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(54) Title: HUMAN DNA SEQUENCES

(57) Abstract: Novel human cDNA sequence of a clones, the encoded protein sequence of a clones, antibodies and variants thereof, are provided. The disclosed sequence of a clones find application in a number of ways, including use in profiling assays. In this regard, various assemblages of nucleic acids or proteins are provided that are useful in providing large arrays of human material for implementing large-scale screening strategies. The disclosed sequence of a clones may also be used in formulating medicaments, treating various disorders and in certain diagnostic applications.

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HUMAN DNA SEQUENCES

Background of the Invention

Current methods for testing pharmacological substances rely on a three-stage testing approach to drug development. First, candidate compounds are typically screened in some sort of *in vitro* system, like inhibition of cancer cell growth. Candidates are then tested in an animal model, as a first approximation of systemic effects, including efficacy and toxicity. Compounds that still show promise after these initial *in vivo* screens, finally are tested in humans. Again, human testing typically occurs in three phases: toxicity; preliminary efficacy; and efficacy. The entire process can take more than a decade and cost hundreds of millions of dollars. Aside from the monetary costs and protracted time scale, moreover, current testing regimes waste the lives of countless laboratory animals and needlessly endanger the lives of human subjects.

A need exists, therefore, for more sophisticated drug screening techniques that can be done rapidly *in vitro*. These screening techniques ideally will be reflective of systemic and/or organ-specific responses, so that they provide a reliable indicator of action in a human body. Current techniques, however, tend to utilize only a single or limited number of markers, thus answering only very simple questions that are of questionable medical import. For example, a typical *in vitro* assay may ask whether a lead compound binds a particular receptor, which has been implicated in a certain disorder. It is presumed that such binding is indicative of therapeutic usefulness, but it does not even purport to address systemic effects.

Not only are screening techniques for efficacy inadequate, the available toxicity screens likewise are inadequate. Toxicity, on a first level, is usually measured by animal testing. Aside from the complications related to *in vivo* versus *in vitro* testing, such screens are insufficient because of differences in metabolism, uptake, etc., relative to humans. Thus, improved methods would be not only be *in vitro*-based, they would also be more "human."

With the increasing miniaturization of screening assays and the growing availability of targets for pharmaceutical intervention, there is increasing interest in developing arrays containing large numbers of these targets that can be assayed simultaneously. If such an

array contains a large enough population of targets, it can be used to essentially mimic the systemic response. In other words, the array becomes an *in vitro* surrogate for the human body. The more refined the array, the more accurate the predictive capability. In theory, an array could be constructed that can detect all of the known human expression products simultaneously, thereby, providing a very reliable indicator of the human response to a given compound. These arrays offer advantages over the present *in vitro* screening systems in that they can assay large numbers of responses simultaneously. They are superior to animal testing because they are more "human" and, thus, more predictive of human responses.

In order to construct such arrays, however, the field is in need of further human targets. Advantageously, such targets will be provided with additional physiologically relevant information, such as whether the target is expressed in a particular tissue and whether it is related to a known functional class of targets. In this way, the artisan can focus as needed, for example, on tissue-specific effects or target class-specific effects, thereby providing information useful in evaluating efficacy and/or toxicity.

In addition to a need for pharmacological screening targets, there is a need for further pharmacological substances. These substances can be used in the formulation of medicinal compositions and in treating a wide variety of disorders.

The present invention responds to the aforementioned and other needs in the field by providing a population of novel targets useful, *inter alia*, in the profiling and medicinal contexts described above.

Summary of the Invention

It is an object of the invention, therefore, to provide a set of human cDNA clones. Further to this object, the invention provides sequences of human cDNA clones that were isolated from libraries generated from different human tissues.

It is another object of the invention to provide assemblages of targets useful in profiling matrices for screening pharmacological test compounds. According to this object, assemblages comprising different populations of human nucleic acids, proteins and antibodies are provided. In different embodiments, cDNA library-specific assemblages and target-family-specific targets are provided.

It is a further object of the invention to provide a database of human nucleotide and protein sequences. Further to this object, novel human nucleotide and protein sequences are provided in electronic form. In one embodiment, one or more of these sequences is provided in a searchable database.

It is still another object of the invention to provide biologically active target molecules useful in treating or detecting human disorders. Further to this object, the invention provides nucleic acid and protein molecules that have the capacity to affect disease etiology or symptoms or correlate with known disease states. Also further to this object, a database is provided which comprises the disclosed molecules in electronic form.

It is still a further object of the invention to provide polypeptides encoded by the human cDNA clones disclosed herein. Further to this object, the invention provides antibodies and fragments thereof that are capable of binding to a specific portion of these polypeptides.

It is yet another object of the invention to provide pharmaceutical compositions which comprise an effective amount of a pharmaceutical agent, wherein the pharmaceutical agent is selected from the group consisting of one or more polypeptides contemplated by the invention, variants or functional derivatives thereof, and antibodies thereto; and a physiologically acceptable carrier or excipient.

It is still another object of the invention to provide expression vectors comprising one or more human cDNA clones disclosed herein or fragments thereof; and optionally a promoter operably linked to the cDNA clone or fragment thereof. Further to this object, the invention provides methodology for recombinantly producing a desired peptide, comprising expressing in a host cell a peptide encoded by a human cDNA clone disclosed herein.

Detailed Description

The invention results from a need in the art for new human nucleic acids and proteins. This need arises in several contexts. First, there is a need to identify targets for therapeutic intervention. Second, there is a need to identify molecules that may be adversely affected in a therapeutic context, thereby resulting in toxicity. Knowledge of these molecules will aid in

the design of new medicaments with enhanced efficacy and decreased toxicity. Finally, the need encompasses human nucleic acids and proteins that have medicinal applicability in their own right.

In view of these needs, the present inventors set out to isolate and sequence human cDNAs from tissue-specific libraries. In this way, they represent subsets of molecules likely to be targets for therapeutic intervention or for avoiding toxicity. In addition, the inventors divided the molecules into various sub-categories, based on suspected functionality, structural similarity etc, which are of interest from a pharmacological perspective. These molecules are disclosed in provisional application serial nos. 60/149,499 and 60/156,503, filed August 18, 1999, and September 28, 1999, respectively, both of which are hereby incorporated by reference in their entirety.

GENERAL DESCRIPTION OF THE INVENTIVE MOLECULES

The present invention provides novel polynucleotide molecules that, in some instances, have similarities with known molecules. The inventive DNAs were cloned from five different human cDNA libraries. In addition to these DNA molecules, the invention provides their protein translations and antibodies derived from them. The inventive DNA and protein sequences are shown individually, below. The inventive nucleic acids also include the complements of these DNA sequences, as well as their RNA counterparts. Methods of producing the molecules also are provided. Further, the invention provides methods for detecting all or part of the molecules and of detecting polynucleotides encoding all or part of the molecules.

The inventive molecules derive from five cDNA libraries: human fetal brain; human fetal kidney; human mammary carcinoma; human testis; and human uterus. For convenience, each sequence bears a designation that indicates from which library it is derived. In particular, these designations are: "hfpbr" for human fetal brain; "hfkf" for human fetal kidney; "hmcf" for human mammary carcinoma; "htes" for human testis; and "hute" for human uterus. The individual libraries were constructed and screened as described below in the examples.

The protein and DNA molecules of the invention are variously described herein as "target" molecules or "inventive" molecules. The sequences and other information pertinent to the nucleic acid and protein molecules of the invention are shown, below.

Interpreting the data disclosed with the Table and cDNA sequences, below:

The table and data below provide the coding sequences of the inventive cDNAs as well as the protein sequences and other useful information, as set out below.

Grouping

The clones were assigned to the following fourteen functional and/or tissue-derived groups:

1. Cell Cycle
2. Cell Structure and Motility
3. Differentiation/Development
4. Intracellular Transport and Trafficking
5. Metabolism
6. Nucleic Acid Management
7. Signal Transduction
8. Transmembrane Protein
9. Transcription Factors
10. Brain derived
11. Kidney derived
12. Mammary Carcinoma derived
13. Testes derived
14. Uterus derived

Description of Clone Files

The individual clone files are structured in the same pattern. The Sections are separated by paragraphs.

1. Clone Name

The clone names are deciphered with reference to the following example:

DKFZphfkd2_24e23, wherein the code represents:

- producer of library ("DKFZ") (for convenience, this reference may be eliminated)
- a "p" for "plasmid cDNA library" (for convenience, this reference may be eliminated)
- library name (e.g. hfbr = human fetal brain; hfkd = human fetal kidney; hmc = human mammary carcinoma; htes = human testes; hute = human uterus)
- an underscore ("_") to separate library information from plate information
- plate number (e.g. "16")
- plate coordinates (letter first; e.g. "f14")

2. Group

3. Introduction

short review of the similarities, function of the protein and possible applications

4. Short Information

specifications about the cDNA (who sequenced, completeness of the cDNA, similarity, who sequenced, chromosomal localisation, length of cDNA, localisation of poly A tail and polyadenylation signal)

5. cDNA-Sequence

6. BLASTn Results

search results of blasting the cDNA sequence against all public databases

7. Medline Entries

information about genes/proteins similar to the novel cDNA (if available)

8. Putative Encoded Protein Information

specifications about the encoded protein (ORF: length and localisation of the reading frame)

9. Protein Sequence

10. BLASTp Results

search results of blasting the protein sequence against all public databases

11. Pedant Information

output of fully automated annotation: summarises peptide information, homologies, patterns as follows:

[Length]

- length of the protein = number of amino acid residues

[MW]

- molecular weight of the protein

[pI]

- isoelectric point

[HOMOL]

- shows protein with closest similarity to the cDNA-encoded protein

[FUNCAT]

- functional information according to a catalogue developed by Munich

Information center for Protein Sequences (MIPS)

[BLOCKS]

- Blocks are multiply aligned ungapped segments corresponding to the most highly conserved regions of proteins. The blocks for the Blocks Database are made automatically by looking for the most highly conserved regions in groups of proteins documented in the Prosite Database. The Prosite pattern for a protein group is not used in any way to make the Blocks Database and the pattern may or may not be contained in one of the blocks representing a group. These blocks are then calibrated against the SWISS-PROT database to obtain a measure of the chance distribution of matches. It is these calibrated blocks that make up the Blocks Database. The WWW versions of the Prosite and SWISS-PROT Databases that are used on this server are located at the ExPASy World Wide Web (WWW) Molecular Biology Server of the Geneva University Hospital and the University of Geneva. World Wide Web URL http://blocks.fhcrc.org/blocks/about_blocks.html/ is the entry point to the database.

- here Blocks segments found in the analysed protein sequences are displayed

[SCOP]

Nearly all proteins have structural similarities with other proteins and, in some of these cases, share a common evolutionary origin. The scop database provides a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known, including all entries in Brookhaven National Laboratory's Protein Data Bank (PDB). It is available as a set of tightly linked hypertext documents which make the large database comprehensible and accessible. In addition, the hypertext pages offer a panoply of representations of proteins, including links to PDB entries, sequences, references, images and interactive display systems. World Wide Web URL <http://scop.mrc-lmb.cam.ac.uk/scop/> is the

entry point to the database. Existing automatic sequence and structure comparison tools cannot identify all structural and evolutionary relationships between proteins. The scop classification of proteins has been constructed manually by visual inspection and comparison of structures, but with the assistance of tools to make the task manageable and help provide generality. Proteins are classified to reflect both structural and evolutionary relatedness. Many levels exist in the hierarchy, but the principal levels are family, superfamily and fold. The exact position of boundaries between these levels are to some degree subjective. Scop evolutionary classification is generally conservative: where any doubt about relatedness exists, we made new divisions at the family and superfamily levels.

- - here SCOPE segments found in the analysed protein sequences are displayed

[EC]

ENZYME is a repository of information relative to the nomenclature of enzymes. It is primarily based on the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) and it describes each type of characterized enzyme for which an EC (Enzyme Commission) number has been provided. World Wide Web URL <http://www.expasy.ch/enzyme/> is the entry point to the database.

- here EC-number and name of enzymes with similarity to the analysed protein sequences are displayed

[PIRKW]

- functional information according to the Protein Information Resource (PIR) database catalogue developed by Munich Information Center for Protein Sequences (MIPS), the National Biomedical Research Foundation (NBRF) and the International Protein Information Database in Japan (JIPID).

[SUPFAM]

- information according to the Protein Information Resource (PIR) database catalogue of protein superfamilies developed by Munich Information Center for Protein Sequences (MIPS), the National Biomedical Research Foundation (NBRF) and the International Protein Information Database in Japan (JIPID).

[PROSITE]

please refer to 12. PROSITE Motifs

[PFAM]

please refer to 13. PFAM Motifs

[KW]

- overall 2dimensional folding information
- 3D indicates that the proteins is similar to a protein of which a 3 dimensional structure is known
- overall structural information

[]

The last PEDANT-block depicts information about the folding structure of the protein generated by PREDATOR. PREDATOR is a secondary structure prediction program. It takes as input a single protein sequence to be predicted and can optimally use a set of unaligned sequences as additional information to predict the query sequence. The mean prediction accuracy of PREDATOR is 68% for a single sequence and 75% for a set of related sequences. PREDATOR does not use multiple sequence alignment. Instead, it relies on careful pairwise local alignments of the sequences in the set with the query sequence to be predicted.

World Wide Web URL http://www.embl-heidelberg.de/argos/predator/predator_info.html is the entry point to the database.

- H = helix, E = extended or sheet, _ = coil, T = transmembrane, B = beta
- x indicates a low-complexity region with repeat-like structure which is omitted in all BLAST searches

12. PROSITE Motifs

PROSITE is a database of protein families and domains. It consists of biologically significant sites, patterns and profiles that help to reliably identify to which known protein family (if any) a new sequence belongs. World Wide Web URL <http://www.expasy.ch/prosite/> is the entry point to the database. A description of the prosite consensus patterns is also provided, below.

13. PFAM Motifs

PFAM (protein families) is a large collection of multiple sequence alignments and hidden

Markov models covering many common protein domains. World Wide Web URL <http://www.sanger.ac.uk/Pfam/> is the entry point to the database.

Deposit of Clones

Clones were deposited as a pool with the American Type Culture Collection under accession number _____, from which each clone comprising a particular polynucleotide is obtainable. Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit.

The clones may also be obtained from the Resource Center of the German Human Genome Project (Heubner Weg 6, 14059 Berlin, GERMANY). The Resource Center library numbers are slightly different than those presented here, but may be readily obtained by the following key or with the assistance of Resource Center personnel.

The library name becomes a number: brain (hfbr2) becomes 564; kidney (hfkd2) becomes 566; mammary carcinoma (hmcfl) becomes 727; testis (htes3) becomes 434; and uterus (hute1) becomes 586. Next, the plate number is converted to two digits (e.g., "2" becomes "02") and is moved behind the plate coordinate, and the underscore is dropped. The following examples are helpful:

<u>Listed Number</u>	<u>Resource Center Number</u>
DKFZphfbr2_16f21	DKFZp564F2116
DKFZphfkd2_1j9	DKFZp566J091
DKFZphmcf1_1c23	DKFZp727C231
DKFZphtes3_14g5	DKFZp434G0514
DKFZphute1_17k7	DKFZp586K0717

The libraries were constructed using two commercially available vectors. The brain (hfbr2 designations) and kidney (hfkd2 designations) libraries utilize pAMP 1 from Life Technologies and are maintained in XL-2Blue (Stratagene); the uterus (hute1), testes (htes3) and mammary carcinoma (hmcfl) libraries are constructed in pSPORT1, also from Life Technologies; and are maintained in DH10B (Life Technologies). In addition to the following techniques, consultation with the commercial literature available on these clones will make evident all of the housekeeping techniques needed to propagate and isolate the individual constructs. All inserts may be excised with a NotI/SalI digestion. Alternatively, universal primers, flanking the cloning region, may be used to amplify the inserts using PCR methods.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. Methods of probe design are presented below.

Oligonucleotide probes may be labeled with γ - ^{32}P ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other, non-radioactive labeling techniques can also be used. Unincorporated label typically is removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe can be quantified by measurement in a scintillation counter. Preferably, specific activity of the resulting probe generally should be approximately 4×10^6 dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 50 - 100 $\mu\text{g/ml}$ (for XL-2Blue strains 25 $\mu\text{g/ml}$ tetracycline should also be used). The culture should preferably be grown to saturation at 37°C ., and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 $\mu\text{g/ml}$ (for XL-2Blue strains 25 $\mu\text{g/ml}$ tetracycline should also be used) and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C . Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them. The filter is then preferably incubated at 65°C . for 1 hour with gentle agitation in 6 x SSC (20 x stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 $\mu\text{g/ml}$ of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1×10^6 dpm/mL. The filter is then preferably incubated at 65°C . with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2 x SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2 x SSC/0.1% SDS at room

temperature with gentle shaking for 15 minutes. A third wash with 0.1 x SSC/0.5% SDS at 65°C. for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Alternatively, clones may be grown as described above, and PCR used to isolate the insert DNAs. Methods of PCR are described below and are otherwise well known.

ERROR SCREENING

The DNA sequences found herein derive from individual clones, which are publicly available, as noted above. Thus, the skilled artisan will recognize that any specific sequence disclosed herein readily can be screened for errors by resequencing a particular fragment, in both directions (*i.e.*, by sequencing both strands). Alternatively, error screening can be performed by amplifying and/or cloning any of the inventive DNAs, using for example RT-PCR, and sequencing the resulting amplified product. In the event that there is a sequencing error, reference should be made to the deposited clone as the correct sequence.

USES AND BIOLOGICAL ACTIVITIES OF THE INVENTIVE MOLECULES

The inventive molecules and their derivatives are susceptible to a wide variety of uses, based on functional and/or structural properties. The skilled worker will appreciate, based on the biological activities detailed below, and discussed with regard to the individual sequences disclosed below, that the inventive molecules will find usefulness in numerous therapeutic and diagnostic applications.

The DNA molecules, especially the potassium salts thereof, can be used as fertilizer supplements due to their high nitrogen and phosphorus contents. Since the DNAs are of defined length, they are also useful in gel electrophoresis as molecular weight markers. Due to their similarity with known molecules, certain of the DNA molecules and their variants and derivatives may be used in any number of different diagnostic procedures and therapeutic applications. They may also be used to make the encoded proteins.

The proteins themselves have many possible uses. They may be used as a nutritional supplement for humans, animals and even for laboratory use as, for example, medium for bacterial cultures. Moreover, since the proteins are of defined, known sizes, they may be used as molecular weight markers for gel electrophoresis and gel filtration. Because they are of defined sequences, they also have use in microsequencing and protein fingerprinting applications.

Expression Profiling Applications

Given their known tissue expression and functional associations, assemblages of the inventive proteins (or corresponding antibodies) and nucleic acids are particularly suited to expression profiling applications. Expression profiling generally entails constructing an array of indicators that signal the presence of a particular RNA or protein expression product. Such arrays can be used to evaluate, for example, pharmacological effectiveness and toxicity. In particular, expression profiles from such arrays can be generated from cells treated with known compounds, having known properties, and these profiles can be compared to profiles of unknowns to evaluate similarities and differences, which can be correlated with efficacy or toxicity.

Additional uses of profiling include diagnosis, tracking development, and ascertaining signaling and metabolic pathways. For examples of references describing profiling and its uses, see Farr *et al.*, U.S. Patent 5,811,231 (1998); Seilhamer *et al.*, U.S. Patent 5,840,484 (1998); Rine *et al.*, U.S. Patent No. 5,777,888 (1998); WO 97/27317; WO 99/05323; WO 99/09218; and WO 99/14369. For a device for implementing such techniques, see Lipshutz *et al.*, U.S. Patent No. 5,856,174 (1999) and Anderson *et al.*, U.S. Patent No. 5,922,591 (1999).

In one embodiment, a subset of the inventive DNAs will be arrayed on a substrate, like a gene chip, a filter or a 96-well plate. Test samples containing cells are maintained in the presence of a label capable of incorporation into nascent mRNA. Samples are treated with test and control compounds, which will induce mRNA expression in the sample, resulting in incorporation of label. Whole mRNA is isolated and applied to the array such that it hybridizes with the DNAs contained therein. After washing, the amount of hybridization is quantified and a profile is generated. These steps are repeated with various control and test compounds, thereby generating a library of profiles, which can be used to ascertain the relationships relevant to pharmacological efficacy or toxicity.

The matrices used in such profiling, however, need not be limited to those utilizing DNAs. Rather, other nucleic acids, like RNAs and protein nucleic acids (PNAs), as well as the inventive proteins and antibodies corresponding to the inventive proteins may also be employed. Hence, for example, antibodies could form the array and the samples could be treated in order to label nascent proteins. Whole proteins then would be isolated and applied to the antibody matrix. Developing the resulting signal would result in a protein expression profile, which is useful in essentially the same manner as the nucleic acid profile. A protein matrix could be used, for example, in evaluating antibody responses to pharmaceutical agents in order to eliminate possible cross-reactivity.

Moreover, where nucleic acids are used in the matrix, it is often beneficial to use variants (as defined below) of the molecules described herein. This can be used to account for genetic variations that are of little or no consequence to the function of the resultant gene product. Hence, they can account for wobble or conservative amino acid variations that do not perturb function, like variations in some of the protein motifs elucidated below. Thus, each position in the matrix can employ multiple nucleic acid probes that account for a series of variants.

Expression profiling may also be done, in another embodiment, using two-dimensional protein gels in which the inventive proteins are detected. The resultant profiles can be used in the same way as described.

Matrices useful for profiling may be constructed based on different criteria. Of course, the more relevant profiles will take into account expression of most human genes, preferably all of them. In certain situations, however, it is advantageous to look at a smaller subset. For example, if one were concerned about fetal neural toxicity, a fetal brain-specific matrix might be chosen. On the other hand, if one were interested in targeting mammary carcinoma tissue, a corresponding matrix could be used. Thus, matrices may be constructed using all of the sequences available from a tissue-specific library.

* * *

The following discussion relates to some of the various functional and structural groupings that would be of interest to the artisan wishing to construct profiling matrices. Of course, the artisan will also recognized that these functional descriptions may find additional applicability in the therapeutic and diagnostic applications discussed below.

Cell Cycle

A proliferating cell must coordinate replication and chromosomal separation to ensure that the genome is replicated completely, and that a single copy is correctly inherited by each daughter cell. The cell cycle is the coordinated series of events that achieves these aims. Many of the key events are initiated by a family of conserved Serine/threonine protein kinases, the cyclin-dependent kinases (CDKs), that are activated by the cyclin family of proteins (cyclins A-H). In turn, the cyclin-CDK complexes are modulated by other protein kinases or phosphatases, and by binding specific inhibitor proteins. The enormous variety of ways in which CDK activity can be regulated allows the cell to respond to internal signals generated by preceding events in the cell cycle and to external growth signals.

The somatic cell cycle is divided into four phases: DNA replication (S phase) and chromosome separation (M phase) are separated by gap phases (G1 and G2). At specific control points the decision to begin the next stage (DNA synthesis or mitosis) is carefully regulated.

Cdc2, the primary kinase, is especially required for the G1-S transition and S phase. Cdc4 and Cdc6 are involved at the restriction point, where the cell can decide to proliferate or arrest (G1 \leftrightarrow G0) and Cdc7 is a CDK activating kinase (CAK) as well as a subunit of TFIIH.

The Cyclin-CDK complexes are regulated in various ways. One is through phosphorylation by CDK activating kinases (CAK), like the Y15 kinase (Wee1) and dephosphorylation by CDK associated phosphatases (CAP), like Cdc25A a member of the Cdc25 family (Cdc25A, B and C).

An other way of regulation occurs through two classes of CDK inhibitors (CKI), the INK4 proteins p15, p16, p18, and p19, who negatively regulates the cyclin D CDK complexes and second the p21 family with p21, p27, and p57.

The cell cycle is also regulated through ubiquitin-mediated proteolysis involving the destruction of both cyclins and CDK inhibitors by the 26S proteasome, that requires an ubiquitin conjugating enzyme (UBC) and an ubiquitin ligase. The instability is conferred by PEST regions (cyclin D and E) or a ten amino acid region in the amino terminus (degradation box) in the A- and B-type cyclins.

All these modifications play an important role for the cellular localization, because only the nuclear CDK-cyclin complexes are functional for cell cycle. During G1 phase of the cell cycle, cyclins A, E and D are synthesized and bind to their cyclin-dependent kinase (CDK) partners. CDK complexes containing cyclins A, E and D1 are then imported into and concentrated within nuclei. Cdk6- cyclin D3 has been localized to both cytoplasmic and nuclear compartments, although only the nuclear complex is active. As cells enter S phase, cyclin A and cyclin E complexes remain within the nucleus, whereas cyclin D1 relocates to the cytoplasm for proteolysis at the onset of S phase. Like Cdk2-cyclin A, Cdc2-cyclin A is nuclear and remains so until it is degraded during mitosis. By contrast, as a result of ongoing nuclear import and more rapid re-export, cyclin B1, which binds to Cdc2 upon synthesis during S phase, is predominantly cytoplasmic. Cdc2-cyclin B2 is also cytoplasmic, although this might occur through anchoring of the complex to some cytoplasmic constituent. At prophase, phosphorylation of cyclin B1 promotes accumulation of Cdc2-cyclin B1 in the nucleus, whereas cyclin B2 remains in the cytoplasm until nuclear envelope breakdown.

Two crucial regulators of Cdc2-cyclin B-Wee1 and Cdc25C exist and are responsible for the G2 to M control point. Wee1 is a nuclear protein throughout the cell cycle, whereas Cdc25C binds to 14-3-3 proteins during interphase and remains predominantly cytoplasmic. In some systems Cdc25C, like cyclin B1, rushes precipitously into the nucleus just before entry into mitosis.

The 110-kDa retinoblastoma (tumor suppressor) protein (RB), a pRB-family member is an important regulator of cell-cycle progression and differentiation. Like the E2F family (E2F1-5) or DP family (DP1-3) of transcription activators, RB suppresses inappropriate proliferation by arresting cells in G1 by repressing the transcription of genes required for the transition into S phase. Before the cell proceeds into S phase, RB becomes phosphorylated at multiple sites by the cyclin dependent protein kinases (CDKs) and loses its transcriptional repressing activity. Phosphorylation of RB during late G1 phase results in the dissociation of the E2F-RB repressor complex which allows S-phase specific genes to be transcribed. Cyclin E is the evolutionary conserved target for E2F and interacts together with CDC2 in late G1.

For a proliferating cell it is vital that only undamaged DNA is replicated because if DNA damage is substantial, its replication can lead to chromosome loss or rearrangement.

Thus, we find a G1<->S checkpoint in late G1 that requires tumor suppressor p53. A p53-dependent G1 arrest is effected by the cyclin dependent kinase inhibitor p21 through higher expression levels that inhibits almost all cyclin CDK complexes.

The kinase responsible for phosphorylating the unidentified kinetochore component in metaphase may be a member of the MAP kinase family and appears to be the proto oncogene c-MOS, a cytostatic factor (CSF) in meiosis.

Several categories of proteins are coded for by clones of the invention within the overall group of "Cell cycle" and include, among others, the following:

Tumor suppressors (e.g. N33): Tumour-suppressor genes are known to be involved in the control of cell growth and division, interacting with proteins which control the cell cycle. The N33 gene is significantly methylated in tumour cells, a mechanism by which tumor-suppressor genes are inactivated in cancer. The N33 gene has been reported by OMIM (Online Mendelian Inheritance in Man at <http://www.ncbi.nlm.nih.gov/htbin-post/Omim>) to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) prostate cancer suppression (OMIM *601385). Clones in this category include: fbr2_2k14.

C-TAK1 Cdc25c associated protein kinase: Cdc25C is a protein kinase that controls entry into mitosis by dephosphorylation of Cdc2. Cdc25C function is regulated by phosphorylation, too. Serine 216 phosphorylation of Cdc25C mediates the binding of 14-3-3 protein to Cdc25C. C-TAK1 (Cdc twenty-five C associated protein kinase) phosphorylates Cdc25C on serine 216 in vitro. Alterations in the gene coding for the above protein kinase has been reported by OMIM to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with Pancreatic cancer (OMIM *60278). Clones in this category include: tes3_7j3.

Cell structure and motility

One of the major differences between prokaryotes and eukaryotes is the ability of the eukaryotic cell to adopt very different shapes dependent on its function during the differentiation process. Animal cells vary from being round to extended cylindric forms like motoneurons or muscle cells. In humans, more than 100 different cell types can be distinguished, each having a characteristic shape. The form of a cell often is closely related to



its capacity to move. Some completely differentiated cells like fibroblasts can still change their form actively, thereby migrating. Other cell types serve as motor elements - "macroscopically" like muscle cells or "microscopically" like ciliated epithelia. Such tasks are fulfilled by a big class of proteins; on the one hand responsible for maintenance of cell structure and contacting neighbor cells or the intercellular matrix and on the other hand for cell motility. These topics cannot be regarded separately: The motility apparatus e.g. must be fixed in the cytoskeleton. Three different types of filaments can be distinguished: Actin filaments, tubulin filaments and intermediate filaments, each present in almost all types of cells.

Actin filaments (F-actin) are built up of monomers (G-Actin). In muscle cells, actin, myosin, for both of which several paralogous genes are known, as well as many more proteins are constituents of the contractile apparatus.

The "thin" and "thick filaments" in a muscle cell consist mainly of actin and myosin, respectively.

Several different proteins are responsible for the anchoring of the actin filaments in the Z-disks (e.g. alpha-actinin and desmin) or at the end of the myofibers in the cell membrane.

Troponin I, -C, -T and Tropomyosin - associated with actin - confer the Ca^{++} -dependent triggering of contraction.

Length of the sarcomere is controlled by the giant protein titin.

In smooth muscle, there is no troponin. Contraction activity is controlled by phosphorylation / dephosphorylation of myosin by a specialized kinase instead. Contractile fibers are not organized in sarcomeres.

Apart from contributing to muscle contraction, the actomyosin system is responsible for many other motions at cellular level, e.g. the amoeboid movement of pseudopodia or the fission of cells at the end of mitosis by a contractile ring.

Besides this, actin fibers fulfill structural tasks like maintenance of the shape of stereocilia or microvilli. Here, actin filaments are connected by proteins like fimbrin. But not

only specialized structures like the mentioned ones contain actin fibers. There is a network covering the complete cell volume with F-actin as a major constituent. Whereas the actin filaments in the structures mentioned above are relatively stable, this F-actin is highly dynamic. Management of the network structure and turnover is achieved by connecting proteins like alpha-actinin, fimbrin or filin; turnover is regulated by gelsolin, villin, and different capping- and fragmentation-proteins.

Microtubules are built up of alpha-beta tubulin heterodimers. Turnover of filaments is achieved by building-in and releasing of monomers with different time constant rates at both ends. The resulting cycle is called "treadmilling". Thirteen strings of tubulin duplets build up one subfiber, whereas one fiber contains two or three of those. A complete axoneme consists of 9 radial and 2 central fibers. This "9+2" - structure is the basis both of flagella, their basal bodies and centrioles. In flagella, several additional structures like radial elements exist. Nexin connects the fibers and dyneine is the motor ATPase which shifts the fibers relative to each other. Several genetic diseases like the Kartagener syndrome are caused by deficiencies of distinct proteins in cilia.

Besides this, microtubules are abundant in all types of cells. They are part of a delivery system for organelles, e.g. in the golgi apparatus. A further very important system based on microtubules is the mitotic spindle, it is organized by the centrosomes. Besides many other components, the major part of a centrosome are two centrioles which are built up of nine microtubule-triplets. Most remarkably, new centrioles are not synthesized de novo but generated by duplication of old ones.

Cytoplasmic microtubules are associated with many different proteins. Two major classes are known: The MAPs ("microtubule-associated proteins", with molecular masses between 200 and 300 kD) and the much smaller tau-Proteins with a MW between 60 and 70 kD. These proteins regulate the treadmill-process and the interaction with other structures in the cell.

Besides actin and myosin the so-called intermediate filaments constitute a third class of filaments. In contrast to the former two groups, they do not participate in motility, nor are they dynamic structures subject to a vivid turnover. The most important ones are

neurofilaments (in neurons), keratin filaments (mainly in epithelial cells), and vimentin filaments (in many sorts different cell types).

The biological function of both the cytoskeleton as well as contractile apparatus of a cell does not end at the cell membrane. Cells must be embedded in the extracellular matrix, all cells of a muscle must act as one single mechanical unit and epithelia must resist macroscopic mechanical forces. Hence, cell adhesion and the extracellular matrix are closely connected to the cytoskeleton. Vincullin is one of the proteins which serve as an anchor for intracellular fibers (actin). Different types of desmosomes and tight junctions connect neighbor cells with intercellular fibers. On the inside, cytoplasmic plaques connect them to the cytoskeleton. These structures, on the one hand, serve as mechanical elements whereas gap junctions, on the other hand, connect cells metabolically.

The extracellular matrix consists of a network of proteins, glycoproteins and polysaccharides. Different proteins are present in relation to different mechanical demands: Elastin is found in tissues with high elasticity (lungs, heart) whereas collagen, a more hard-wearing protein, is found in tendons and ligaments. Fibronectin is an extracellular protein highly important for cell adhesion.

Reference: Murray J *et al* (1992): Cell Motil Cytoskeleton 22: 211-223.

Within the overall group of Cell Structure and Motility several categories of proteins are coded for by clones of the invention:

Collagen alpha chain proteins: Proteins with the typical (xxG)_n repeat of collagen proteins and Pfam von Willebrand factor type A domain(s) suggest they are collagen alpha chains. These proteins can find application in modulation of connective tissue, bone and cartilage development and maintainance. OMIN reports collagen alpha chains have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Osteogenesis imperfecta, type I (OMIN #166200); 2) Osteogenesis imperfecta congenita (OMIN #166210); 3) Alport Syndrome, X-linked (OMIN #301050); 4) Thrombastenia of Glanzmann and Naegeli (OMIN *273800); 5) Ehlers-Danlos Syndrome, Type VII (OMIN #130060); 6) Marfan Syndrome (OMIN #154700); 7) Alport Syndrome, Autosomal Recessive (OMIN #203780); 8) Alpha-2-Deficient Collagen Disease (OMIN 203760); 9) Goodpasture Syndrome (Omin 233450); 10) Osteogenesis Imperfecta,

progressively deforming, with normal sclerae (OMIN #259420); 11)) Ehlers-Danlos Syndrome, Type VII Autosomal Recessive (OMIN *225410); and 12)) Osteogenesis imperfecta, Type IV (OMIN #166220). OMIN reports that von Willebrand factor type A domains have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases:: 1) Hemophilia A (OMIN *306700); 2) Von Willebrand Disease (OMIN *193400); 3) Giant Platelet Syndrome (OMIN *231200); 4) Thrombastenia of Glanzmann and Naegeli (OMIN *273800); 5) Congenital Thrombotic Diseases due to protein C deficiency (OMIN #176860); 6) Polycystic Kidney Disease 1 (OMIN *601313); 7) Nephrogenic Diabetes Insipidus (OMIN *304800); 8) Factor V Deficiency (OMIN *227400); and 9) Dentatorubral-Pallidoluyasian Atrophy (Omin *125370). Clones in this category include: fbr2_2b5.

Radial spokehead protein: Radial spokehead proteins, e.g., Chlamydomonas reinhardtii radial spokehead protein of flagella or axoneme and the Strongylocentrotus purpuratus sea urchin spermatozoa protein p63, and human proteins with similarity thereto are important for the maintenance of a planar form of sperm flagellar beating. The human protein(s) can find application in modulating the structure of the human spermatozoa radial spoke head and modulation of sperm motility in men (e.g., in sterility). Clones in this category include: tes3_15i5.

Ankyrins: Ankyrins are peripheral membrane proteins which interconnect integral proteins with the spectrin-based membrane skeleton. Thus these proteins are involved in coupling of cyto skeleton and cell membrane. OMIN reports that Ankyrins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Hereditary Spherocytosis (OMIN *182900); 2) Hemolytic Poikilocytic Anemia due to reduced ankyrin binding sites (OMIN 141700); 3) Atypical Elliptocytosis (OMIN 225450); 4) Autosomal recessive spherocystosis (OMIN #270970); 5) Werner Syndrome (OMIN *277700); and 6) Rhesus-unlinked type Elliptocytosis (OMIN #130600). Clones in this category include: tes3_18i7.

FGD1-related F-actin binding protein (Farbin/FGD1): FGD1-related F-actin-binding protein (Farbin/FGD1) is a novel F-actin-binding protein. The gene locus fgd1 seems to be responsible for faciogenital dysplasia or Aarskog-Scott syndrome. (OMIN 305400). Frabin binds F-actin and shows F-actin-cross-linking activity. Overexpression of frabin in Swiss 3T3 cells and COS7 cells induces cell shape change and c-Jun N-terminal kinase activation, as

described for FGD1. Because FGD1 has been shown to serve as a GDP/GTP exchange protein for Cdc42 small G protein, it is likely that frabin is a direct linker between Cdc42 and the actin cytoskeleton. Cdc42p is an esin yeast, Cdc42p transduces signals to the actin cytoskeleton to initiate and maintain polarized growth and to mitogen-activated protein morphogenesis. In mammalian cells, Cdc42p regulates a variety of actin-dependent events and induces the JNK/SAPK protein kinase cascade, which leads to the activation of transcription factors within the nucleus. Clones in this category include: tes3_72k15.

Paramyosins: Paramyosin is a major structural component of thick filaments and invertebrate muscle. Paramyosins are promising antigens for immunization against several parasites, such as *Schistosoma mansoni*. Clones in this category include: tes3_7b22.

Tuftelin: Tuftelin/enamelin are matrix proteins of the teeth. As other proteins involved in calcification, these proteins are also expressed in the uterus matrix. The new protein can find application in modulation of tissue-calcification, especially the uterus. As reported by OMIN, tuftelin has been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with amelogenesis imperfecta (OMIN *600087). Clones in this category include: ute1_19g22.

Cell Adhesion Regulator (CAR1): CAR1 is involved in the regulation of cell-cell adhesion. OMIN reports the association (as potentially diagnostic, therapeutic, causative, and/or related, etc...) of CAR1 with tumor suppression by the reduction of tumor invasion (OMIN *116935). Clones in this category include: ute1_24j6.

Differentiation/Development

Almost every multicellular organism originates from meiotic cell divisions and the recombination of a paternal and a maternal set of chromosomes. After fertilization of the egg, all cells of a body originate from this one cell. Thus the cells of the developing body are initially genetically alike. But phenotypically they become very different. They are specialized to a certain cell type and arranged in an organized pattern to a certain type of tissue and the whole structure has the well-defined shape of an organ. All these features are determined by the DNA sequence of the genome, which is reproduced in every cell. Each cell acts on the genetic instructions given to a certain time and at a certain place of development and plays its individual part in the multicellular organism. Cell differentiation may be divided into three general steps: cell cycle exit, apoptosis protection and tissue specific gene

expression. These processes are coordinated to provide the final and unique tissue characteristics.

An animal cell that has achieved a certain level of development is said to be determined. This differentiation of a cell may be irreversible and in that case the cell may be renewed only by simple duplication. Other cells are renewed by means of stem cells which are immortal (e.g. stem cells of the bone marrow, epidermal stem cells). The genetic control of development is extensively studied in non-vertebrates and vertebrates. The classical animal model is the fruit fly *Drosophila* and the modern model is the transgenic mouse. Animal transgenesis has proven to be useful for physiological as well as physiopathological studies. Besides the approach based on the random integration of a DNA construct in the mouse genome, gene targeting can be achieved using totipotent embryonic stem cells for targeted transgenesis. Transgenic mice are then derived from the embryonic stem cells. This allows the introduction of null mutations in the genome (so-called knock-out) or the control of the transgene expression by the endogenous regulatory sequence of the gene of interest (so-called knock-in). Mice can be created that express wild-type genes, mutant genes, marker genes or cell lethal genes in a tissue specific manner. These animal models allow to follow changes in tissue and organ development and lead to a better understanding of the cellular function of many genes or to the generation of animal models for human diseases. Fundamental problems in immunology, onset and development of cancer, regulation in fatty acid metabolism, aspects of cardiovascular function, control of the central nervous system development, analysis of reproductive development and function are only some examples of research interests.

The final stage of cell differentiation is growth arrest. In animal tissues with rapid cell turnover terminally differentiated cells undergo programmed cell death. The cells have the ability to kill themselves by activating an intrinsic cell suicide program when they are no longer needed or have become seriously damaged. The execution of this program is termed apoptosis. Apoptosis is of importance for development and homeostasis of animals. The key components of this program have been conserved in evolution from worms (*C. elegans*) to insects (*Drosophila*) to humans. The roles of apoptosis include the sculpting of structures during development, deletion of unneeded cells and tissues, regulation of growth and cell number, and the elimination of abnormal and potentially dangerous cells. In this way

apoptosis provides "quality control mechanism" that limits the accumulation of harmful cells, such as virus-infected cells and tumor cells. On the other hand inappropriate apoptosis is associated with a wide variety of diseases, including AIDS, neuro-degenerative disorders and ischemic stroke. Because it is now clear that apoptosis is a result of an active, gene-directed process, it should be eventually possible to manipulate this form of cell death by developing drugs that interact with its recently identified mechanisms of action. Inducers of cell differentiation, cell cycle arrest and apoptosis might be the novel molecular targets for new anticancer agents in addition to the signaling pathways for growth factors and cytokines.

Proteins, factors, receptors and genes of importance in apoptosis:

Proteases:

- Calpain, an intracellular cysteine protease, exact role unknown.
- Caspase-1 to Caspase-11, a family of proteases synthesized as an inactive proenzyme. Targets of the activated enzymes include: poly(ADP-ribose) polymerase, DNA-dependent protein kinase, U1 ribonucleoprotein, nuclear laminins and cytoskeleton components (actin).
- Granzyme B, a serine protease released by cytotoxic T-cells.

Receptors:

- CD 95 (synonyms: Fas, APO-1), a receptor protein of the TNF-receptor family which includes TNF-R1 and TNF-R2 with the common characteristic of a 70 amino acid cytoplasmic domain.
- FADD (synonym: MORT-1), a cytoplasmic protein
- DR-3 (synonym: APO-3) a member of the TNF-receptor-family
- DR-4 and DR-5

Genes:

- ced-3, ced-4 and ced-9 encode the general apoptotic and antiapoptotic program in *Caenorhabditis elegans*. Apaf-3 is the mammalian homologue of ced-3.

- Bcl-2 / Bcl-xL / Bax / Bcl-xS / Bak: a large gene family that can either inhibit or promote apoptosis.

- Cytokine response modifier A, a cowpox virus gene whose gene product inhibits caspases.

Others:

- Caspase-activated DNase (CAD) and its inhibitor (ICAD), causes DNA fragmentation in the nucleus

- Ceramide, a complex lipid that acts as a second messenger.

- c-Jun N-terminal kinase (JNK) is a proline-directed kinase

- p53 protein, is essential for the induction of apoptosis as a response to chromosomal damage.

- RAIDD, a death signal-transducing protein.

- Receptor interacting protein (RIP) is an accessory protein with a death domain and a serine/threonine kinase activity.

- Sphingomyelinase, an enzyme that hydrolyzes the complex lipid sphingomyelin to ceramide.

- Tumor necrosis factor (TNF) is a type -II membrane protein

- TNF-receptor associated factor (TRAF2), is an accessory protein that can bind to both TNF-R1 and TNF-R2.

Within the overall group of Differentiation/Development, several categories of proteins are coded for by clones of the invention:

Interleukins (e.g. Interleukin-7): Interleukin precursors related to interleukin-7, for example, are expected to act as new growth factors for human B lineage cells. Additionally,

these proteins should induce the gene rearrangement of the T-cell receptor repertoire, leading to thymocyte commitment, and subsequently induce both cytotoxic T-cell- and lymphocyte-activated killer cells. These interleukins could find clinical application in a variety of conditions of hematolymphopoietic failure and different tumours, because of its recruitment of B cell lineage cells, cytotoxic T-cell- and lymphocyte-activated killer cells. (OMIN *146660). Clones in this category include: tes3_35e21.

Testis-specific Y-encoded proteins: The TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. Proteins of the TSPY-SET-NAP1L1 family represent proteins closely related to TSPY. These proteins seem to be involved in early spermatogenesis. Clones in this category include: fbr2_2d15.

Intracellular transport and trafficking

Eukaryotic cells rely for their viability on the partitioning of many basic cellular processes into membrane-bounded organelles. These are the nucleus, endoplasmic reticulum (ER), Golgi apparatus, endosomes, lysosomal compartments, mitochondria and peroxisomes. Most molecules destined for the lysosome, cell surface and outside the cell are routed through the ER and Golgi, which together with the vesicular intermediates between them, comprise the secretory pathway (Palade 1975). In the ER and Golgi compartments proteins are sorted, modified and often assembled into complexes *en route* to their final destination. Incorrectly assembled proteins are retained in the ER until they fold correctly or are targeted for degradation. Additional proteins are translocated into and function within the luminal spaces of organelles or are secreted. Thus a large proportion of proteins synthesized require targeting to membranes either for insertion into or transport across them. A major purpose of this is growth. The secretory pathway is dependent on an intact cytoskeleton and also closely linked to general metabolism by affecting ribosome biogenesis (Mizuta and Warner, 1994). A huge number of proteins is required for targeting, translocation and sorting of newly synthesized proteins.

The first step in sorting is the recognition of cis-acting targeting or signal sequences that organelle-targeted proteins contain. This is carried out by cytosolic targeting factors and/or receptors on the membrane to which the protein is targeted. In some cases the primary

sequences are extremely degenerate, with only the overall character being conserved (hydrophobicity for an ER signal sequence, helical amphiphilicity for mitochondrial targeting sequence (Kaiser *et al.*, 1987; Lemire *et al.*, 1989). Following the targeting step, proteins are either inserted into or transported across the membrane (translocated) through a proteinaceous apparatus (termed the translocon). The translocon include or recruit motors to drive the translocation process in the correct direction (Schatz and Dobberstein, 1996).

Defined intracellular protein transport steps:

- ER
 - targeting to the ER
 - translocation into the lumen of the ER, and, depending on the presence of certain signals in the peptide sequence transport through the golgi complex
- Mitochondria
 - targeting
 - translocation
- Peroxisomes
- The general secretory pathway
 - protein modification, assembly and quality control in the ER
 - vesicle-mediated trafficking
 - vesicle docking and fusion
 - transport through the golgi apparatus and sorting at the trans-golgi
 - transport to the cell surface
 - transport routes to the lysosome
- Endocytosis
- Specialized protein transport routes
- Protein export from the cytoplasm

References: Palade, G (1975) Science 189:347-358; Mizuta et al. (1994) Mol Cell Biol 14: 2493-2502; Kaiser *et al.* (1987) Science 235: 312-317; Lemire *et al.* (1989) J Biol Chem 264: 20206-20215; Schatz et al. (1996) Science 271: 1519-1526.

Rab proteins

In eukaryotic cells the compartmentalisation of processes is a prerequisite for a tight regulation of processes and activities. The cells contain a highly dynamic set of membrane compartments that are responsible for packaging, sorting, secreting, and recycling proteins

and other molecules. Trafficking between organelles within the secretory pathway occurs as vesicles derived from a donor compartment fuse with specific acceptor membranes, resulting in the directional transfer of cargo molecules. This process is tightly controlled by the Rab/Ypt family of proteins (reviewed by Novick and Zerial, 1997), a branch of the superfamily of small GTPases. Rab proteins regulate a variety of functions, including vesicle translocation and docking at specific fusion sites. Rabs may also play critical roles in higher order processes such as modulating the levels of neurotransmitter release in neurons, a likely mechanism in synaptic plasticity that underlies learning and memory (Geppert and Südhof, 1998).

Small GTPases share a common three-dimensional fold that, in the GTP bound state, can bind a variety of downstream effector proteins. GTP hydrolysis leads to a conformational change in the "switch" regions that renders the GTPase unrecognizable to its effectors. In this way, by localizing and activating a select set of effectors, a common structural motif is used to control a wide array of distinct cellular processes.

The final steps in membrane fusion are likely to be driven by a set of proteins known as SNAREs. After a vesicle becomes docked, the cytoplasmic domains of VAMP (also termed synaptobrevin) and syntaxin on opposing membranes, in combination with a SNAP-25 molecule, coalesce into an elongated α -helical bundle (Poirier et al., 1998 ; Sutton et al., 1998), which may lead to fusion. Because numerous SNARE isoforms have been identified that localize to distinct membrane compartments, it was originally proposed that the specificity of interaction between the SNARE proteins accounted for the specificity in membrane trafficking. Recent results, however, suggest that SNAREs are not specific in their ability to form complexes in vitro, suggesting that trafficking specificity requires additional factors (Yang et al., 1999). In this regard, Rab proteins are strong candidates for governing the specificity of vesicle trafficking. Like the SNAREs, many isoforms (40) of the Rab family have been identified that localize to specific membrane compartments (reviewed by Novick and Zerial, 1997).

Concomitant with the SNARE cycle, Rab proteins undergo a intricate cycle of membrane and protein interactions. Rabs are posttranslationally modified at C-terminal cysteines by the addition of two geranylgeranyl groups, which mediate membrane association when the Rab is in the GTP-bound state. After guanine nucleotide hydrolysis occurs, the Rab is extracted from the membrane upon forming a complex with a cytosolic GDP-dissociation

inhibitor (GDI). This cytosolic intermediate is then recycled onto a newly forming vesicle, most likely through a secondary factor termed a GDI dissociation factor (GDF), which displaces GDI. After the Rab becomes membrane bound, a guanidine nucleotide exchange factor (GEF) promotes release of GDP and the subsequent loading of GTP. In its GTP-bound conformation, the Rab is then free to associate with its specific set of effectors, which can in turn trigger events leading to the eventual fusion of the vesicle with a target membrane. To complete the cycle, perhaps after or concurrent with membrane fusion, a GTPase activating protein (GAP) accelerates nucleotide hydrolysis, switching off the GTPase. The remaining GDP-bound Rab can then participate in a new round of fusion.

Rab interactions with effectors are likely to regulate vesicle targeting and membrane fusion in three ways. First, a Rab may specifically facilitate vectorial vesicle transport. Vesicles are transported from their site of origin to acceptor compartments likely through associations with cytoskeletal elements and transport motors. A protein has been identified with a domain structure that suggests a connection between the cytoskeleton and the Rabs. This protein, called Rabkinesin-6, contains a kinesin-like ATPase motor domain followed by a coiled-coil stalk region and a RBD that specifically binds Rab6 (Echard et al., 1998). An additional link with the cytoskeleton is provided by the Rab effector, Rabphilin-3A. Rabphilin-3A has been shown in vitro to interact with -actinin, an actin-bundling protein, but only when not bound to Rab3A (Kato et al., 1996). These results raise the intriguing possibility that Rab proteins regulate vesicle interactions with the cytoskeleton and thereby play an active role in targeting vesicles to their appropriate destinations.

Second, Rab proteins may regulate membrane trafficking at the vesicle docking step. A number of Rab effectors, including Rabaptin-5, EEA1, Rabphilin-3A, and Rim, may serve as molecular tethers. Each effector protein contains a RBD, followed by a linker region (some having the potential to form elongated coiled-coil structures), and a domain capable of interacting with a second Rab or the target membrane. Rabaptin-5, for example, contains two RBDs, one near the N terminus that specifically recognizes Rab4 and a second near the C terminus that binds Rab5 (Vitale et al., 1998). Both Rim, which is localized to the target membrane, and Rabphilin-3A, which is localized to the vesicle, contain N-terminal RBDs and C-terminal Ca^{2+} -binding C2 domains, implicating these effectors in synaptic vesicle localization or docking in response to Ca^{2+} influx (Wang et al., 1997). Tethering effectors may also recognize protein complexes on the acceptor membrane. Sec4p, a yeast Rab3A

homolog, interacts with the exocyst (Guo et al., 1999), a complex of seven or more subunits that is assembled at sites of vesicle fusion along the plasma membrane. The exocyst complex may therefore function as a landmark for Rab/effector-mediated vesicle docking.

Third, once a vesicle has become tethered to its fusion site, Rab proteins may selectively activate the SNARE fusion machinery. The mechanism of this activation is unknown but may involve direct interactions of Rabs or, more likely, their effectors with SNAREs. For example, Hrs-2 is a protein that binds to SNAP-25 and contains a Zn²⁺-finger motif characteristic of Rab-binding proteins such as Rabphilin-3A, Rim, EEA1, and Noc2, suggesting that Hrs-2 may form a physical link between Rabs and SNAREs (Bean et al., 1997). In addition, certain mutations in the syntaxin-binding protein Sly1p, the Sec1p homolog utilized in ER to Golgi trafficking, eliminate the requirement for Ypt1p, a Rab protein that functions at this trafficking step (Dascher et al., 1991). Rabs may therefore regulate SNARE associations through Sec1 family members. In support of this idea, a Rab effector was recently found to interact with a vacuole Rab, a Sec1p homolog, and a SNARE protein (Peterson et al., 1999), which suggests that this effector serves to connect Rab and SNARE function. In this way, Rabs and their effectors may facilitate the correct pairing of SNAREs.

References: Dascher et al. (1991) *Mol. Cell. Biol.* 11, 872-885; Echard et al. (1998). *Science*. 279, 580-585; Geppert et al. (1998) *Annu. Rev. Neurosci.* 21, 75-95; Guo et al. (1999). *EMBO J.* 18, 1071-1080; Kato et al. (1996) *J. Biol. Chem.* 271, 31775-31778; Novick et al. (1997) *Curr. Opin. Cell Biol.* 9, 496-504; Peterson (1999) *Curr. Biol.* 9, 159-162; Poirier et al. (1998) *Nat. Struct. Biol.* 5, 765-769; Vitale et al. (1998) *EMBO J.* 17, 1941-1951; Wang et al. (1997) *Nature*. 388, 593-598; Yang et al. (1999) *J. Biol. Chem.* 274, 5649-5653.

Within the overall group of Intracellular Transport and Trafficking several categories of proteins are coded for by clones of the invention.

Rab proteins:

Rab1B is essential for the intracellular transport of nascent low density lipoprotein (LDL) receptor. It is discussed as a universal mediator of endoplasmatic reticulum to Golgi transport of membrane glycoproteins in mammalian cells. . Clones in this category include: fbr2_2i17, fbr2_3b16.

Rab10 appear concentrated on membranes in the perinuclear region. Rab 10 has been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases as reported by OMIN: 1) Choroideremia (OMIN *303199); and 2) RETT Syndrome (OMIN 312750). Clones in this category include: fbr2_62119.

In mice, Rab17 shows epithelial cell specificity. Rab 17 is discussed as candidate gene for the mouse mutations In (leaden), Tw (twirler), and ax (ataxia). Cloned from a brain cDNA library, the new putative Rab-protein is expected to be involved in vesicle trafficking within neuronal cells. These proteins can find application in modulating the transport of vesicles inside neuronal cells, which are essential for development of functional dendritic processes. . . Clones in this category include: fbr2_41m15.

Ankyrin G: The ankyrin 3 gene encodes a novel ankyrin, which is expressed in multiple tissues, with very high expression at the axonal initial segment and nodes of Ranvier of neurons in the central and peripheral nervous systems. Ankyrin G shows several tissue-specific alternative mRNA processing. The different ankyrin G proteins participate in maintenance/targeting of ion channels and cell adhesion molecules to nodes of Ranvier and axonal initial segments. Ankyrin G has been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with Werner disease (OMIN *277700). Clones in this category include: fkd2_24p5.

Zn-T-transporters: The Zn-T-transporters are membrane proteins that facilitates sequestration of zinc in endosomal vesicles. In the brain, ZnT-3 mRNA seems to be involved in the accumulation of zinc in synaptic vesicles. Zinc (Zn) is an essential element in normal development and metabolism. Recent studies show that in Alzheimer's disease, Zn functions as a double-edged sword; affording protection against Alzheimer's amyloid beta peptide (the major component of senile plaques) at low concentrations and enhancing toxicity at high concentrations by accelerated aggregation of the amyloid beta peptide. These proteins can find application in modulation of Zinc transport in neuronal cells, thus providing means for a modulation of Alzheimer's amyloid beta peptide plaque formation. (OMIN *602878, *602095). Clones in this category include: fbr2_62f10.

Metabolism

This group includes proteins which are involved in the uptake and consumption of nutrients, and enzymes which are part of the biochemical pathways for energy metabolism or

which are involved in the supply of building blocks of nucleic acids, proteins (NTPs, dNTPs, amino acids) for DNA/RNA and protein synthesis, and fatty acids (membranes), to allow for the generation of higher order structures. This group constitutes the most important and largest group in prokaryotes and lower eukaryotes. The higher the evolutionary level of an organism is, however, the more other protein classes like 'signal transduction', 'cell cycle' and 'differentiation and development' increase in importance and number of representatives.

Proteins involved in the metabolism of energy and compounds (here: other than nucleic acids or proteins) are usually the products of house keeping genes, they are often constitutively and/or ubiquitously expressed.

Several categories of proteins are coded for by clones of the invention within the overall group of Metabolism:

NAT1, ARD1: In yeast, ARD1 and NAT1, are required for the expression of an N-terminal protein acetyltransferase 1. NAT1 controls full repression of the silent mating type locus HML, sporulation and entry into G0. ARD1 is involved in the assembly of the NAT 1-complex. These can find application modulating NAT assembly and action and therefore could be important in metabolism of drugs and environmental mutagens.(OMIN *108345). Clones in this category include: fbr2_3g8.

Apolipoprotein E receptor: In LDL-receptors the class A domains form the binding site for LDL and calcium. The acidic residues between the fourth and sixth cysteines are important for high-affinity binding of positively charged sequences in LDLR's ligands. These proteins can find application in modulation of cholesterol binding and transport by LDL-receptors and LDL-binding proteins. In normal individuals, chylomicron remnants and very low density lipoprotein (VLDL) remnants are rapidly removed from the circulation by receptor-mediated endocytosis in the liver. In familial dysbetalipoproteinemia, or type III hyperlipoproteinemia (HLP III), increased plasma cholesterol and triglycerides are the consequence of impaired clearance of chylomicron and VLDL remnants because of a defect in apolipoprotein E. Accumulation of the remnants can result in xanthomatosis and premature coronary and/or peripheral vascular disease. OMIN reports that apolipoprotein has associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Familial hypercholesterolemia (OMIN 143890); 2) Familial combined hyperlipidemia (OMIN 144250); and 3) Alzheimer disease. (OMIN #104300). Clones in this category include: fbr2_62017.

Ubiquitin carboxyl-terminal hydrolases: Ubiquitin carboxyl-terminal hydrolases (EC 3.1.2.15) (UCH) (deubiquitinating enzymes) are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins. OMIN reports that Ubiquitin-specific proteases have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Lung carcinoma (OMIN *603486); 2) x-linked retinal diseases (OMIN *300050); 3) oncogenesis (OMIN *300050); 4) ovarian cancer (OMIN *300050). Clones in this category include: fbr2_78k24; htes3_27d1.

Phosphoserine signature (phosphoglucosyltransferases, phosphomannomutase): These proteins take part in the conversion of hexose phosphates. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following disease: Fanconi-Bickel Syndrome (OMIN #227810). Clones in this category include: fkd2_24b15.

NADH ubiquinone oxidoreductase: NADH:ubiquinone oxidoreductase is the first enzyme in the respiratory electron transport chain of mitochondria. It is a membrane-bound multi-subunit protein. The bovine heart enzyme contains about 40 different polypeptides. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following disease: Brancio-oto-renal syndrome (OMIN *6601445). Clones in this category include: fkd2_3o17.

Transketolases: Transketolase requires thiamin pyrophosphate as cofactor and shows a wide specificity for both reactants, e.g. converts hydroxypyruvate and R-CHO into CO(2) and R-CHOH-CO-CH(2)OH. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: Wernicke-Korsakoff Syndrome (OMIN *277730). Clones in this category include: tes3_17i17.

Fatty acid-CoA synthetases/ligases: These proteins contain AMP-binding domain signature(s), which is present in enzymes which act via an ATP-dependent covalent binding of AMP to their substrate. This domain is found in several CoA synthetases, such as acetate-CoA ligase (EC 6.2.1.1), long-chain-fatty-acid-CoA ligase (EC 6.2.1.3), bile acid-CoA ligase. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic,

causative, and/or related, etc...) with the following diseases: 1) Alport syndrome , mental retardation and elliptocytosis (OMIN *300157); 2) Adrenoleukodystrophy (OMIN *300100). Clones in this category include: tes3_35k17.

ADP/ATP or Adenine Nucleotide Translocators: These proteins contain mitochondrial energy transfer signature(s) and are most abundant in mitochondria. In its functional state, it is a homodimer of 30-kD subunits embedded asymmetrically in the inner mitochondrial membrane. The dimer forms a gated pore through which ADP is moved from the matrix into the cytoplasm.. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) cardiomyopathy (OMIN *103220); 2) myopathy (OMIN *103220); 3) Progressive external ophthalmoplegia (OMIN *601227). Clones in this category include: tes3_35n12.

Carboxylesterases: OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) hepatic carboxylesterase with detoxification of foreign compounds (OMIN *114835); 2) non-Hodgkin lymphoma (OMIN *114835); 3) B-cell chronic lymphocytic leukemia (OMIN *114835); 4) rheumatoid arthritis (OMIN *114835). Clones in this category include: tes3_35n9.

Heat shock proteins: OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) 27 kd heat shock protein has been correlated with thermotolerance in response to environmental challenges and developmental transitions. (OMIN *6021295). Clones in this category include: utell_23e13.

Nucleic acid management

The genetic information is stored in the form of nucleic acids in all organisms. Two kinds of nucleic acids exist, DNA and RNA. Whereas the more stable DNA in most organisms constitutes the storage form of the genetic information, the labile RNA and in particular mRNA is an intermediate used for the temporal expression of specific genes.

In eukaryotes, DNA is usually a double stranded linear molecule consisting of two antiparallel strands and made up of a deoxyribose, a phosphorus backbone and the four bases A, C, G, and T. The DNA of some organisms has a ring structure. The structure of DNA was

unraveled years ago by Watson and Crick. DNA is directional molecule determined by the C-atoms of the sugar.

The most important processes dealing with nucleic acids are:

- replication (e.g. DNA polymerases, Telomerase)
- transcription (RNA polymerases)
- RNA processing (maturation - splicing and degradation)
- in addition, enzymes and proteins exist which require a nucleic acid (mostly RNA) in the active center to be functional (ribozymes - e.g. RNase, Ribosomal proteins)

The DNA of a cell is replicated in the S-phase of the cell cycle. Several enzymes carry out the task of doubling this nucleic acid. As all steps of the cell cycle, also the process of replication is tightly regulated. The enzyme DNA polymerase and several other proteins are involved in this process. Whereas many prokaryotes do have only one origin of replication (i.e., the starting point of the replication cycle), in eukaryotic DNAs (chromosomes) multiple such start points exist. The switch from the synthesis (S) phase to the subsequent G2 or M phases of the cell cycle are dependent on the completion of the replication. This makes clear, that a number of proteins are involved in the replication itself as well as in the control of the process. Since most eukaryotic chromosomes are linear structures, additional proteins and enzymes are necessary to make sure that the structure is maintained through successive generations. This includes those proteins necessary to build the three dimensional structure of chromosomes (e.g. histones) and the structural network of the nucleus and nucleolus (including the defined localization of transcriptionally active genes in the vicinity of nucleoli) but also such enzymes as telomerase which guarantees the integrity of the chromosomal ends.

The expression of genes is usually performed in two steps. First a messenger RNA (mRNA) is produced (transcribed) in one to many copies and second this mRNA is translated into the protein product. The regulation of transcription is discussed under the separate heading 'transcription factors', but also the classes 'signal transduction', 'development', 'cell cycle' and others are affected as the expression of certain genes determines the fate of a cell or organism.

The primary transcript (hnRNA - heterogeneous nuclear RNA) is a single stranded one-to-one copy of the gene as it is located on the chromosome. Before a protein can be translated, already during transcription the process of maturation is initiated. Firstly, a 5' cap structure is enzymatically and covalently added to the RNA, blocking the 5' end of the RNA.

Second, when the RNA polymerase has terminated polymerization, the enzyme poly A polymerase adds varying numbers of adenine residues to the 3' end of the transcript. This enzyme recognizes the sequence AAUAAA or AUUAAA (+ some minor variations), cuts the RNA 10 - 30 nucleotides downstream and adds the A residues. The size of the poly A sequence affects the stability of the RNA. Finally, in the process of splicing, the introns present on the genomic level and also present in the hnRNA are spliced out by a multi-protein complex consisting of several proteins and RNAs. The finally matured mRNA is exported to the cytoplasm where it is translated with help of the ribozymes.

The half life of RNA is usually much shorter than that of DNA. Usually, the mRNA is degraded shortly after synthesis, to guarantee a very defined window of expression of a given gene. This regulation is necessary to specifically maintain or change the set of proteins present at any time in a cell. Specific regions in the 3'UTR (untranslated region) determine the stability of the mRNA in the cytoplasm before it is degraded by RNases, enzymes consisting both of protein and RNA.

References: Watson and Crick (1953) *Nature* **171**: 737-738.

Several categories of proteins are coded for by clones of the invention within the overall group of "Nucleic acid management" and include, among others, the following:

RNA helicases including DEAD/H box helicases: RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. DEAD box proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) as reported by with the following disease processes and/or genes: 1) ataxia-telangiectasia gene: "A human gene (DDX10) encoding a putative DEAD-box RNA helicase at 11q22-q23" *Genomics* 33:199-206, 1996, Savitsky et al., (OMIN *601235); 2) hematopoietic tumors: "Cloning and expression of a murine cDNA homologous to the human RCK/P54, a lymphoma-linked chromosomal breakpoint 11q23", *Gene* 166:293-6, 1995, Seto et al. (OMIN *600326); 3) dermatomyositis: a) "The major dermatomyositis-specific Mi-2 autoantigen is a presumed helicase involved in transcriptional activation."

Arthritis Rheum. 38: 1389-1399, 1995, Seelig et al. (OMIN *603277); b) "Two forms of the major antigenic protein of the dermatomyositis-specific Mi-2 autoantigen." (Letter), *Arthritis Rheum.* 39: 1769-1771, 1996., Seelig et al. (OMIN *603277); c) "The dermatomyositis-specific autoantigen Mi2 is a component of a complex containing histone deacetylase and nucleosome remodeling activities", *Cell* 95: 279-289, 1998. Zhang et al. (OMIN *603277); 4) Muscular Dystrophy, Pseudohypertrophic Progressive Duchenne and Becker Types (OMIN *310200); 5) Mucopolysaccharidosis Type IVA (OMIN *253000); 6) Albinism I (OMIN *203100); 7) Wilms Tumor 1 (OMIN *194070); 8) Spinocerebellar Ataxia 7 (OMIN *164500). Clones in this category include: fbr2_23b10, fbr2_3cl8, fbr2_6o17, fbr2_82i24, and tes3_14h21.

Inorganic pyrophosphatase: Inorganic pyrophosphatase (EC 3.6.1.1) (PPase) is the enzyme responsible for the hydrolysis of pyrophosphate (PPi) which is formed as the product of the many biosynthetic reactions that utilize ATP. All known PPases require the presence of divalent metal cations, with magnesium conferring the highest activity. Clones in this category include: fbr2_64a15.

DNA-damage -inducible protein (dinP) or Proteins induced by DNA-Damage: The dinB/P pathway is a second SOS-pathway in E.coli. Genes related to this seem to be involved in modulating DNA repair and mutagenesis. Clones in this category include: fbr2_72b18.

Proteins with myc-type, helix-loop-helix dimerization domain signature(s). This helix-loop-helix domain mediates protein dimerization has been found in proteins such as the myc family of cellular oncogenes, proteins involved in myogenesis and vertebrate proteins that bind specific DNA sequences in various immunoglobulin chains enhancers. Therefore, these proteins could be novel DNA-binding proteins. Clones in this category include: fbr2_72i12.

Cytosolic ribosomal proteins L36: L36 seems to be part of the eukaryotic ribosomal peptidyl transferase center and can find application in modulation of ribosome assembly, maintenance and activity. Clones in this category include: fkd2_3b2.

Ribonuclease H: Ribonuclease H proteins are RNA modifying proteins and have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases as reported by OMIN: 1) Adenomatous Polyposis of the Colon (OMIN

*175100); 2) Retinoblastoma (OMIN *180200) ; and 3) Von Hippel-Lindau Syndrome (OMIN *193300). Clones in this category include: phtes3_15j3.

Signal transduction

Cells in higher order organisms need to continuously communicate with its environment especially with other cells of the same organism in order to maintain the function and specialization of the whole system these cells are part of. This important task of communication is performed with help of cell-surface receptors which receive and transmit signals from outside into the cell.

G-proteins

The largest known family of cell-surface receptors is that of the G-protein-coupled receptors, which mediate the transmission of diverse stimuli such as neurotransmitters, glycopeptides, hormones, peptides, odorant molecules, and photons. The functional unit of these receptors is composed of the receptor molecule itself (GPCR) which is anchored in the cytoplasmic membrane with seven membrane spanning domains, the heterotrimeric G-protein which is composed of α and $\beta\gamma$ -subunits ($G\alpha$ and $G\beta\gamma$), and the effectors that interact with $G\alpha$ and / or $G\beta\gamma$. In particular, the dissociated $G\alpha$ and $G\beta\gamma$ can regulate the activities of a number of effector molecules such as adenylate cyclases, phospholipase C isoforms, ion channels, and tyrosine kinases, resulting in a variety of cellular functions. The process of signal transduction must be tightly regulated and reversible in order to avoid overstimulation, to achieve signal termination, and render the receptor responsive to subsequent stimuli [Iacovelly L. et al., (1999) *FASEB J.* 13, 1-8, Hamm, H.E. (1998) *J. Biol. Chem.* 273, 669-672].

G-proteins are GTPases that, upon binding of GTP change their conformation which in return unmasks structural motives, in particular the so called effector loop, which can mediate the interactions to target proteins, or effectors, for the GTPases. This ability enables the GTPases to cycle between active, GTP-bound and inactive, GDP bound conformations and in the process to function as molecular traffic lights in a multitude of signal transduction pathways. The most important of these signal transduction pathways that are regulated with help of G-proteins are that of the phospholipase C / protein kinase C and that of the adenylate cyclase / protein kinase A.

The cycling of GTPases is tightly regulated by three main classes of proteins: The exchange of hydrolyzed GDP for a fresh GTP is facilitated by guanosine nucleotide exchange factors (GEFs), the hydrolysis of GTP to GDP is sped up by GTPase-activating proteins (GAPs), and the dissociation of GDP from the GTPases is inhibited by GDP dissociation inhibitors (GDIs) [Tapon and Hall (1997) *Curr. Opin. Cell. Biol.* **9**, 86-92, Van Aelst and D-Souza-Schorey (1997) *Genes Dev.* **11**, 2295-2322].

SOC-family

A conserved motif that was originally identified in proteins that negatively regulate the signaling action of cytokines was termed SOCS box, the Suppressor Of Cytokine Signaling. Based on homology, five distinct structural protein classes have been identified since that carry this motif. The function of most of these proteins is presently not known. Common to the proteins is only the SOCS box which is located near the C-terminus of the respective peptides. Recently, the SOCS box has been demonstrated to induce binding of proteins to elongins B and C which could target the proteins (and bound substrates) to the proteasomal protein degradation pathway (Kamura, T. *et al.* (1998) *Genes Dev.* **12**, 3872-3881; Zhang, J.-G. *et al.* (1999) *Proc. Natl. Acad. Sci. USA* **96**, 2071-2076).

The class where the SOCS box was originally described contains several members (SOCS-1-SOCS-7 and CIS). In addition to the SOCS box, these proteins also contain a SH2 (Src-homology 2) domain and a variable N-terminus. These SOCS proteins appear to form part of a classical negative feedback loop that regulates cytokine signal transduction. Upon cytokine stimulation, expression of SOCS proteins is rapidly induced and the proteins inhibit further cytokine action. The mode of action of the SOCS proteins is variable. While SOCS-1 binds and inhibits the JAK (Janus kinases) family of cytoplasmic protein kinases [Narazhaki M. *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95**, 13130-13134, Nicholson, S.E. *et al.* (1999) *EMBO J.* **18**, 375-385], CIS appears to act by competing with signaling molecules such as the STATs (Transducers and Activators of Transcription) family for binding to phosphorylated receptor cytoplasmic domains [Yoshimura, A. *et al.* (1995) *EMBO J.* **14**, 2816-2826; Matsumoto, A. *et al.* (1997) *Blood* **89**, 3148-3154].

A second class of SOCS box protein contains additionally WD-40 repeats which were initially identified in the mouse WSB-1 and -2 proteins. The functions of WD-40 proteins are not completely understood but seem to be rather divergent. In Cdc4p the WD-40 repeats probably are necessary for binding the substrate for Cdc34p [Mathias, N. *et al.* (1999) *Mol.*

Cell Biol. **19**, 1759-1767]. Cdc4p is a component of a ubiquitin ligase that tethers the ubiquitin-conjugating enzyme Cdc34p to its substrates. The posttranslational modification of a protein by ubiquitin usually results in rapid degradation of the ubiquitinated protein by the proteasome. The transfer of ubiquitin to substrate is a multistep process where WD-40 repeats might play an important function.

Other WD-40 containing proteins (e.g. the retino blastoma binding protein RbAp48) have been shown to bind metal ions (Zinc) and that this metal binding might mediate and/or regulate protein-protein interactions which are functionally important in chromatin metabolism [Kenzior, A.L. and Folk, W.R. (1998) *FEBS Lett.* **440**, 425-429]. These proteins are involved in the RAS-cAMP pathway that regulates cellular growth [Ach R.A. *et al.* (1997) *Plant Cell* **9**, 1595-1606].

The SPRY domain has been identified in pyrin or marenostrin, a protein which is mutated in patients with Mediterranean fever and which is similar to the butyrophilin family. While butyrophilins seem to be involved in the lactation process in mammals, the function pyrin is unknown. Three proteins (SSB-1 to -3) have been identified to contain both SPRY and SOCS box motifs. The function of these proteins is also not known.

Ankyrin repeat containing proteins share a 33-residue repeating motif, an L-shaped structure with protruding β -hairpin tips which mediate specific macromolecular interactions with cytoskeletal, membrane, and regulatory proteins. These proteins play fundamental roles in diverse biological activities including growth and development, intracellular protein trafficking, the establishment and maintenance of cellular polarity, cell adhesion signal transduction, and mRNA transcription. Three proteins that contain ankyrin repeats (ASB-1 to -3) have been identified to contain a C-terminal SOCS box additionally to the ankyrin repeats. The function of these proteins or the individual domains remains to be discovered [Hilton, D.J. *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95**, 114-119].

A few small GTPases (RAR and RAR like) do also contain a SOCS box. GTPases are involved in signal transduction during cellular communication. The function of the SOCS box in this type of proteins is currently unclear [Hilton, D.J. *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95**, 114-119].

Ca²⁺ as second messenger

The bivalent cation Ca²⁺ is, besides cAMP, one of the two major second messengers in eukaryotic cells. Its intracellular concentration is tightly regulated and usually kept very

low compared to the cell's environment. Ca^{2+} binding proteins and transporters (Gap junction, Voltage-gated, second messenger-gated) help to sequester huge amounts of the ion in various organelles from where Ca^{2+} can be released upon extracellular stimuli. E.g. the contraction of the muscle is dependent on the presence of Ca^{2+} ions which are readily transported back into the organelles in order for the muscle to relax. In signal transduction, Ca^{2+} functions as a second messenger that activates Ca^{2+} dependent processes through the activation of Ca^{2+} /calmodulin dependent protein kinases (CaM kinases) which are the major effector molecules of Ca^{2+} . In the signaling cascades, the CaM dependent kinases activate phospholipases (e.g. phospholipase C) that in return activate other protein kinases such as protein kinase C.

cAMP

The cyclic AMP is produced by the enzyme adenylate cyclase in response to extracellular signals. Certain G-proteins stimulate the activity of adenylate cyclase which converts ATP to cAMP and PPI. Two molecules of cAMP bind to each of two regulatory subunits of cAMP dependent protein kinase which in turn dissociate from the two catalytic subunits of the heterotetramer R_2C_2 . Upon release of the C-subunits, they become active and phosphorylate substrate proteins at Ser and Thr residues. The process leading from binding of extracellular molecules to their receptors, the transmission of the stimuli into the cell, the activation of adenylate cyclase and the subsequent activation of cAMP dependent protein kinase is one of two major signal transduction pathways in eukaryotic cells. Since the phosphorylation of proteins is a posttranslational modification of proteins, the kinases are described in the class "signal transduction."

SARA

Members of the transforming growth factor β (TGF β) superfamily signal through a family of cell-surface transmembrane serine/threonine kinases, known as type I and type II receptors (Heldin et al., 1997 ; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). Ligand induces formation of heteromeric complexes of these receptors, and signaling is initiated when receptor I is phosphorylated and activated by the constitutively active kinase of receptor II (Wrana et al., 1994). The activated type I receptor kinase then propagates the signal to a family of intracellular signaling mediators known as Smads (contraction of the C.elegans Sma and Drosophila Mad genes which were the first identified members of this class of signaling effectors).

Three classes of Smads with distinct functions have been defined: the receptor-regulated Smads, which include Smad1, 2, 3, 5, and 8; the common mediator Smad, Smad4; and the antagonistic Smads, which include Smad6 and 7 (Heldin et al., 1997; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). Receptor-regulated Smads (R-Smads) act as direct substrates of specific type I receptors, and the proteins are phosphorylated on the last two serines at the carboxyl terminus within a highly conserved SSXS motif (Macías-Silva et al., 1996 ; Abdollah et al., 1997 ; Kretzschmar et al., 1997 ; Liu et al., 1997b ; Souchelnytskyi et al., 1997). Regulation of R-Smads by the receptor kinase provides an important level of specificity in this system. Thus, Smad2 and Smad3 are substrates of TGF β or activin receptors and mediate signaling by these ligands (Macías-Silva et al., 1996 ; Liu et al., 1997b ; Nakao et al., 1997), whereas Smad1, 5, and 8 are targets of BMP receptors and propagate BMP signals (Hoodless et al., 1996 ; Chen et al., 1997b ; Kretzschmar et al., 1997 ; Nishimura et al., 1998). Once phosphorylated, R-Smads associate with the common Smad, Smad4 (Lagna et al., 1996 ; Zhang et al., 1997), and mediate nuclear translocation of the heteromeric complex. In the nucleus, Smad complexes then activate specific genes through cooperative interactions with DNA and other DNA-binding proteins such as FAST1, FAST2, and Fos/Jun (Chen et al., 1996 , Chen et al., 1997a ; Liu et al., 1997a ; Labbé et al., 1998 ; Zhang et al., 1998 ; Zhou et al., 1998). In contrast to R-Smads and Smad4, the antagonistic Smads, Smad6 and 7, appear to function by blocking ligand-dependent signaling (reviewed in Heldin et al., 1997).

Phosphorylation of R-Smads by the type I receptor is essential for activating the TGF β signaling pathway (Heldin et al., 1997 ; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). However, little is known of how Smad interaction with receptors is controlled. A novel Smad2/Smad3 interacting protein has been described (Tsukazaki T. et al., 1998) that contains a double zinc finger, or FYVE domain, and which has been called SARA (Smad anchor for receptor activation). The SARA motif recruits Smad2 into distinct subcellular domains and co-localizes and interacts with TGF β receptors. TGF β signaling induces dissociation of Smad2 from SARA with concomitant formation of Smad2/Smad4 complexes and nuclear translocation. Moreover, deletion of the FYVE domain in SARA causes mislocalization of Smad2 and inhibits TGF β -dependent transcriptional responses. Thus, SARA defines a component of TGF β signaling that functions to recruit Smad2 to the receptor by controlling the subcellular localization of Smad.

References: Abdollah et al. (1997) J. Biol. Chem. 272, 27678-27685; Attisano et al. (1998) Curr. Opin. Cell Biol. 10, 188-194; Chen et al. (1996) Nature 383, 691-696; Chen et al. (1997a) Nature 389, 85-89; Chen et al. (1997b) Proc. Natl. Acad. Sci. USA 94, 12938-12943; Heldin et al. (1997) Nature 390, 465-471; Hoodless et al. (1996) Cell 85, 489-500; Kretzschmar et al. (1998) Curr. Opin. Genet. Dev. 8, 103-111; Kretzschmar et al. (1997) Genes Dev. 11, 984-995; Labbé et al. (1998) Mol. Cell 2, 109-120; Lagna et al. (1996) Nature 383, 832-836; Liu et al. (1997a) Genes Dev. 11, 3157-3167; Liu et al. (1997b) Proc. Natl. Acad. Sci. USA 94, 10669-10764; Macías-Silva et al. (1996) Cell 87, 1215-1224; Nakao et al. (1997) EMBO J. 16, 5353-5362; Nishimura et al. (1998) J. Biol. Chem. 273, 1872-1879; Souchelnytskyi et al. (1997) J. Biol. Chem. 272, 28107-28115; Tsukazaki et al. (1998) Cell 95, 779-791; Wrana et al. (1994) Nature 370, 341-347; Zhang et al. (1997) Curr. Biol. 7, 270-276; Zhang et al. (1998) Nature 394, 909-913; Zhou et al. (1998) Mol. Cell 2, 121-127.

Calcium

The bivalent cation Ca^{2+} is, along with cAMP, one of the two major second messengers in eukaryotic cells. Its intracellular concentration is tightly regulated and usually kept very low compared to the cell's environment. Ca^{2+} binding proteins and transporters (Gap junction, Voltage-gated, second messenger-gated) help to sequester huge amounts of the ion in various organelles from where Ca^{2+} can be released upon extracellular stimuli. E.g. the contraction of the muscle is dependent on the presence of Ca^{2+} ions which are readily transported back into the organelles in order for the muscle to relax. In signal transduction, Ca^{2+} functions as a second messenger that activates Ca^{2+} dependent processes through the activation of Ca^{2+} /calmodulin dependent protein kinases (CaM kinases) which are the major effector molecules of Ca^{2+} . In the signaling cascades, the CaM dependent kinases activate phospholipases (e.g. phospholipase C) that in return activate other protein kinases such as protein kinase C.

Rab proteins

In eukaryotic cells the compartmentalization of processes is a prerequisite for a tight regulation of processes and activities. The cells contain a highly dynamic set of membrane compartments that are responsible for packaging, sorting, secreting, and recycling proteins and other molecules. Trafficking between organelles within the secretory pathway occurs as

vesicles derived from a donor compartment fuse with specific acceptor membranes, resulting in the directional transfer of cargo molecules. This process is tightly controlled by the Rab/Ypt family of proteins (reviewed by Novick and Zerial, 1997), a branch of the superfamily of small GTPases. Rab proteins regulate a variety of functions, including vesicle translocation and docking at specific fusion sites. Rabs may also play critical roles in higher order processes such as modulating the levels of neurotransmitter release in neurons, a likely mechanism in synaptic plasticity that underlies learning and memory (Geppert and Südhof, 1998).

Small GTPases share a common three-dimensional fold that, in the GTP bound state, can bind a variety of downstream effector proteins. GTP hydrolysis leads to a conformational change in the "switch" regions that renders the GTPase unrecognizable to its effectors. In this way, by localizing and activating a select set of effectors, a common structural motif is used to control a wide array of distinct cellular processes.

The final steps in membrane fusion are likely to be driven by a set of proteins known as SNAREs. After a vesicle becomes docked, the cytoplasmic domains of VAMP (also termed synaptobrevin) and syntaxin on opposing membranes, in combination with a SNAP-25 molecule, coalesce into an elongated α -helical bundle (Poirier et al., 1998 ; Sutton et al., 1998), which may lead to fusion. Because numerous SNARE isoforms have been identified that localize to distinct membrane compartments, it was originally proposed that the specificity of interaction between the SNARE proteins accounted for the specificity in membrane trafficking. Recent results, however, suggest that SNAREs are not specific in their ability to form complexes in vitro, suggesting that trafficking specificity requires additional factors (Yang et al., 1999). In this regard, Rab proteins are strong candidates for governing the specificity of vesicle trafficking. Like the SNAREs, many isoforms (40) of the Rab family have been identified that localize to specific membrane compartments (reviewed by Novick and Zerial, 1997).

Concomitant with the SNARE cycle, Rab proteins undergo a intricate cycle of membrane and protein interactions. Rabs are posttranslationally modified at C-terminal cysteines by the addition of two geranylgeranyl groups, which mediate membrane association when the Rab is in the GTP-bound state. After guanine nucleotide hydrolysis occurs, the Rab is extracted from the membrane upon forming a complex with a cytosolic GDP-dissociation inhibitor (GDI). This cytosolic intermediate is then recycled onto a newly forming vesicle,

most likely through a secondary factor termed a GDI dissociation factor (GDF), which displaces GDI. After the Rab becomes membrane bound, a guanidine nucleotide exchange factor (GEF) promotes release of GDP and the subsequent loading of GTP. In its GTP-bound conformation, the Rab is then free to associate with its specific set of effectors, which can in turn trigger events leading to the eventual fusion of the vesicle with a target membrane. To complete the cycle, perhaps after or concurrent with membrane fusion, a GTPase activating protein (GAP) accelerates nucleotide hydrolysis, switching off the GTPase. The remaining GDP-bound Rab can then participate in a new round of fusion.

Rab interactions with effectors are likely to regulate vesicle targeting and membrane fusion in three ways. First, a Rab may specifically facilitate vectorial vesicle transport. Vesicles are transported from their site of origin to acceptor compartments likely through associations with cytoskeletal elements and transport motors. A protein has been identified with a domain structure that suggests a connection between the cytoskeleton and the Rabs. This protein, called Rabkinesin-6, contains a kinesin-like ATPase motor domain followed by a coiled-coil stalk region and a RBD that specifically binds Rab6 (Echard et al., 1998). An additional link with the cytoskeleton is provided by the Rab effector, Rabphilin-3A. Rabphilin-3A has been shown in vitro to interact with -actinin, an actin-bundling protein, but only when not bound to Rab3A (Kato et al., 1996). These results raise the intriguing possibility that Rab proteins regulate vesicle interactions with the cytoskeleton and thereby play an active role in targeting vesicles to their appropriate destinations.

Second, Rab proteins may regulate membrane trafficking at the vesicle docking step. A number of Rab effectors, including Rabaptin-5, EEA1, Rabphilin-3A, and Rim, may serve as molecular tethers. Each effector protein contains a RBD, followed by a linker region (some having the potential to form elongated coiled-coil structures), and a domain capable of interacting with a second Rab or the target membrane. Rabaptin-5, for example, contains two RBDs, one near the N terminus that specifically recognizes Rab4 and a second near the C terminus that binds Rab5 (Vitale et al., 1998). Both Rim, which is localized to the target membrane, and Rabphilin-3A, which is localized to the vesicle, contain N-terminal RBDs and C-terminal Ca^{2+} -binding C2 domains, implicating these effectors in synaptic vesicle localization or docking in response to Ca^{2+} influx (Wang et al., 1997). Tethering effectors may also recognize protein complexes on the acceptor membrane. Sec4p, a yeast Rab3A homolog, interacts with the exocyst (Guo et al., 1999), a complex of seven or more subunits

that is assembled at sites of vesicle fusion along the plasma membrane. The exocyst complex may therefore function as a landmark for Rab/effector-mediated vesicle docking.

Third, once a vesicle has become tethered to its fusion site, Rab proteins may selectively activate the SNARE fusion machinery. The mechanism of this activation is unknown but may involve direct interactions of Rabs or, more likely, their effectors with SNAREs. For example, Hrs-2 is a protein that binds to SNAP-25 and contains a Zn²⁺-finger motif characteristic of Rab-binding proteins such as Rabphilin-3A, Rim, EEA1, and Noc2, suggesting that Hrs-2 may form a physical link between Rabs and SNAREs (Bean et al., 1997). In addition, certain mutations in the syntaxin-binding protein Sly1p, the Sec1p homolog utilized in ER to Golgi trafficking, eliminate the requirement for Ypt1p, a Rab protein that functions at this trafficking step (Dascher et al., 1991). Rabs may therefore regulate SNARE associations through Sec1 family members. In support of this idea, a Rab effector was recently found to interact with a vacuole Rab, a Sec1p homolog, and a SNARE protein (Peterson et al., 1999), which suggests that this effector serves to connect Rab and SNARE function. In this way, Rabs and their effectors may facilitate the correct pairing of SNAREs.

References: Dascher et al. (1991). *Mol. Cell. Biol.* 11, 872-885; Echard et al. (1998). *Science*. 279, 580-585; Geppert et al. (1998). *Annu. Rev. Neurosci.* 21, 75-95; Guo et al. (1999). *EMBO J.* 18, 1071-1080; Kato et al. (1996). *J. Biol. Chem.* 271, 31775-31778; Novick et al. (1997). *Curr. Opin. Cell Biol.* 9, 496-504; Peterson et al. (1999). *Curr. Biol.* 9, 159-162; Poirier et al. (1998). *Nat. Struct. Biol.* 5, 765-769; Vitale et al. (1998). *EMBO J.* 17, 1941-1951; Wang et al. (1997). *Nature*. 388, 593-598; Yang et al. (1999). *J. Biol. Chem.* 274, 5649-5653.

Kinases

Reversible posttranslational modifications of proteins are major means of regulating cellular activities. Among the various modifications that are carried out by the cells, the addition of phosphoryl groups to Ser/Thr or Tyr residues is the most important and widely used. The phosphorylation of proteins is accomplished by protein kinases, while the reverse reaction, the removal of phosphoryl groups, is carried out by phosphatases. Kinases / Phosphatases regulate key positions e.g. in the processes of cell proliferation, differentiation and communication/signaling. These processes must be tightly regulated in order to maintain a steady state level of cellular fate. Mis-regulation of kinase activities (or that of

phosphatases) is made responsible for a multitude of disease processes such as oncogenesis, inflammatory processes, arteriosclerosis, and psoriasis.

Protein kinases constitute the largest protein family that is currently known. Several hundred kinases have been identified already. Classically, kinases are subdivided into two classes based on the amino acid residues in their substrates that are phosphorylated by the particular enzymes. The kinases specifically add phosphoryl groups from adenosine triphosphate (ATP) or, less frequently, guanosine triphosphate (GTP), either to serine and/or threonine or to tyrosine residues of substrate proteins. An estimated 1,000 to 10,000 proteins present in a typical mammalian cell are believed to be regulated also by the action of protein kinases.

Protein kinases are frequently integral parts of signaling cascades that transmit extracellular stimuli (e.g. hormones, neurotransmitters, growth- or differentiation factors) into the cell and result in various responses by the cells. The kinases play key roles in these cascades as they constitute a sort of 'molecular switches' turning on or off the activities of other enzymes and proteins, e.g. metabolic, regulatory, channels and pumps, receptors, cytoskeletal, transcription factors.

The regulation of kinase activities is accomplished by various means:

The best characterized example for the regulation via regulatory subunits is the cAMP-dependent protein kinase (PKA) which is also a prototype for second messenger activated protein kinases. This enzyme consists of a heterotetramer of two catalytic (C) and two regulatory (R) subunits. Upon binding of two molecules of second messenger (cAMP) in each R subunit, the catalytic subunits are released and active. Both of the catalytic and the regulatory subunits several isoforms exist. The combination of catalytic and regulatory subunits determines the localization of the holoenzyme and also the substrate spectrum that is available for phosphorylation. The consensus pattern necessary to be present in the substrate for PKA action is RRXS/T where X can be any amino acid.

The casein kinase II comprises another examples for holoenzymes that consist of catalytic and regulatory subunits. Other kinases that are activated by second messengers are cGMP-dependent protein kinase and Protein kinase C (PKC) which is activated by diacylglycerol, which in turn is produced by phospholipases by cleavage of phosphatidylcholine.

Receptor kinases usually consists of an extracellular domain which can bind effector molecules (e.g. growth factors and hormones) and transfer the stimulus to the intracellular domain of these proteins which usually is a protein tyrosine kinase. Other tyrosine kinases lack an extracellular domain but are associated with receptors which transfer the signal after effector binding by activating the associated protein kinase enzyme (e.g. Src kinase family; Src, Blk, Fgr, Fyn, Lck Lyn, Yes and Janus kinase family; Jak1-3, Tyk2).

Dysfunction of kinases, e.g. caused by non-functioning regulation, can be the cause of inflammatory diseases and uncontrolled proliferation. v-Src which is a truncated version of the C-Src protooncogene tyrosine kinase is a classical example for this process as v-Src does not contain the regulatory domain of the cellular gene and is thus constitutively active.

Several categories of proteins are coded for by clones of the invention within the overall group of "Signal transduction" and include, among others, the following:

Neurocalcin (Recoverin): Neurocalcin is a $\text{Ca}(2+)$ -binding protein with three putative $\text{Ca}(2+)$ -binding domains (EF-hands). In cattle, 6 isoforms are differentially expressed in the central nervous system, retina and adrenal gland. Homology with recoverin indicates involvement in Ca^{2+} dependent activation of guanylate cyclase.. These proteins can find application in modulating/blocking the guanylate cyclase-pathway. Diseases associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with these proteins include as reported by OMIN 1) autosomal dominant cone dystrophy (OMIN *600364); 2) cone dystrophy 3 (OMIN *600364); 3) cancer associated retinopathy (OMIN *179618). Clones in this category include: fbr2_23b21.

Proteins with a WW Domain: Proteins that contain a WW domain which has been originally described as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes. Examples of proteins containing the WW domain are Dystrophin, Utrophin, vertebrate YAP protein (binds the SH3 domain of the Yes oncoprotein), murine NEDD-4 (embryonic development and differentiation of the central nervous system), IQGAP (human GTPase activating protein acting on ras). Therefore these proteins should be involved in intracellular signal transduction. Diseases associated (as

potentially diagnostic, therapeutic, causative, and/or related, etc...) with these proteins include as reported by OMIN 1) Muscular Dystrophy, Pseudohypertrophic Progressive Duchenne and Becker Types (OMIN *310200). Clones in this category include: fbr2_23n16.

Protein substrates for cAMP-dependent protein kinase: Acting as a choride channel or chloride channel inhibitor these proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) as reported by OMIN with Cystic Fibrosis (OMIN #219700). Clones in this category include fbr2_82i17.

Sphingosine kinase: Sphingosine kinase is a new type of lipid kinase, which is regulated by growth factors. The enzyme phosphorylates sphingosine, which subsequently exerts intracellular and extracellular actions. Intracellularly, sphingosine 1-phosphate (SPP) promotes proliferation and inhibits apoptosis. In yeast, survival of cells exposed to heat shock indicates is dependent on SPP. Extracellularly, SPP inhibits cell motility and influences cell morphology, effects that appear to be mediated by the G protein-coupled receptor EDG1. These proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) as reported by OMIN with Gaucher Disease, Type I (OMIN *230800). Clones in this category include fbr2_82m6.

Vanilloid Receptors: VR1 seems to play an important role in the activation and sensitization of nociceptors. It is the receptor for e.g. capsaicin, a selective activator of nociceptors, a natural product of capsicum peppers. Related can find application as a target for the development of new nociception-modulating drugs. Clones in this category include tes3_20k2.

RCC1 (Regulator of chromosome condensation): RCC1 (regulator of chromosome condensation) is a eukaryotic protein which binds to chromatin and interacts with ran, a nuclear GTP-binding protein. RCC1 promotes the exchange of bound GDP with GTP, acting as a guanine-nucleotide dissociation stimulator. These proteins can find application in the regulation of gene expression by activation of nuclear GTP-binding proteins. The X-linked retinitis pigmentosa is a result of a defect GTPase regulator, which contains a RCC1-type repeat. OMIN also reports that RCC1 has associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with retinitis pigmentosa (OMIN *312610). Clones in this category include tes3_21d4.

Ras inhibitor proteins: Ras is a signal transducing molecule involved in the receptor tyrosine kinase/RAS/Map kinase signalling cascade. Ras proteins bind GDP/GTP and show

intrinsic GTPase activity. Mutations in ras, which change aa 12, 13 or 61 activate the potential of ras to transform cultured cells and are implicated in a variety of human tumours. Ras inhibitor proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with many disease processes as reported by OMIN including: 1) Tumors of the lung, breast, brain, pituitary, pancreas, bone, skin, bladder, kidney, ovary, prostate and lymphocyte, Melanoma (OMIN *600160); 2) X-linked non-specific mental retardation (OMIN *300104); 3) adenomatous polyposis of the colon (OMIN *175100); 4) Beckwith-Wiedemann Syndrome (#130650); and 5) Major affective disorder 1 (OMIN *125480). Clones in this category include utel_22g21.

Mammalian proteins cornicon involving the EGF-receptor: Cornicon proteins are part of a signal transduction pathway involving the EGF-receptor. The EGF-receptor has been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Familial hypercholesterolemia (OMIN 143890); 2) Leprechaunism (OMIN #246200); 3) Hemophilia B (OMIN *306900); 4) Ectodermal dysplasia 1; 5) Kartagener syndrome (OMIN *244400) and 6) Glioma of the brain (OMIN *137800).). Clones in this category include utel_22e12.

Transmembrane proteins

Membrane region prediction was effected using the ALOM2 software (Klein et al., 1985; version 2 by K. Nakai). Similar to many other methods, the Kyte & Doolittle (1982) amino acid hydrophobicity scale is used in ALOM2 as the primary variable for classifying sequences in terms of their localization. High prediction accuracy is achieved through the system of intelligent decision rules and the utilization of a carefully selected training data set. The method also generates reliability estimates which makes it possible to distinguish between membrane-spanning proteins (I, intrinsic) and globular proteins with regions of high hydrophobicity buried in the core.

For a protein of length L , the block of length l with maximum hydrophobicity is found:

$$\max H = \max_{k=1, \dots, L-l+1} (1/l) \sum_{i=k}^{k+l-1} H_i$$

where H_i represents the hydrophobicity of an individual residue.

Let $P(I/\max H)$ and $P(E/\max H)$ be the conditional probabilities that a protein is integral or peripheral, respectively, given its value of maximal hydrophobicity $\max H$, and let $P(I)$ and $P(E)$ be the prior probabilities of intrinsic and extrinsic membrane proteins estimated from the training set. Then a sequence is assigned to E if

$$P(E/\max H) > P(I/\max H)$$

or, after applying the Bayes rule,

$$P(E)P(\max H/E) > P(I)P(\max H/I),$$

where the conditional probabilities $P(\max H/E)$ and $P(\max H/I)$ can be determined based on the estimates of probability distributions of $\max H$ in both groups.

Discriminant analysis allows to simplify this task by calculating the odds $P(E/\max H):P(I/\max H)$ as e^b , where b is the left-hand side of a linear or quadratic inequality. For example, for the window of length 17, the protein is allocated to the peripheral category E based on the empirically derived quadratic inequality:

$$1.05(\max H)^2 + 12.30\max H + 17.49 > 0,$$

whereas the optimal inequality for assigning membrane proteins (category I) is linear:

$$-9.02\max H + 14.27 > 0$$

The odds parameter can be made more or less stringent. For example, one can require odds at least 1:10 for a protein to be classified as integral. This leads to higher selectivity but less sensitivity.

The boundaries of membrane-spanning regions in putative membrane proteins are detected by means of an iterative procedure whereby the most hydrophobic region corresponding to the value $\max H$ is considered to be membrane and removed from the sequence. The classification procedure is then repeated again for the remaining sequence, and, if such a protein is again classified as integral, the next most hydrophobic region is considered.

Reference: Klein, P., Kanehisa, M., DeLisi, C. (1985) The detection and classification of membrane-spanning proteins. *Biochem Biophys Acta* **815**: 468-476

Transcription factors

Purified eukaryotic RNA polymerase II is unable to initiate promoter-specific transcription. A family of factors that collectively confer RNAPII promoter specificity is known as the general transcription factors (GTFs). They include the TATA-binding Protein (TBP) TFIIB, TFIIE, TFIIF and TFI IH. These factors are conserved among all eukaryotes.

RNAPII complexes containing the entire set of GTFs or a subset of GTFs together with other proteins have been isolated from mammalian and yeast cells. Although purified RNAPII and GTFs are sufficient for promoter-specific initiation, this system fails to respond to activators. This is mediated by a further complex termed mediator complex which associates with the carboxy-terminal heptapeptide domain (CTD) of the largest subunit of RNAPII.

Purification of human RNAPII complexes resulted in two distinct forms of human RNAPII after analysis of functional properties. One complex contained chromatin remodeling activities but was devoid of GTFs. The other complex did not contain factors that modify chromatin but contained a subset of SRB/mediator subunits and GTFs and other polypeptides that mediate transcriptional activation, a scenario similar to that reported for yeast.

A complex designated NAT (~20 SU) for negative regulator of transcription contains RNAPII, Cdk8, homologs of the yeast mediator complex as well as Rgr1 and Srb10/11 known as negative regulators of transcription.

A complex with striking similar structural and functional properties to NAT has been identified designated SMCC (~15 SU) (SRB/mediator coactivator complex), that can also mediate transcriptional activation.

The SMCC complex includes all reported NAT subunits including subunits of the TRAP complex. TRAP is a coactivator complex isolated on the basis of its interaction with the thyroid hormone receptor. Another coactivator complex DRIP, isolated on the basis of its

ability to interact with the vitamin D3 receptor, contains novel subunits as well as subunits of NAT/SMCC and TRAP complexes.

The effects of each of these coactivator complexes is dependent on the TFIID complex. It is not known if the TAF subunits of TFIID are required. It is likely that new coactivator complexes will be uncovered containing both novel and previously defined components.

Beside the huge amount of transcription factors which can be part of the RNAIIP holoenzyme or the coactivator complexes there is an even larger quantity of specific transcription factors binding to promoter elements within the DNA sequences of a given gene leading to activation or repression of transcription. A broad range of cellular responses like differentiation, proliferation, cell death and others are elicited through activating or repressing the transcription of target genes.

There are at least five superclasses of transcription factors:

1. Superclass contains members with characteristic basic domains:

Members are:

Leucine zipper factors, where the basic domain is followed by a leucine zipper of repeated leucine residues at every seventh position. The zipper mediates protein dimerization as a prerequisite for DNA-binding.

Helix-loop-helix factors (bHLH) contain a DNA-binding basic region followed by a motif of two potential amphipathic alpha-helices connected by a loop of variable length also mediating dimerization.

Factors with a combination of Helix-loop-helix and leucine zipper.

Further members of this superclass are NF- κ B, RF-X, and bHLH like proteins.

2. Superclass comprises factors containing zinc-coordinating DNA-binding domains.

Members are:

Proteins with Cys4 zinc finger of nuclear receptor type, where two such motifs differing in size, composition and function are present in each receptor molecule. Each finger comprises 4 cysteine residues coordinating one zinc ion. The second half including the second cysteine pair has alpha-helix conformation and the helix of the first finger binds to the DNA through the major groove. The sequence between the first two cysteines of the second finger mediates dimerization upon DNA-binding. This class includes the steroid hormone receptors and the thyroid hormone receptor-like factors. Other diverse cys4 zinc fingers have a motif of GATA-type.

Proteins with Cys2His2 zinc finger domain(s). Each finger comprises 2 cysteine and 2 histidine residues coordinating one zinc ion, and in some cases one histidine is replaced by another cysteine. The zinc ion is essential for DNA-binding.

Proteins with Cys6 cysteine-zinc cluster(s). Six cysteine residues coordinate two zinc ions, i. e. two of the thiol groups are coordinating two zinc ions each. Present in many fungal regulators.

Zinc fingers of alternating composition.

3. Superclass contains factors of helix-turn-helix type.

Members are:

Proteins with homeo domains. Homeo domains are three consecutive alpha-helix structures. Helix 3 contacts mainly the major groove of the DNA, some contacts at the minor groove are observed as well. Helix 2 and 3 resemble the helix-turn-helix structure of prokaryotic regulators.

Proteins with Paired box domain(s). This is a DNA-binding domain of approximately 130 amino acid residues. Its N-terminal half is basic, its C-terminal half is highly charged in general. It probably comprises 3 alpha-helices.

Proteins with Fork head / winged helix domain(s). This domain was identified by homology between HNF-3A and fkh. The domain comprises approx. 110 AA. Analysis of the crystal structure has revealed a compact structure of three alpha-helices, the third alpha-helix

being exposed towards the major groove of the DNA. The domain also exerts minor groove contacts. Upon binding to DNA, it induces a bend of 13 degree.

Heat shock factors

Proteins with Tryptophan clusters. The tryptophan clusters comprise several tryptophan residues with a spacing of 12-21 amino acid residues; the subclass of myb-type DNA-binding domains typically exhibit a spacing of 19-21 amino acid residues.

Proteins with TEA domain(s). The TEA domain has been identified as a region which is conserved among the transcription factors TEF-1, TECl and abaA. This domain in TEF-1 has been shown to interact with DNA, although two additional regions may also contribute to DNA-binding. It is predicted to fold into three alpha-helices, with a randomly coiled region of 16-18 amino acid residues between helices 1 and 2, and a short stretch between helices 2 and 3 of 3-8 residues.

4. Superclass contains beta-Scaffold Factors with Minor Groove Contacts

Members are:

Proteins with RHR (Rel homology) region.

The structure of the Rel-type DBD exhibits a bipartite subdomain structure, each subdomain comprising a beta-barrel with five loops that form an extensive contact surface to the major groove of the DNA. Particularly, the first loop of the N-terminal subdomain (the highly conserved recognition loop) performs contacts with the recognition element on the DNA, but other loops are involved. The fact that the main DNA-contacts are made through loops has been suggested to provide a high degree of flexibility in binding to a range of different target sequences. Augmenting interactions are achieved by two alpha-helices within the N-terminal Part that form strong minor groove contacts to the A/T-rich center of the B-element. In p65, the sequence between both alpha-helices is much shorter and even helix 2 is truncated. The second, C-terminal domain is necessary mainly for protein dimerization.

p53 proteins

MADS (MCM1-agamous-deficiens-SRF) box proteins. Proteins of this class comprise a region of homology. The DNA-binding domain also comprises the dimerization capability. In the DNA-bound dimer (shown for SRF), two antiparallel amphipathic alpha-helices (alpha-I), form a coiled coil and are oriented approximately parallel on the minor groove. These helices make minor and major groove contacts, the N-terminal extensions form minor groove contacts. The bound DNA is bent and wrapped around the protein. It exhibits a compressed minor groove in the center and widened minor groove in the flanks.

Beta-Barrel alpha-helix transcription factors.

TATA-binding proteins

HMG proteins

Proteins of this class comprise a region of homology with the chromosomal non-histone HMG proteins such as HMG1. This region comprises the DNA-binding domain which in some instances such as HMG1 mediates sequence-unspecific, in other cases such as LEF-1 sequence-specific binding to DNA. This domain exhibits a typical L-shaped conformation made up of 3 alpha-helices and an extended N-terminal extension of the first helix. The latter together with helix 1, which contains a kink, form the long arm of the L, whereas helices 1 and 2 form the short arm. Binding to the minor groove induces a sharp bending of the DNA by more than 90 degree, away from the bound protein. The overall topology of the DNA-protein complexes resembles somewhat that of the TBP-TATA box complex.

Heteromeric CCAAT factors

Proteins with Grainyhead domain(s)

Cold-shock domain factors. Cold-shock domain proteins are characterized by a highly conserved region first found in prokaryotic cold-shock proteins. This domain is a single-stranded nucleic acid-binding structure interacting with DNA or RNA. It consists of an antiparallel five-stranded beta-barrel, the strands of which are connected by turns and loops. Within this structure, a three-stranded beta-strand contains a conserved RNA-binding motif, RNPI. Not all CSD proteins are transcription factors. Those which specifically bind to a

certain-sequence are termed Y-box proteins. Proteins of this class were previously called protamine-like domain proteins because of having a highly positively charged domain with interspersed proline residues.

Proteins with Runt homology domain

The members of this transcription factor class have been identified on the basis of their homology to a defined region within the *Drosophila* protein Runt. The runt domain is part of the DNA-binding domain of these factors. It consists mainly of beta-strands, does not contain alpha-helical regions and seems to be most similar to the palm domain found in DNA polymerase beta (rat).

5. Superclass contains other transcription factors like Copper fist proteins, HMGI(Y), STAT, Pocket domain proteins and Ap2/EREBP-related factors.

The classification of transcription factors originates from TRANSFAC database:

<http://transfac.gbf.de/TRANSFAC/>

Reference: Heinemeyer

Several categories of proteins are coded for by clones of the invention within the overall group of "Transcription Factors" and include, among others, the following:

Dcoh: Dcoh is a bifunctional protein, complexed with bioppterin. It serves as dimerization cofactor of hepatocyte nuclear factor-1 and catalyzes the dehydration of the bioppterin cofactor of phenylalanine hydroxylase. The Dcoh protein has been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) hyperphenylalanemia (OMIN 126090, #264070). Clones in this category include fkd2_46k12.

Signal transducing proteins: Beta-transducin subunits of G-proteins contain WD-40 repeats. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. Due to the zinc finger the novel protein seems to be a new molecule involved in signal transduction and transcription. These proteins have been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) essential hypertension (OMIN *139130). Clones in this category include utel_1i2.

* * *

The invention, therefore, specifically contemplates the following assemblages of materials, which track the above-identified fourteen functional groupings, that are useful in practicing the profiling aspects of the invention. One type of assemblage is nucleic acid-based and can include the following groupings of sequences and their derivatives: all sequences; human fetal brain sequences; brain derived sequences; human fetal kidney library sequences; kidney derived sequences; human mammary carcinoma library sequences; mammary carcinoma derived sequences; human testis library sequences; testes derived sequences; cell cycle genes; cell structure and motility genes; differentiation and development genes; intracellular transport and trafficking genes; metabolism genes; nucleic acid management genes; signal transduction genes; transmembrane protein genes; and transcription factor genes. Other assemblages contain proteins or their corresponding antibodies or antibody fragments, divided along the same groupings.

Database Applications

Because they are human genes and gene products, the inventive molecules are useful as members of a database. Such a database may be used, for example, in drug discovery and rationale drug design or in testing the novelty and non-obviousness of newly sequenced materials. In addition, they are particularly suited in designing variants for the profiling (and other) applications described herein. Hence, the following discussion of electronic embodiments applies equally to such variants, which, naturally, will be generated and stored using a computer using known methodologies.

Accordingly, one aspect of the invention contemplates a database of at least one of the inventive sequences stored on computer readable media. Again, the individual sequences may be grouped with regard to the individual functional and structural groups mentioned above. While the individual sequences of a database may exist in printed form, they are preferably in electronic form, as in an ascii or a text file. They may also exist as word processing files or they may be stored in database applications like DB2, Sybase, Oracle, GCG and GenBank. One skilled in the art will understand the range of applications suitable for using and storing the electronic embodiments of the invention.

"Computer readable media" refers to any medium which can be read and accessed by a computer. These include: magnetic storage media, like floppy discs, hard drives and magnetic tape; optical storage media, like CD-ROM; electrical storage media, like RAM

and ROM; and hybrids of these categories, like magnetic/optical storage media. One skilled in the art will readily understand the scope of computer readable media and how to implement them.

Biological Activities and Assays for Implementing Therapeutic and Diagnostic Applications

This section provides assays for biological activity that are useful in characterizing and quantifying the biological activity of the inventive molecules and their derivatives, which is relevant to the pharmacological effects of the inventive molecules. As used in this section, it will be understood that "protein" may also refer to the inventive antibodies (including fragments).

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M + (preB M +), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin gamma, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-Nordan, R. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9-Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to modify immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the

tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient.

The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and beta 2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of

Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the

treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and

cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112 (Maibach, H. I. and Rooye, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. *Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle

stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin alpha family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- beta group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of

cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such

receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of

cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in

a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Particular Applications for Certain Clones

The following sets out a non-exclusive list of applications for certain embodiments of the invention. In the interest of economy, applications relevant to multiple embodiments are not duplicated in this list. Other embodiments described in below have similar characteristics, as described therein. The artisan is directed, therefore, to this section for similar descriptions of the functions of other embodiment.

Testes

htes3_15c24: The new protein can find application in modulation of 2-hydroxyacid dehydrogenases-dependent pathways and as a new enzyme for biotechnologic production processes.

htes3_15i5: The new protein can find application in modulating the structure of the human spermatozoa radia spoke head and modulation of sperm motility in men.

htes3_15k11: The novel protein contains a protein kinase ATP-binding region signature and a serine/threonine protein kinase active-site signature. The new protein can find application in modulation of intracellular signal pathways dependent on this kinase.

htes3_17n12: The new protein can find application in modulating/blocking the expression of SOX-controlled genes.

htes3_20k2: The new protein can find application as a target for the development of new nociception-modulating drugs.

htes3_20m18: The new protein can find application in modulation of mitochondrial DNA replication and maintenance.

htes3_20d4: The new protein can find application in the regulation of gene expression by activation of nuclear GTP-binding proteins. The X-linked retinitis pigmentosa is a result of a defect GTPase regulator, which contains a RCC1-type repeat.

htes3_21j15: NY-CO-33 is a protein recognised by autologous antibodies of human colon cancer patients. The novel protein contains 4 C2H2 Zinc fingers and is a new putativ transcription factor. The new protein can find application in modulating/blocking the expression of genes controlled by this transcription factor.

The new protein can find application in modulating chromosome transport in mitosis and meiosis and modulation of cell division.

htes3_26g22: The new protein can find application in modulating chromosome transport in mitosis and meiosis and modulation of cell division. The novel TBP-binding protein is considered to participate in transcription regulation through the interaction with TBP. The new protein can find application in modulation of gene transcription.

htes3_21i16: The new protein can find application in modulation of protein translocation into the endoplasmic reticulum.

htes3_27d1: The novel protein can find application in modulation of ubiquitin- and protein metabolism in cells.

htes3_2m18: The novel protein can find application as multifunctional nuclease / exoribonuclease.

htes3_35b4: The new protein can find application in modulation of the mitotic spindle.

htes3_35b5: The novel protein can find application in modulating the v-ATPase activity in endocytic and secretory organelles.

htes3_35e21: Due to the close relationship to human interleukin-7, the novel interleukin is expected to act as a new growth factor for human B lineage cells. Additionally, the protein should induce the gene rearrangement of the T-cell receptor repertoire, leading to thymocyte commitment, and subsequently induce both cytotoxic T-cell- and lymphocyte-activated killer cells. This new interleukin could find clinical application in a variety of conditions of hematolymphopoietic failure and different tumours, because of its recruitment of B cell lineage cells, cytotoxic T-cell- and lymphocyte-activated killer cells.

htes3_35k16: Therefore it is a new fatty acid-CoA synthetases/ligase with unknown substrate. The new protein can find application in modulation of fatty acid metabolism and as a new enzyme for biotechnologic production processes.

htes3_35n12: The new protein can find application in modulation of ADP-transport and energy metabolism in cells/mitochondria.

htes3_35n9: The new protein can find application in modulation of carboxylester metabolism and as a new enzyme for biotechnologic production processes.

htes3_35p22: The novel protein is closely related to human tre-2 and other enzymes involved in the degradation of ubiquitinated proteins. The human tre-2 oncogene encodes a deubiquitinating enzyme, indicating a role for the ubiquitin system in mammalian growth control. The novel protein can find application in cancer diagnostics and treatment, and in regulating protein stability and growth control via regulation of ubiquitination.

htes3_4h6: The novel kinesin protein can find application in modulating the function of kinesin and modulating intracellular transport via/on microtubules.

htes3_72k15: FGD1-related F-actin-binding protein (Frabin/FGD1) is a novel F-actin-binding protein. The gene locus *fgd1* seems to be responsible for faciogenital dysplasia or Aarskog-Scott syndrome. Frabin binds F-actin and shows F-actin-cross-linking activity. Overexpression of frabin in Swiss 3T3 cells and COS7 cells induces cell shape change and c-Jun N-terminal kinase activation, as described for FGD1. Because FGD1 has been shown to serve as a GDP/GTP exchange protein for Cdc42 small G protein, it is likely that frabin is a direct linker between Cdc42 and the actin cytoskeleton. Cdc42p is an actin yeast, Cdc42p transduces signals to the actin cytoskeleton to initiate and maintain polarized growth and to mitogen-activated protein morphogenesis. In mammalian cells, Cdc42p regulates a variety of actin-dependent events and induces the JNK/SAPK protein kinase cascade, which leads to the activation of transcription factors within the nucleus. The novel protein seems to be the human orthologue of rat frabin.

The new protein can find application in modulating of cell structure and motility as well as modulation of the JNK/SAPK pathway.

htes3_72p16: As Mem3, the novel protein is similar to yeast VPS (vacuolar protein sorting) 35. The null allele of VPS35 results in yeast in a differential defect in the sorting of vacuolar carboxypeptidase Y (CPY), proteinase A (PrA), proteinase B (PrB), and alkaline phosphatase (ALP). The new protein can find application in modulation the sorting of proteins into different compartments.

htes3_7b22: The novel protein is related to paramyosin, a major structural component of thick filaments and invertebrate muscle. Paramyosins are promising antigens for immunization against several parasites, such as *Schistosoma mansoni*. The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamic.

htes3_7j3: The new protein is closely related to C-Tak1 and therefore should be involved in cell-cycle regulation, too. The new protein can find application in modulating/blocking the cell cycle.

htes3_7p9: The nuclear domain (ND)10 also described as POD or Kr bodies is involved in the development of acute promyelocytic leukemia and virus-host interactions. The NDP52 protein is part of this complex structure. In vivo, NDP52 is transcribed in all human tissues, but is redistributed upon viral infection and interferon treatment. ND10 plays an important role in the viral life cycle. The novel protein is similar to NDP52. It contains three leucine zippers and a RGD cell attachment site. This protein seems to be a novel part of the ND819) complex. The new protein can find application in modulation of viral infections and tumour events.

htes3_8m10: The poly(A)-binding protein (PABP) binds to the messenger (mRNA) 3'-poly(A) tail found on most eukaryotic mRNAs and together with the poly(A) tail has been implicated in governing the stability and the translation of mRNA. The new protein can find application in modulation of mRNA translation and processing/stability.

Kidney

hfk2_24b15: The new protein can find application in modulation of hexose metabolism pathways and as a new enzyme for biotechnologic production processes.

hfk2_24n20: The new protein seems to be part of the signalling pathway between tyrosine kinases and the membrane/cyto skeleton. The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamics.

hfk2_3o17: The new protein can find application in modulation of the respiratory electron transport chain pathways of mitochondria.

hfk2_46j20: The new protein can find application in modulating the homoprotocatechuate degradative pathway and as a enzyme for biotechnologic production processes.

hfk2_46k19: The new protein can find application in modulating/blocking the expression of genes controlled by the hepatocyte nuclear factor-1.

hfk2_46m4: SAR1 proteins are involved in vesicular transport between the endoplasmic reticulum and the Golgi apparatus.

hfk2_46k14: rab6 is a ubiquitous ras-like GTPase involved in intra-Golgi transport. The new protein can find application in modulating the transport of vesicles inside the Golgi apparatus.

Uterus Associated:

hutel_18i19: The SREBP-2 protein is embedded in the membranes of the nucleus and endoplasmic reticulum. In cholesterol-depleted cells the proteins are cleaved to release soluble NH2-terminal fragments that enter the nucleus and activate genes encoding the low density lipoprotein receptor and enzymes of cholesterol synthesis. The new protein is a putative transcription factor capable of protein-protein interaction via a lim domain and additionally shows similarity to the common sunflower transcription factor SF3.

hutel_18i1: The novel protein is similar to several 40S ribosomal proteins and therefore seems to part of the corresponding ribosome sub-unit.

hutel_19g22: The new protein can find application in modulation of tissue-calcification, especially the uterus.

hutel_19h17: The new protein can find application in modulating the response of cells to oxysterols.

hutel_20b19: The novel protein seems to be a novel enzyme with sarcosine oxidase activity. The new protein can find application in modulation of sarcosine metabolism and as a new enzyme for biotechnologic production processes.

hutel_20g21: The novel protein seems to be a new ras inhibitor protein. The new protein can find application in modulating/blocking ras dependent signal transduction pathways.

hutel_20h13: The novel protein is a new human alpha-adaptin. The new protein can find application in modulating endocytosis and vesicle trafficking in cells.

hutel_20m11: The new protein can find application in modulating/blocking the activity of protein phosphatase-1 and in modulating the cell cycle.

hutel_20m24: This protein is a putative mannosyl transferase that is involved in the assembly of the core oligosaccharide Glc3Man9GlcNAc2. The new protein can find application in modulation of glycosylation of proteins and as a new enzyme for biotechnologic production processes.

hutel_22e12: The new protein can find application in modulating the cornichon modulated signal transduction way and also the EGF receptor signaling processes.

hutel_23e13: The novel protein contains a serine protease of the subtilase family with an aspartic acid-containing active site. The new protein can find application in modulation of proteinase activity in cells and as a new enzyme for proteomics and biotechnologic production processes.

hutel_24j6: The new protein can find application in modulation of cell-cell-adhesion.

hutel_24h3: The new protein can find application as a useful marker for chondro-osteogenic cell differentiation and for the modulation of chondro-osteogenic cell differentiation.

Fetal Brain:

hfbr2_16c16: The new protein can find application in modulating/blocking of cyto skeleton-membrane protein interaction.

hfbr2_23b21: The new protein can find application in modulating/blocking the guanylate cyclase-pathway.

hfbr2_23b10: The new protein can find application in modulation of splicing.

hfbr2_2b5: The novel protein contains the typical (xxG)_n repeat of collagen proteins and a Pfam von Willebrand factor type A domain. Therefore, the protein seems to be a new collagen alpha chain. The new protein can find application in modulation of connective tissue, bone and cartilage development and maintainance.

hfbr2_2c17: The new protein can find application in modulating/blocking G-protein-dependent pathways.

hfbr2_2d15: The new protein can find application in modulating early spermatogenesis.

hfbr2_2i17: The new protein can find clinical application in modulating the transport of glycoproteins inside cells, especially of the LDL receptor.

hfbr2_2k14: Tumour-suppressor genes are known to be involved in the control of cell growth and division, interacting with proteins which control the cell cycle. The N33 gene is significantly methylated in tumour cells, a mechanism by which tumor-suppressor genes are inactivated in cancer. In addition, the novel protein contains a RGD cell attachment site. Therefore the novel protein is a new putative tumour-suppressor gene.

hfbr_3c18: RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. The novel protein contains a DEAD-box and is a new member of this subgroup.

hfbr_3g8: The new protein can find application modulating NAT assembly and action and therefore be important in metabolism of drugs and environmental mutagens.

hfbr2_62b11: The rac small GTPase is associated with type-I phosphatidylinositol 4-phosphate 5-kinase and regulating the production of phosphatidylinositol 4,5-bisphosphate. The new protein is expected to activate p21rac-related small GTPases.

hfbr2_62o17: The new protein can find application in modulation of cholesterol binding and transport by LDL-receptors and LDL-binding proteins.

hfbr_6b24: The new protein can find application in modulation of rhamnose metabolism and as a new enzyme for biotechnologic production processes.

hfbr_72b18: The new protein can find application in modulating DNA repair and mutagenesis.

hfbr_78c4: The new protein can find application in modulating/blocking the response of cells to interferons.

hfbr_78k24: These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins. The new protein can find application in modulation of protein stability/degradation in cells.

hfbr_82e4: The new protein can find clinical application in modulating/blocking calmodulin-mediated pathways in human neuronal cells.

VARIANTS OF THE INVENTIVE DNA MOLECULES

Variants in General

"Variants," according to the invention, include DNA and/or protein molecules that resemble, structurally and/or functionally, those set forth in herein. Variants may be isolated from natural sources ("homologs"), may be entirely synthetic or may be based in part on both natural and synthetic approaches.

The section set forth below presents various structural and functional characteristics of molecules within the invention. Preferred molecules are characterized by a combination of one or more of these characteristics. For instance, some preferred molecules are described with reference to at least two structural characteristics, while others may be described with reference to at least one structural and at least one functional characteristic.

It will be recognized by the skilled artisan that structure ultimately defines function, *i.e.* the functions of the molecules described herein derives from the structures of those

molecules. Accordingly, the structural variants described below that bear the closest structural relationship (as variously defined below) to the inventive molecules are the variants that most likely will preserve biological function. This relationship between structure and function will guide the skilled artisan in identifying the preferred embodiments of the invention.

Splicing Variants

It is well-known that eukaryotic structural genes are comprised of both protein coding and non-coding portions. When the messenger RNA is transcribed from the DNA template, it contains introns, which are non-coding, and exons, which are coding. In order to form a translation competent mRNA, the introns must be "spliced" out of this initial pre mRNA.

Specific sequences within the pre mRNA represent "splice junctions" that direct the cellular splicing machinery to the appropriate position. The splice junctions are loosely conserved sequence regions of the pre mRNA, which almost invariably begin with GT and end with AG (DNA perspective). The 5' end of the splice junction typically contains about nine somewhat conserved residues, for example, C/AAGTA/GAGT. The 3' end usually contains a pyrimidine rich stretch of at least about 11 nucleotides, followed by NC/TAGG. Splicing occurs before the GT and after the AG. Mount, *Nucleic Acids Res.* 10:459-72 (1982).

Interestingly, exons often correspond to discrete functional domains of the protein product. The intron/exon arrangement thus creates a linear array of nucleotides which can be correlated to discrete, and often interchangeable, functional protein fragments. Go, *Nature* 291:90-92 (1981); Branden *et al.*, *EMBO J.* 3:1307-10 (1984). This linear arrangement creates the possibility of generating multiple different full length proteins by rearranging the order of the different functional portions in the array. For example, if a set of exons are arranged 1-2-3-4, where (-) represents the introns separating the exons, a splicing event need not simply produce 1234, but may produce 123, 134, 124 and so on. Production of different mRNA products in this way is commonly called "alternative splicing." Andreadis *et al.*, *Ann. Rev. Cell Biol.* 3:207-42 (1987).

Some of the present DNA molecules can be represented in modular fashion in terms of their coding regions. Essentially, these modules are exons (though each "exon" may in fact be made up of several exons), which may be combined in different ways to form a variety of

different DNA molecules, each encoding a different functional protein. Splicing variants are indicated below.

Degenerate Variants

One aspect of the present invention provides "degenerate variants" of the nucleic acid fragments of the present invention. A "degenerate variant" is a nucleotide fragment which differs from those of inventive molecules by nucleotide sequence, but due to the degeneracy of the genetic code, encodes an identical polypeptide sequence.

Given the known relationship between DNA sequences and the proteins they encode, degenerate variants typically are described by reference to this relationship. It is well known that the degeneracy of the genetic code results in many possible DNA sequences which encode a particular protein. Indeed, of the three bases which comprise an amino acid-encoding triplet, the third position, and often the second, almost always may vary. This fact alone allows for a class of variant DNA molecules which encode protein sequences identical to those disclosed herein, yet have about 30% sequence variation. In other words, the variant DNA molecules are about 70% identical to the inventive DNAs, having no additional or deleted sequences. Thus, one aspect of the invention provides degenerate variant DNA molecules encoding the inventive protein sequences.

In one embodiment, these variants have at least about 70% sequence identity with the DNA molecules described herein. In a preferred embodiment, these variants have at least about 80% sequence identity to the inventive molecules. In a more preferred embodiment these variants have at least about 90% sequence identity with the inventive molecules.

Conservative Amino Acid Variants

Variants according to the invention also may be made that conserve the overall molecular structure of the encoded proteins. Given the properties of the individual amino acids comprising the disclosed protein products, some rational substitutions will be recognized by the skilled worker. Amino acid substitutions, *i.e.* "conservative substitutions," may be made, for instance, on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine;

(c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α -helices. Similarly, certain amino acids, such as alanine, cysteine, leucine, methionine, glutamic acid, glutamine, histidine and lysine are more commonly found in α -helices, while valine, isoleucine, phenylalanine, tyrosine, tryptophan and threonine are more commonly found in β -pleated sheets. Glycine, serine, aspartic acid, asparagine, and proline are commonly found in turns. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative amino acid variants.

As used herein, "sequence identity" between two polypeptide sequences indicates the percentage of amino acids that are identical between the sequences. "Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions.

Functionally Equivalent Variants

Yet another class of DNA variants within the scope of the invention may be described with reference to the product they encode. As shown below, some of the inventive DNA molecules encode a protein having a degree of homology with known proteins, or protein domains. It is expected, therefore, that they will have some or all of the requisite functional features of such molecules. These "functionally equivalent variants" products are characterized by the fact that they are functionally equivalent, with respect to biological activity, to certain known molecules.

The instant invention provides information on common structural motifs, including consensus sequences that will guide the artisan in constructing functionally equivalent variants. It will be understood that the motifs, identified for each inventive protein, may be modified within the identified consensus sequences. Thus, the invention contemplates the proteins disclosed herein that contain variability in the consensus sequences identified, and the invention further contemplates the full range of nucleic acids encoding them, and the complements of those nucleic acids.

Hybridizing Variants

DNA variants within the invention also may be described by reference to their physical properties in hybridization. One skilled in the field will recognize that DNA can be used to identify its complement and, since DNA is double stranded, its equivalent or homolog, using nucleic acid hybridization techniques. It will also be recognized that hybridization can occur with less than 100% complementarity. However, given appropriate choice of conditions, hybridization techniques can be used to differentiate among DNA sequences based on their structural relatedness to a particular probe. For guidance regarding such conditions see, for example, Sambrook *et al.*, 1989, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, N.Y.; and Ausubel *et al.*, 1989, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Green Publishing Associates and Wiley Interscience, N.Y.

Structural relatedness between two polynucleotide sequences can be expressed as a function of "stringency" of the conditions under which the two sequences will hybridize with one another. As used herein, the term "stringency" refers to the extent that the conditions disfavor hybridization. Stringent conditions strongly disfavor hybridization, and only the most structurally related molecules will hybridize to one another under such conditions. Conversely, non-stringent conditions favor hybridization of molecules displaying a lesser degree of structural relatedness. Hybridization stringency, therefore, directly correlates with the structural relationships of two nucleic acid sequences. The following relationships are useful in correlating hybridization and relatedness (where T_m is the melting temperature of a nucleic acid duplex):

- a. $T_m = 69.3 + 0.41(G+C)\%$
- b. The T_m of a duplex DNA decreases by 1°C with every increase of 1% in the number of mismatched base pairs.
- c. $(T_m)_{\mu 2} - (T_m)_{\mu 1} = 18.5 \log_{10} \mu 2 / \mu 1$
where $\mu 1$ and $\mu 2$ are the ionic strengths of two solutions.

Hybridization stringency is a function of many factors, including overall DNA concentration, ionic strength, temperature, probe size and the presence of agents which disrupt hydrogen bonding. Factors promoting hybridization include high DNA

concentrations, high ionic strengths, low temperatures, longer probe size and the absence of agents that disrupt hydrogen bonding.

Hybridization usually is done in two stages. First, in the "binding" stage, the probe is bound to the target under conditions favoring hybridization. Stringency is usually controlled at this stage by altering the temperature. For high stringency, the temperature is usually between 65°C and 70°C, unless short (<20 nt) oligonucleotide probes are used. A representative hybridization solution comprises 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100µg of non-specific carrier DNA. See Ausubel *et al.*, *supra*, section 2.9, supplement 27 (1994). Of course many different, yet functionally equivalent, buffer conditions are known. Where the degree of relatedness is lower, a lower temperature may be chosen. Low stringency binding temperatures are between about 25°C and 40°C. Medium stringency is between at least about 40°C to less than about 65°C. High stringency is at least about 65°C.

Second, the excess probe is removed by washing. It is at this stage that more stringent conditions usually are applied. Hence, it is this "washing" stage that is most important in determining relatedness via hybridization. Washing solutions typically contain lower salt concentrations. One exemplary medium stringency solution contains 2X SSC and 0.1% SDS. A high stringency wash solution contains the equivalent (in ionic strength) of less than about 0.2X SSC, with a preferred stringent solution containing about 0.1X SSC. The temperatures associated with various stringencies are the same as discussed above for "binding." The washing solution also typically is replaced a number of times during washing. For example, typical high stringency washing conditions comprise washing twice for 30 minutes at 55° C. and three times for 15 minutes at 60° C.

The present invention includes nucleic acid molecules that hybridize to the inventive molecules under high stringency binding and washing conditions. More preferred molecules (from an mRNA perspective) are those that are at least 50 % of the length of any one of those depicted in below. Particularly preferred molecules are at least 75 % of the length of those molecules.

Substitutions, Insertions, Additions and Deletions

In a general sense, the preferred DNA variants of the invention are those that retain the closest relationship, as described by "sequence identity" to the inventive DNA molecules. According to another aspect of the invention, therefore, substitutions, insertions, additions and deletions of defined properties are contemplated. It will be recognized that sequence

identity between two polynucleotide sequences, as defined herein, generally is determined with reference to the protein coding region of the sequences. Thus, this definition does not at all limit the amount of DNA, such as vector DNA, that may be attached to the molecules described herein. Preferred DNA sequence variants include molecules encoding proteins sharing some or all of any relevant biological activity of the native molecule.

In creating these variants, the skilled worker will be guided by reference to the protein structure. First, insertions and deletions in any recognized functional domain, above, generally should be avoided, except as noted below in the section entitled "Proteins," where this domain is discussed in detail. Alterations in such domains usually will be limited to conservative amino acid substitutions. In addition, where insertions and deletions are desired, this may be accomplished at the N- and/or C-terminus of the protein molecule (or the corresponding coding regions of the DNA). If insertions or deletions are made within the protein, deletions of major structural features usually should be avoided. Thus, a preferred place to make insertion or deletion variants is in non-structural regions, such as linker regions between two alpha helices.

"Substitutions" generally refer to alterations in the DNA sequence which do not change its overall length, but only alter one or more nucleotide positions, substituting one for another in the common sense of the word. One class of preferred substitutions, "degenerate substitutions," are those that do not alter the encoded amino acid sequence. Some substitutions retains 50%, 55%, 60% or 65% identity. Preferred substitutions retain at least about 70% identity, more preferably at least 70% or 75% identity, with the inventive DNAs. Some more preferred molecules have at least about 80% identity, more preferably at least 80% or 85% identity. Particularly preferred DNAs share at least about 90% identity, more preferably at least 90% or 95% identity.

"Insertions," unlike substitutions, alter the overall length of the DNA molecule, and thus sometimes the encoded protein. Insertions add extra nucleotides to the interior (not the 5' or 3' ends) of the subject DNAs. Preferred insertions are made with reference to the protein sequence encoded by the DNA. Thus, it is most preferred to provide an insertion in the DNA at a location that corresponds to an area of the encoded protein which lacks structure. For instance, it typically would not be beneficial, if the preservation of biological activity is desired, to provide an insertion within an alpha-helical region or a beta-pleated sheet. Accordingly, non-structural areas, such as those containing helix-breaking glycines

and proline residues, are most preferred sites of insertion. Other preferred sites of insertion are the splice sites, which are indicated above in the description of the inventive DNA molecules.

While the optimal size of insertions will vary depending upon the site of insertion and its effect on the overall conformation of the encoded protein, some general guides are useful. Generally, the total insertions (irrespective of their number) should not add more than about 30% (or preferably not more than 30%) to the overall size of the encoded protein. More preferably, the insertion adds less than about 10-20% (yet more preferably 10-20%) in size, with less than about 10% being most preferred. The number of insertions is limited only by the number of suitable insertions sites, and secondarily by the foregoing size preferences.

"Additions," like insertions, also add to the overall size of the DNA molecule, and usually the encoded protein. However, instead of being made within the molecule, they are made on the 5' or 3' end, usually corresponding to the N- or C- terminus of the encoded protein. Unlike deletions, additions are not very size-dependent. Indeed, additions may be of virtually any size. Preferred additions, however, do not exceed about 100% of the size of the native molecule. More preferably, they add less than about 60 to 30% to the overall size, with less than about 30% being most preferred.

"Deletions" diminish the overall size of the DNA and, therefore, also reduce the size of the protein encoded by that DNA. Deletions may be made from either end of the molecule or internal to it. Typical preferred deletions remove discrete structural features of the encoded protein. For example, some deletions will comprise the deletion of one or more exons which may define a structural feature. Preferred deletions remove less than about 30% of the size of the subject molecule. More preferred deletions remove less than about 20% and most preferred deletions remove less than about 10%.

Computer-Defined Variants and Definition of "Sequence Identity"

In general, both the DNA and protein molecules of the invention can be defined with reference to "sequence identity." As used herein, "sequence identity" refers to a comparison made between two molecules using, for example, the standard Smith-Waterman algorithm that is well known in the art.

Some molecules have at least about 50%, 55% or 60% identity. Preferred molecules are those having at least about 65% sequence identity, more preferably at least 65% or 70% sequence identity. Other preferred molecules have at least about 80%, more preferably at

least 80% or 85%, sequence identity. Particularly preferred molecules have at least about 90% sequence identity, more preferably at least 90% sequence identity. Most preferred molecules have at least about 95%, more preferably at least 95%, sequence identity. As used herein, two nucleic acid molecules or proteins are said to "share significant sequence identity" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) identity.

"Sequence identity" is defined herein with reference the Blast 2 algorithm, which is available at the NCBI (<http://www.ncbi.nlm.nih.gov/BLAST>), using default parameters.

References pertaining to this algorithm include: those found at

http://www.ncbi.nlm.nih.gov/BLAST/blast_references.html; Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649-656.

METHODS OF MAKING VARIANTS

It will be recognized that variants of the inventive molecules can be constructed in several different ways. For example, they may be constructed as completely synthetic DNAs. Methods of efficiently synthesizing oligonucleotides in the range of 20 to about 150 nucleotides are widely available. See Ausubel *et al.*, *supra*, section 2.11, Supplement 21 (1993). Overlapping oligonucleotides may be synthesized and assembled in a fashion first reported by Khorana *et al.*, J. Mol. Biol. 72:209-217 (1971); see also Ausubel *et al.*, Section 8.2. The synthetic DNAs are designed with convenient restriction sites engineered at the 5' and 3' ends of the gene to facilitate cloning into an appropriate vector.

An alternative method of generating variants is to start with one of the inventive DNAs and then to conduct site-directed mutagenesis. See Ausubel *et al.*, *supra*, chapter 8, Supplement 37 (1997). In a typical method, a target DNA is cloned into a single-stranded

DNA bacteriophage vehicle. Single-stranded DNA is isolated and hybridized with an oligonucleotide containing the desired nucleotide alteration(s). The complementary strand is synthesized and the double stranded phage is introduced into a host. Some of the resulting progeny will contain the desired mutant, which can be confirmed using DNA sequencing. In addition, various methods are available that increase the probability that the progeny phage will be the desired mutant. These methods are well known to those in the field and kits are commercially available for generating such mutants.

ISOLATING HOMOLOGS

Methods

By using the sequences disclosed herein as probes or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs. "Homologs" are essentially naturally-occurring variants and include allelic, species-specific and tissue-specific variants.

Region-specific primers or probes derived from the nucleotide sequence(s) provided can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog using known methods (Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)). Such an application is useful in diagnostic methods, as described in more detail below, as well as in preparing full-length DNAs from various sources. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. As a general guide, the formula $3(G+C) + 2(A+T) = ^\circ\text{C}$, is useful.

When using primers derived from the inventive sequences, one skilled in the art will recognize that by employing high stringency conditions (e.g., annealing at 50-60°C), only sequences with greater than 75% sequence identity to the primer will be amplified. By employing lower stringency conditions (e.g., annealing at 35-37°C), sequences which have greater than 40-50% sequence identity to the primer also will be amplified.

The PCR product may be subcloned and sequenced to confirm that it indeed displays the expected sequence identity. The PCR fragment may then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled

and used to screen a bacteriophage cDNA library. Alternatively, the labeled fragment may be used to screen a genomic library.

PCR technology may also be utilized to isolate full length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source. A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal transferase reaction, the hybrid may be digested with RNAase H, and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of cloning strategies which may be used, see e.g., Sambrook et al., 1989, *supra*.

When using DNA probes derived from the inventive sequences for colony/plaque hybridization, one skilled in the art will recognize that by employing medium to high stringency conditions (e.g., hybridizing at 50-65°C in 5X SSPC and 50% formamide, and washing at 50-65°C in 0.5X SSPC), sequences having regions with greater than 90% sequence identity to the probe can be obtained, and that by employing lower stringency conditions (e.g., hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in SSPC), sequences having regions with greater than 35-45% sequence identity to the probe will be obtained.

Suitably, genomic or cDNA libraries can be constructed and screened in accord with the previous paragraph. The libraries should be derived from a tissue or organism that is known to express the gene of interest, or that is suspected of expressing the gene. The clone containing the homolog may then be purified through methods routinely practiced in the art, and subjected to sequence analysis.

Additionally, an expression library can be constructed utilizing DNA isolated from or cDNA synthesized from a tissue or organism that is known to express the gene of interest, or that is suspected of expressing the gene. In this manner, clones may be induced and screened using standard antibody screening techniques in conjunction with antibodies raised against the normal gene product, as described herein. (For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, *ANTIBODIES: A LABORATORY MANUAL*, Cold Spring Harbor Press, Cold Spring Harbor Press.)

Human Homologs

Any organism or tissue can be used as the source for homologs of the present invention so long as the organism or tissue naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs is human.

PROTEINS OF THE INVENTION

One class of proteins included within the invention is encoded by the inventive DNA molecules presented. Other proteins according to the invention are those encoded by the DNA variants described above. As noted, these variants are designed with the encoded proteins in mind.

A preferred class of protein fragments includes those fragments which retain any biological activity. These molecules share functional features common the family of proteins, although these characteristics may vary in degree.

According to one aspect of the invention fragments of the inventive proteins are contemplated. Some preferred fragments are those which are capable of eliciting an immune response. Generally these "antigenic" fragments will be from about five amino acids in length to about fifty amino acids in length. Some preferred antigenic fragments are from five to about twenty amino acids long. "Antigenic" response may refer to a T cell response, a B cell response or a response by cells of the macrophage/monocyte lineages. In most cases, however, it will refer to the immune response involved in the generation of antibodies. In other words, the relevant immune response is that of helper T cells and/or B cells. These preferred molecules comprise one or more T cell and /or B cell epitopes.

ANTIBODIES OF THE INVENTION

Antibodies raised against the proteins and protein fragments of the invention also are contemplated by the invention. Described below are antibody products and methods for producing antibodies capable of specifically recognizing one or more epitopes of the presently described proteins and their derivatives.

Antibodies include, but are not limited to polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies including single chain Fv (scFv) fragments, Fab fragments, F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, epitope-binding fragments, and humanized forms of any of the above.

As known to one in the art, these antibodies may be used, for example, in the detection of a target protein in a biological sample. They also may be utilized as part of treatment methods, and/or may be used as part of diagnostic techniques whereby patients may be tested for abnormal levels or for the presence of abnormal forms of the such proteins.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., *J. Immunol. Methods* 35:1-21 (1980); Kohler and Milstein, *Nature* 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72 (1983); Cole et al., in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985), pp. 77-96). Antibodies may also be generated by the known techniques of phage display and *in vitro* immunization.

Polyclonal Antibodies

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as an inventive protein or an antigenic derivative thereof.

Polyclonal antiserum, containing antibodies to heterogeneous epitopes of a single protein, can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified, as known in the art, to enhance immunogenicity. Immunization methods include subcutaneous or intraperitoneal injection of the polypeptide.

Effective polyclonal antibody production is affected by many factors related both to the antigen and to the host species. For example, small molecules tend to be less immunogenic than other and may require the use of carriers and/or adjuvant. In addition, host animal response may vary with site of inoculation. Both inadequate or excessive doses of antigen may result in low titer antisera. In general, however, small doses (high ng to low µg levels) of antigen administered at multiple intradermal sites appears to be most reliable. Host animals may include but are not limited to rabbits, mice, chickens and rats, to name but a few. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al., *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

The protein immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin β -galactosidase) or through the inclusion of an adjuvant during immunization. Adjuvants include Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Booster injections can be given at regular intervals, with at least one usually being required for optimal antibody production. The antiserum may be harvested when the antibody titer begins to fall. Titer may be determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen. See, for example, Ouchterlony *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). The antiserum may be purified by affinity chromatography using the immobilized immunogen carried on a solid support. Such methods of affinity chromatography are well known in the art.

Affinity of the antisera for the antigen may be determined by preparing competitive binding curves, as described, for example, by Fisher, Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D.C. (1980).

In addition to using protein as the immunogen, DNA molecules may be used directly. In this manner, a DNA encoding the protein immunogen is administered. Boosting and harvesting is done in a manner analogous to that detailed above. Yet another method of producing antibodies entails immunizing chickens and harvesting the antibodies from their eggs.

Monoclonal Antibodies

Monoclonal antibodies (MAbs), are homogeneous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture or *in vivo*. MAbs may be produced

by making hybridomas which are immortalized cells capable of secreting a specific monoclonal antibody.

Monoclonal antibodies to any of the proteins, peptides and epitopes thereof described herein can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495-497 (1975) (and U.S. Patent No. 4,376,110) or modifications of the methods thereof, such as the human B-cell hybridoma technique (Kosbor *et al.*, 1983, *Immunology Today* 4:72; Cole *et al.*, 1983, *Proc. Natl. Acad. Sci. USA* 80: 2026-2030), and the EBV-hybridoma technique (Cole *et al.*, 1985, *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc., pp. 77-96).

In one method a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen are isolated.

The spleen cells are fused, typically using polyethylene glycol, with mouse myeloma cells, such as SP2/0-Ag14 myeloma cells. The excess, unfused cells are destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted, and aliquots are plated to microliter plates where growth is continued.

Antibody-producing clones (hybridomas) are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures. These include ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419 (1980), western blot analysis, radioimmunoassay (Lutz *et al.*, *Exp. Cell Res.* 175:109-124 (1988)) and modified methods thereof.

Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* *BASIC METHODS IN MOLECULAR BIOLOGY*, Elsevier, New York. Section 21-2 (1989). The hybridoma clones may be cultivated *in vitro* or *in vivo*, for instance as ascites. Production of high titers of mAbs *in vivo* makes this the presently preferred method of production. Alternatively, hybridoma culture in hollow fiber bioreactors provides a continuous high yield source of monoclonal antibodies.

The antibody class and subclass may be determined using procedures known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

MAbs may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. Methods of purifying monoclonal antibodies are well known in the art.

Antibody Derivatives and Fragments

Fragments or derivatives of antibodies include any portion of the antibody which is capable of binding the target antigen, or a specific portion thereof. Antibody derivatives include poly-specific (*e.g.*, bi-specific) antibodies, which contain binding sites specific for two or more different epitopes. These epitopes may be from the same or different inventive molecules or one or more epitope may be from a molecule not specifically disclosed here.

Antibody fragments specifically include $F(ab')_2$, Fab, Fab' and Fv fragments. These can be generated from any class of antibody, but typically are made from IgG or IgM. They may be made by conventional recombinant DNA techniques or, using the classical method, by proteolytic digestion with papain or pepsin. See CURRENT PROTOCOLS IN IMMUNOLOGY, chapter 2, Coligan *et al.*, eds., (John Wiley & Sons 1991-92).

$F(ab')_2$ fragments are typically about 110 kDa (IgG) or about 150 kDa (IgM) and contain two antigen-binding regions, joined at the hinge by disulfide bond(s). Virtually all, if not all, of the Fc is absent in these fragments. Fab' fragments are typically about 55 kDa (IgG) or about 75 kDa (IgM) and can be formed, for example, by reducing the disulfide bond(s) of an $F(ab')_2$ fragment. The resulting free sulfhydryl group(s) may be used to conveniently conjugate Fab' fragments to other molecules, such as detection reagents (*e.g.*, enzymes).

Fab fragments are monovalent and usually are about 50 kDa (from any source). Fab fragments include the light (L) and heavy (H) chain, variable (V_L and V_H , respectively) and constant (C_L C_H , respectively) regions of the antigen-binding portion of the antibody. The H and L portions are linked by an intramolecular disulfide bridge.

Fv fragments are typically about 25 kDa (regardless of source) and contain the variable regions of both the light and heavy chains (V_L and V_H , respectively). Usually, the V_L and V_H chains are held together only by non-covalent interacts and, thus, they readily dissociate. They do, however, have the advantage of small size and they retain the same binding properties of the larger Fab fragments. Accordingly, methods have been developed to crosslink the V_L and V_H chains, using, for example, glutaraldehyde (or other chemical crosslinkers), intermolecular disulfide bonds (by incorporation of cysteines) and peptide linkers. The resulting Fv is now a single chain (*i.e.*, SCFv).

Other antibody derivatives include single chain antibodies (U.S. Patent 4,946,778; Bird, *Science* 242:423-426 (1988); Huston *et al.*, *Proc. Natl. Acad. Sci. USA* 85:5879-5883 (1988); and Ward *et al.*, *Nature* 334:544-546 (1989)). Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain FV (SCFv).

One preferred method involves the generation of scFvs by recombinant methods, which allows the generation of Fvs with new specificities by mixing and matching variable chains from different antibody sources. In a typical method, a recombinant vector would be provided which comprises the appropriate regulatory elements driving expression of a cassette region. The cassette region would contain a DNA encoding a peptide linker, with convenient sites at both the 5' and 3' ends of the linker for generating fusion proteins. The DNA encoding a variable region(s) of interest may be cloned in the vector to form fusion proteins with the linker, thus generating an scFv.

In an exemplary alternative approach, DNAs encoding two Fvs may be ligated to the DNA encoding the linker, and the resulting tripartite fusion may be ligated directly into a conventional expression vector. The scFv DNAs generated any of these methods may be expressed in prokaryotic or eukaryotic cells, depending on the vector chosen.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab)₂ fragments. Alternatively, Fab expression libraries may be constructed (Huse *et al.*, 1989, *Science*, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Derivatives also include "chimeric antibodies" (Morrison *et al.*, *Proc. Natl. Acad. Sci.*, 81:6851-6855 (1984); Neuberger *et al.*, *Nature*, 312:604-608 (1984); Takeda *et al.*, *Nature*, 314:452-454 (1985)). These chimeras are made by splicing the DNA encoding a mouse antibody molecule of appropriate specificity with, for instance, DNA encoding a human antibody molecule of appropriate specificity. Thus, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. These are also known sometimes as "humanized" antibodies and they offer the added

advantage of at least partial shielding from the human immune system. They are, therefore, particularly useful in therapeutic *in vivo* applications.

Labeled Antibodies

The present invention further provides the above-described antibodies in detectably labeled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example see (Sternberger *et al.*, *J. Histochem. Cytochem.* 18:315 (1970); Bayer *et al.*, *Meth. Enzym.* 62:308 (1979); Engval *et al.*, *Immunol.* 109:129 (1972); Goding, *J. Immunol. Meth.* 13:215 (1976)). The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* diagnostic assays.

Immobilized Antibodies

The foregoing antibodies also may be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby *et al.*, *Meth. Enzym.* 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immunoaffinity purification of the proteins of the present invention.

THERAPEUTIC AND DIAGNOSTIC COMPOSITIONS

The proteins, antibodies and polynucleotides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in *Remington's Pharmaceutical Sciences* (16th ed., Osol, A., Ed., Mack, Easton PA (1980)). In order to form a pharmaceutically acceptable composition suitable for effective administration,

such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvate may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the composition may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.* gelatin for

use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

RECOMBINANT CONSTRUCTS AND EXPRESSION

The present invention further provides recombinant DNA constructs comprising one or more of the nucleotide sequences of the present invention. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a DNA or DNA fragment, typically bearing an open reading frame, is inserted, in either orientation.

The gene products encoded by the subject DNAs may be produced by recombinant DNA technology using techniques well known in the art. See, for example, the techniques described in Sambrook et al., 1989, *supra*, and Ausubel et al., 1989, *supra*. Alternatively, the DNA sequences may be chemically synthesized using, for example, synthesizers. See, for

example, the techniques described in OLIGONUCLEOTIDE SYNTHESIS, 1984, Gait, ed., IRL Press, Oxford, which is incorporated by reference herein in its entirety. They may be assembled from fragments and short oligonucleotide linkers, or from a series of oligonucleotides. They are preferably made by RT-PCR methods. The resulting synthetic gene is capable of being expressed in a recombinant vector.

In some cases the recombinant constructs will be expression vectors, which are capable of expressing the RNA and/or protein products of the encoded DNA(s). Thus, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the open reading frame (ORF). The vector may further comprise a selectable marker sequence.

Specific initiation signals may also be required for efficient translation of inserted target gene coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where a target DNA includes its own initiation codon and adjacent sequences is inserted into the appropriate expression vector, no additional translation control signals may be needed. However, in cases where only a portion of an ORF is used, exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire target. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner *et al.*, *Methods in Enzymol.* 153:516-544 (1987)). Some appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Patent No. 5,082,767.

The present invention further provides host cells containing at least one of the DNAs of the present invention. The host cell can be virtually any cell for which expression vectors are available. It may be, for example, a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic

cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis *et al.*, *Basic Methods in Molecular Biology* (1986)).

A wide variety of expression systems are available, such as: yeast (*e.g.* *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing the target DNA; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing the target DNA sequences; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.* Ti plasmid) containing target DNA coding sequences; or mammalian cell systems (*e.g.* COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (*e.g.*, metallothionein promoter) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the vaccinia virus 7.5K promoter).

Depending on the system chosen, the resulting product may differ. For example, proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

Vectors

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting selection of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), α -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequence, and in one aspect of the invention, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal or C-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Bacterial Expression

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, if desirable, to provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may, also be employed as a matter of choice.

Bacterial vectors may be, for example, bacteriophage-, plasmid- or cosmid-based. These vectors can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids typically containing elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, GEM 1 (Promega Biotec, Madison, WI, USA), pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pKK232-8, pDR540, and pRIT5 (Pharmacia).

These "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Bacterial promoters include lac, T3, T7, lambda P_R or P_L, trp, and ara.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is derepressed/induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the protein being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of antibodies or to screen peptide libraries, for example, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, *EMBO J.* 2:1791), in which the coding sequence may be ligated into the vector in frame with the *lac Z* coding region so that a fusion protein is produced; pIN vectors (Inouye et al. 1985, *Nucleic Acids*

Res. 13:3101-3109; Van Heeke *et al.*, 1989, *J. Biol. Chem.* 264:5503-5509); pET vectors, Studier *et al.*, *Methods in Enzymology* 185: 60-89 (Academic Press 1990); and the like.

Moreover, pGEX vectors may be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and easily can be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene protein can be released from the GST moiety.

In a one embodiment, full length cDNA sequences are appended with in-frame *Bam*HI sites at the amino terminus and *Eco*RI sites at the carboxyl terminus using standard PCR methodologies (Innis *et al.*, 1990, *supra*) and ligated into the pGEX-2TK vector (Pharmacia, Uppsala, Sweden). The resulting cDNA construct contains a kinase recognition site at the amino terminus for radioactive labeling and glutathione S-transferase sequences at the carboxyl terminus for affinity purification (Nilsson, *et al.* 1985, *EMBO J.* 4: 1075; Zabeau and Stanley, 1982, *EMBO J.* 1:1217).

Eukaryotic Expression

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Mammalian promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Exemplary mammalian vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). Selectable markers include CAT (chloramphenicol transferase).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the coding sequence of interest

may be ligated to an adenovirus transcription/translation control complex, *e.g.*, the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (*e.g.*, region E1 or E3) will result in a recombinant virus that is viable and capable of expressing a target protein in infected hosts. (*E.g.*, See Logan *et al.*, 1984, *Proc. Natl. Acad. Sci. USA* 81:3655-3659).

In one embodiment, cDNA sequences encoding the full-length open reading frames are ligated into pCMV β replacing the β -galactosidase gene such that cDNA expression is driven by the CMV promoter (Alam, 1990, *Anal. Biochem.* 188: 245-254; MacGregor *et al.*, 1989, *Nucl. Acids Res.* 17: 2365; Norton *et al.* 1985, *Mol. Cell. Biol.* 5: 281).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (*e.g.*, glycosylation) and processing (*e.g.*, cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins.

Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, etc.

For long-term, high-yield production of recombinant proteins in eukaryotic cells, stable expression is preferred. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (*e.g.*, promoter, enhancer, sequences, transcription terminators, polyadenylation sites, *etc.*), and a selectable marker.

Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the target protein. Such engineered cell lines may be

particularly useful in screening and evaluation of compounds that affect the endogenous activity of the protein.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, *et al.*, *Cell* 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska *et al.*, *Proc. Natl. Acad. Sci. USA* 48:2026 (1962)), and adenine phosphoribosyltransferase (Lowy, *et al.*, *Cell* 22:817 (1980)) genes can be employed in tk⁻, hgp^rt⁻ or ap^rt⁻ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate (Wigler, *et al.*, *Proc. Natl. Acad. Sci. USA* 77:3567 (1980)); O'Hare, *et al.*, 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan *et al.*, *Proc. Natl. Acad. Sci. USA* 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, *et al.*, 1981, *J. Mol. Biol.* 150:1); and hydro, which confers resistance to hygromycin (Santerre, *et al.*, 1984, *Gene* 30:147) genes.

An alternative fusion protein system allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, *et al.*, *Proc. Natl. Acad. Sci. USA* 88: 8972-8976 (1991)). In this system, the gene of interest is subcloned into a vaccinia-based plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni²⁺ nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The target coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of a target gene coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (E.g., see Smith *et al.*, 1983, *J. Virol.* 46: 584; Smith, U.S. Patent No. 4,215,051).

While the present proteins can be expressed in recombinant systems, as described above, cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

Purification of Recombinant Proteins

Recombinant proteins produced may be isolated by host cell lysis. This may be followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, like lysozyme and chelators.

If inclusion bodies are formed in bacterial systems, they may be extracted from cell pellets using, for example, detergents, reducing agents, salts, urea, guanidinium chloride and extremes of pH (*e.g.* <4 or >10). If denaturation occurs, protein refolding steps (*e.g.*, dialysis) can be used, as necessary, in completing configuration of the mature protein. If disulfide bridges are present in the native protein, they may be reoxidized using known methods.

By way of specific non-limiting example, the recombinant bacterial cells, for example *E. coli*, are grown in any of a number of suitable media, for example LB, and the expression of the recombinant protein induced by adding IPTG (*e.g.*, *lac* operator-promoter) to the media or switching incubation to a higher temperature (*e.g.*, λ cI⁸⁵⁷). After culturing the bacteria for a further period of between 2 and 24 hours, the cells are collected by centrifugation and washed to remove residual media. The bacterial cells are then lysed, for example, by disruption in a cell homogenizer and centrifuged to separate the cell membranes from the soluble cell components. If the protein aggregates into inclusion bodies, this centrifugation can be performed under conditions whereby the dense inclusion bodies are selectively enriched by incorporation of sugars such as sucrose into the buffer and centrifugation at a selective speed. The inclusion bodies can then be washed in any of several solutions to remove some of the contaminating host proteins, then solubilized in solutions containing high concentrations of urea (*e.g.* 8M) or chaotropic agents such as guanidinium hydrochloride in the presence of reducing agents such as β -mercaptoethanol or DTT (dithiothreitol).

At this stage it may be advantageous to incubate the protein for several hours under conditions suitable for the protein to undergo a refolding process into a conformation which

more closely resembles that of the native protein. Such conditions generally include low protein concentrations less than 500 µg/ml), low levels of reducing agent, concentrations of urea less than 2 M and often the presence of reagents such as a mixture of reduced and oxidized glutathione which facilitate the interchange of disulphide bonds within the protein molecule. The refolding process can be monitored, for example, by SDS-PAGE or with antibodies which are specific for the native molecule. Following refolding, the protein can then be purified further and separated from the refolding mixture by chromatography on any of several supports including ion exchange resins, gel permeation resins or on a variety of affinity columns.

Labeling Proteins

When used as a component in assay systems such as those described, below, the target protein may be labeled, either directly or indirectly, to facilitate detection of the present *res*-like molecules either *in vitro* or *in vivo*. Any of a variety of suitable labeling systems may be used including but not limited to radioisotopes such as ¹²⁵I; enzyme labeling systems that generate a detectable colorimetric signal or light when exposed to substrate; and fluorescent labels.

Where recombinant DNA technology is used for protein production the, it may be advantageous to engineer fusion proteins that can facilitate labeling, immobilization and/or detection. These fusion proteins may, for example, add amino acids which facilitate further chemical modification. They also may add a functional moiety, such as an enzyme, which directly facilitates detection.

TRANSGENIC ANIMALS

The invention further contemplates animal models for studying the function of the present molecules and for overproducing the protein products. The disclosed DNA sequences may be used in conjunction with techniques for producing transgenic animals that are well known to those of skill in the art.

To prepare transgenic animals, target gene sequences may for example be introduced into, and overexpressed in, the genome of the animal of interest, or, if endogenous target gene sequences are present, they may either be overexpressed or, alternatively, be disrupted in order to underexpress or inactivate target gene expression, such as described for the disruption of apoE in mice (Plum *et al.*, *Cell* 71: 343-353 (1992)).

In order to overexpress a target gene sequence, the coding portion of the target gene sequence may be ligated to a regulatory sequence which is capable of driving gene expression in the animal and cell type of interest. Such regulatory regions will be well known to those of skill in the art, and may be utilized in the absence of undue experimentation.

For underexpression of an endogenous target gene sequence, such a sequence may be isolated and engineered such that when reintroduced into the genome of the animal of interest, the endogenous target gene alleles will be inactivated. Preferably, the engineered target gene sequence is introduced via gene targeting such that the endogenous target sequence is disrupted upon integration of the engineered target gene sequence into the animal's genome.

Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, *e.g.*, baboons, monkeys, and chimpanzees may be used to generate cardiovascular disease animal models. Goats, cows and sheep are particularly preferred for producing protein *in vivo*.

Any technique known in the art may be used to introduce a target gene transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe *et al.*, U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten *et al.*, *Proc. Natl. Acad. Sci., USA* 82:6148-6152 (1985)); gene targeting in embryonic stem cells (Thompson *et al.*, *Cell* 56:313-321 (1989)); electroporation of embryos (Lo, *Mol. Cell. Biol.* 3:1803-1814 (1983)); and sperm-mediated gene transfer (Lavitrano *et al.*, *Cell* 57:717-723 (1989)); *etc.* For a review of such techniques, see Gordon, Transgenic Animals, *Intl. Rev. Cytol.* 115:171-229 (1989).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, *i.e.*, mosaic animals. The transgene may be integrated as a single transgene or in concatamers, *e.g.*, head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching

of Lasko et al. (Lasko *et al.*, *Proc. Natl. Acad. Sci. USA* 89:3232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the target gene be integrated into the chromosomal site of the endogenous target gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous target gene of interest are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous target gene.

The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene of interest in only that cell type, by following, for example, the teaching of Gu *et al.* *Science* 265: 103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant target gene and protein may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include but are not limited to Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and RT-PCR. Samples of target gene-expressing tissue, may also be evaluated immunocytochemically using antibodies specific for the target gene transgene gene product of interest.

The transgenic animals that express target gene mRNA or target gene transgene peptide (detected immunocytochemically, using antibodies directed against the target gene product's epitopes) at easily detectable levels should then be further evaluated to identify those animals which display characteristic increased susceptibility to carcinogenesis. Additionally, specific cell types within the transgenic animals may be analyzed and assayed *in vitro* for cellular phenotypes characteristic of mutant phenotype.

Once target gene transgenic founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include but are not limited to: outbreeding of founder animals with more

than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound target gene transgenics that express the target gene transgene of interest at higher levels because of the effects of additive expression of each target gene transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order both to augment expression and eliminate the possible need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; breeding animals to different inbred genetic backgrounds so as to examine effects of modifying alleles on expression of the target gene transgene and the possible development of carcinogenesis. One such approach is to cross the target gene transgenic founder animals with a wild type strain to produce an F1 generation that exhibits increased susceptibility to carcinogenesis. The F1 generation may then be inbred in order to develop a homozygous line, if it is found that homozygous target gene transgenic animals are viable.

Methods of generating "knockout" mice using homologous recombination in embryonic stem cells are well known in the art. Suitable methods are described, for example, in Mansour *et al.*, *Nature*, 336:348 (1988); Zijlstra *et al.*, *Nature*, 342:435 (1989) and 344:742 (1990); and Hasty *et al.*, *Nature*, 350:243 (1991). This genomic DNA can be obtained by conventional methods using the cDNA sequence as a probe in a commercially-available genomic DNA library.

Briefly, a genomic fragment is cleaved with a restriction endonuclease and a heterologous cassette containing a neomycin-resistance gene is inserted at the cleavage site. A suitable cassette is the GTI-II *neo* cassette described by Lufkin *et al.*, *Cell* 66:1105 (1991). The modified genomic fragment is cloned into a suitable targeting vector that is introduced into murine embryonic stem cells by electroporation. Cells that have undergone homologous recombination (and hence disruption of the gene) are selected by resistance to G418, and used to generate chimeric mice using well known methods. See Lufkin *et al.*, *supra*. Traditional breeding methods then can be used to generate mice that are homozygous for the disrupted gene.

The phenotype of mice that are homozygous for the mutation then can be studied to provide insights into the role of the protein in, for example, carcinogenesis. These mice also can be used as models for developing new treatments for cancers. If this mutation is lethal in

homozygous mice (for example during embryogenesis) heterozygous mice, which express only half the amount of the protein can also be studied.

GENE THERAPY APPLICATIONS

When mutations in the inventive protein, or in the elements controlling expression of that protein, are found to be associated with a malignant phenotype, control of cellular proliferation can be restored by gene therapy methods. For example, overexpression of the protein can be counteracted by concurrent expression of an antisense molecule that binds to and inhibits expression of the mRNA encoding the protein. Alternatively, overexpression can be inhibited in an analogous manner using a ribozyme that cleaves the mRNA. In another embodiment, where expression of a mutated protein induces the malignant phenotype, concomitant expression of the non-mutated molecule via introduction of an exogenous gene may be used. Methods of using antisense and ribozyme technology to control gene expression, or of gene therapy methods for expression of an exogenous gene in this manner are well known in the art.

Each of these methods requires a system for introducing a vector into the cells containing the mutated gene. The vector encodes either an antisense or ribozyme transcript of the inventive protein. The construction of a suitable vector can be achieved by any of the methods well-known in the art for the insertion of exogenous DNA into a vector. *See, e.g., Sambrook et al., Molecular Cloning* (Cold Spring Harbor Press 2d ed. 1989), which is incorporated herein by reference. In addition, the prior art teaches various methods of introducing exogenous genes into cells *in vivo*. *See Rosenberg et al., Science* 242:1575-1578 (1988) and Wolff *et al.*, *PNAS* 86:9011-9014 (1989), which are incorporated herein by reference. The routes of delivery include systemic administration and administration *in situ*. Well-known techniques include systemic administration with cationic liposomes, and administration *in situ* with viral vectors. Any one of the gene delivery methodologies described in the prior art is suitable for the introduction of a recombinant vector containing an inventive gene according to the invention into a MTX-resistant, transport-deficient cancer cell. A listing of present-day vectors suitable for the purpose of this invention is set forth in Hodgson, *Bio/Technology* 13: 222 (1995), which is incorporated by reference.

For example, liposome-mediated gene transfer is a suitable method for the introduction of a recombinant vector containing an inventive gene according to the invention

into a MTX-resistant, transport-deficient cancer cell. The use of a cationic liposome, such as DC-Chol/DOPE liposome, has been widely documented as an appropriate vehicle to deliver DNA to a wide range of tissues through intravenous injection of DNA/cationic liposome complexes. See Caplen *et al.*, *Nature Med.* 1:39-46 (1995) and Zhu *et al.*, *Science* 261:209-211 (1993), which are herein incorporated by reference. Liposomes transfer genes to the target cells by fusing with the plasma membrane. The entry process is relatively efficient, but once inside the cell, the liposome-DNA complex has no inherent mechanism to deliver the DNA to the nucleus. As such, the most of the lipid and DNA gets shunted to cytoplasmic waste systems and destroyed. The obvious advantage of liposomes as a gene therapy vector is that liposomes contain no proteins, which thus minimizes the potential of host immune responses.

As another example, viral vector-mediated gene transfer is also a suitable method for the introduction of the vector into a target cell. Appropriate viral vectors include adenovirus vectors and adeno-associated virus vectors, retrovirus vectors and herpesvirus vectors.

Adenoviruses are linear, double stranded DNA viruses complexed with core proteins and surrounded by capsid proteins. The common serotypes 2 and 5, which are not associated with any human malignancies, are typically the base vectors. By deleting parts of the virus genome and inserting the desired gene under the control of a constitutive viral promoter, the virus becomes a replication deficient vector capable of transferring the exogenous DNA to differentiated, non-proliferating cells. To enter cells, the adenovirus fibre interacts with specific receptors on the cell surface, and the adenovirus surface proteins interact with the cell surface integrins. The virus penton-cell integrin interaction provides the signal that brings the exogenous gene-containing virus into a cytoplasmic endosome. The adenovirus breaks out of the endosome and moves to the nucleus, the viral capsid falls apart, and the exogenous DNA enters the cell nucleus where it functions, in an epichromosomal fashion, to express the exogenous gene. Detailed discussions of the use of adenoviral vectors for gene therapy can be found in Berkner, *Biotechniques* 6:616-629 (1988) and Trapnell, *Advanced Drug Delivery Rev.* 12:185-199 (1993), which are herein incorporated by reference. Adenovirus-derived vectors, particularly non-replicative adenovirus vectors, are characterized by their ability to accommodate exogenous DNA of 7.5 kB, relative stability, wide host range, low pathogenicity in man, and high titers (10^4 to 10^5 plaque forming units per cell). See Stratford-Perricaudet *et al.*, *PNAS* 89:2581 (1992).

Adeno-associated virus (AAV) vectors also can be used for the present invention. AAV is a linear single-stranded DNA parvovirus that is endogenous to many mammalian species. AAV has a broad host range despite the limitation that AAV is a defective parvovirus which is dependent totally on either adenovirus or herpesvirus for its reproduction *in vivo*. The use of AAV as a vector for the introduction into target cells of exogenous DNA is well-known in the art. See, e.g., Lebkowski *et al.*, *Mole. & Cell. Biol.* 8:3988 (1988), which is incorporated herein by reference. In these vectors, the capsid gene of AAV is replaced by a desired DNA fragment, and transcomplementation of the deleted capsid function is used to create a recombinant virus stock. Upon infection the recombinant virus uncoats in the nucleus and integrates into the host genome.

Another suitable virus-based gene delivery mechanism is retroviral vector-mediated gene transfer. In general, retroviral vectors are well-known in the art. See Breakfield *et al.*, *Mole. Neuro. Biol.* 1:339 (1987) and Shih *et al.*, in *Vaccines* 85: 177 (Cold Spring Harbor Press 1985). A variety of retroviral vectors and retroviral vector-producing cell lines can be used for the present invention. Appropriate retroviral vectors include Moloney Murine Leukemia Virus, spleen necrosis virus, and vectors derived from retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, human immunodeficiency virus, myeloproliferative sarcoma virus, and mammary tumor virus. These vectors include replication-competent and replication-defective retroviral vectors. In addition, amphotropic and xenotropic retroviral vectors can be used. In carrying out the invention, retroviral vectors can be introduced to a tumor directly or in the form of free retroviral vector producing-cell lines. Suitable producer cells include fibroblasts, neurons, glial cells, keratinocytes, hepatocytes, connective tissue cells, ependymal cells, chromaffin cells. See Wolff *et al.*, *PNAS* 84:3344 (1989).

Retroviral vectors generally are constructed such that the majority of its structural genes are deleted or replaced by exogenous DNA of interest, and such that the likelihood is reduced that viral proteins will be expressed. See Bender *et al.*, *J. Virol.* 61:1639 (1987) and Armento *et al.*, *J. Virol.* 61:1647 (1987), which are herein incorporated by reference. To facilitate expression of the antisense or ribozyme molecule, of the inventive protein, a retroviral vector employed in the present invention must integrate into the genome of the host cell genome, an event which occurs only in mitotically active cells. The necessity for host cell replication effectively limits retroviral gene expression to tumor cells, which are highly

replicative, and to a few normal tissues. The normal tissue cells theoretically most likely to be transduced by a retroviral vector, therefore, are the endothelial cells that line the blood vessels that supply blood to the tumor. In addition, it is also possible that a retroviral vector would integrate into white blood cells both in the tumor or in the blood circulating through the tumor.

The spread of retroviral vector to normal tissues, however, is limited. The local administration to a tumor of a retroviral vector or retroviral vector producing cells will restrict vector propagation to the local region of the tumor, minimizing transduction, integration, expression and subsequent cytotoxic effect on surrounding cells that are mitotically active.

Both replicatively deficient and replicatively competent retroviral vectors can be used in the invention, subject to their respective advantages and disadvantages. For instance, for tumors that have spread regionally, such as lung cancers, the direct injection of cell lines that produce replication-deficient vectors may not deliver the vector to a large enough area to completely eradicate the tumor, since the vector will be released only from the original producer cells and their progeny, and diffusion is limited. Similar constraints apply to the application of replication deficient vectors to tumors that grow slowly, such as human breast cancers which typically have doubling times of 30 days versus the 24 hours common among human gliomas. The much shortened survival-time of the producer cells, probably no more than 7-14 days in the absence of immunosuppression, limits to only a portion of their replicative cycle the exposure of the tumor cells to the retroviral vector.

The use of replication-defective retroviruses for treating tumors requires producer cells and is limited because each replication-defective retrovirus particle can enter only a single cell and cannot productively infect others thereafter. Because these replication-defective retroviruses cannot spread to other tumor cells, they would be unable to completely penetrate a deep, multilayered tumor *in vivo*. See Markert *et al.*, *Neurosurg.* 77: 590 (1992). The injection of replication-competent retroviral vector particles or a cell line that produces a replication-competent retroviral vector virus may prove to be a more effective therapeutic because a replication competent retroviral vector will establish a productive infection that will transduce cells as long as it persists. Moreover, replicatively competent retroviral vectors may follow the tumor as it metastasizes, carried along and propagated by transduced tumor cells. The risks for complications are greater, with replicatively competent vectors, however.

Such vectors may pose a greater risk than replicatively deficient vectors of transducing normal tissues, for instance. The risks of undesired vector propagation for each type of cancer and affected body area can be weighed against the advantages in the situation of replicatively competent versus replicatively deficient retroviral vector to determine an optimum treatment.

Both amphotropic and xenotropic retroviral vectors may be used in the invention. Amphotropic viruses have a very broad host range that includes most or all mammalian cells, as is well known to the art. Xenotropic viruses can infect all mammalian cell cells except mouse cells. Thus, amphotropic and xenotropic retroviruses from many species, including cows, sheep, pigs, dogs, cats, rats, and mice, *inter alia* can be used to provide retroviral vectors in accordance with the invention, provided the vectors can transfer genes into proliferating human cells *in vivo*.

Clinical trials employing retroviral vector therapy treatment of cancer have been approved in the United States. See Culver, *Clin. Chem.* 40: 510 (1994). Retroviral vector-containing cells have been implanted into brain tumors growing in human patients. See Oldfield *et al.*, *Hum. Gene Ther.* 4: 39 (1993). These retroviral vectors carried the HSV-1 thymidine kinase (HSV-tk) gene into the surrounding brain tumor cells, which conferred sensitivity of the tumor cells to the antiviral drug ganciclovir. Some of the limitations of current retroviral based cancer therapy, as described by Oldfield are: (1) the low titer of virus produced, (2) virus spread is limited to the region surrounding the producer cell implant, (3) possible immune response to the producer cell line, (4) possible insertional mutagenesis and transformation of retroviral infected cells, (5) only a single treatment regimen of pro-drug, ganciclovir, is possible because the "suicide" product kills retrovirally infected cells and producer cells and (6) the bystander effect is limited to cells in direct contact with retrovirally transformed cells. See Bi *et al.*, *Human Gene Therapy* 4: 725 (1993).

Yet another suitable virus-based gene delivery mechanism is herpesvirus vector-mediated gene transfer. While much less is known about the use of herpesvirus vectors, replication-competent HSV-1 viral vectors have been described in the context of antitumor therapy. See Martuza *et al.*, *Science* 252: 854 (1991), which is incorporated herein by reference.

DIAGNOSTIC METHODS

The present invention also contemplates, for certain molecules described below, methods for diagnosis of human disease. In particular, patients can be screened for the occurrence of cancers, or likelihood of occurrence of cancers, associated with mutations in the encoded protein. DNA from tumor tissue obtained from patients suffering from cancer can be isolated and the gene encoding the protein can be sequenced. By examining a number of patients in this manner, mutations in the gene that are associated with a malignant cellular phenotype can be identified. In addition, correlation of the nature of the observed mutations with subsequent observed clinical outcomes allows development of prognostic model for the predicted outcome in a particular patient.

Screening for mutations conveniently can be carried out at the DNA level by use of PCR, although the skilled artisan will be aware that many other well known methods are available for the screening. PCR primers can be selected that flank known mutation sites, and the PCR products can be sequenced to detect the occurrence of the mutation. Alternatively, the 3' residue of one PCR primer can be selected to be a match only for the residue found in the unmutated gene. If the gene is mutated, there will be a mismatch at the 3' end of the primer, and primer extension cannot occur, and no PCR product will be obtained. Alternatively, primer mixtures can be used where the 3' residue of one primer is any nucleotide other than the nonmutated residue. Observation of a PCR product then indicates that a mutation has occurred. Other methods of using, for example, oligonucleotide probes to screen for mutations are described, for example, in U.S. Patent No. 4,871,838, which is herein incorporated by reference in its entirety.

Alternatively, antibodies can be generated that selectively bind either mutated or non-mutated protein. The antibodies then can be used to screen tissue samples for occurrence of mutations in a manner analogous to the DNA-based methods described *supra*.

The diagnostic methods described above can be used not only for diagnosis and for prognosis of existing disease, but may also be used to predict the likelihood of the future occurrence of disease. For example, clinically healthy patients can be screened for mutations in the inventive molecule that correlate with later disease onset. Such mutations may be observed in the heterozygous state in healthy individuals. In such cases a single mutation event can effectively disable proper functioning of the gene and induce a transformed or malignant phenotype. This screening also may be carried out prenatally or neonatally.

DNA molecules according to the invention also are well suited for use in so-called "gene chip" diagnostic applications. Such applications have been developed by, *inter alia*, Synteni and Affymetrix. Briefly, all or part of the DNA molecules of the invention can be used either as a probe to screen a polynucleotide array on a "gene chip," or they may be immobilized on the chip itself and used to identify other polynucleotides via hybridization to the surface of the chip. In this manner, for example, related genes can be identified, or expression patterns of the gene in various tissues can be simultaneously studied. Such gene chips have particular application for diagnosis of disease, or in forensic analysis to detect the presence or absence of an analyte. Suitable chip technology is described for example, in Wodicka *et al.*, *Nature Biotechnology*, 15:1359 (1997) which is hereby incorporated by reference in its entirety, and references cited therein.

PROTEIN-PROTEIN INTERACTIONS

Due to their similarity to certain known proteins, it is anticipated that some of the inventive protein molecules will interact with another class of cellular proteins. This is particularly true of those molecule containing leucine zipper motifs.

Any method suitable for detecting protein-protein interactions can be employed for identifying interacting targets. Among the traditional methods which can be employed are co-immunoprecipitation, crosslinking and co-purification through gradients or chromatographic columns. Utilizing procedures such as these allows for the identification of GAP gene products. Once identified, a GAP protein can be used, in conjunction with standard techniques, to identify its corresponding pathway gene. For example, at least a portion of the amino acid sequence of the pathway gene product can be ascertained using techniques well known to those of skill in the art, such as via the Edman degradation technique (see, *e.g.*, Creighton, 1983, *PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES*, W.H. Freeman & Co., N.Y., pp.34-49). The amino acid sequence obtained can be used as a guide for the generation of oligonucleotide mixtures that can be used to screen for pathway gene sequences. Screening can be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and for screening are well-known. (See *e.g.*, Ausubel, *supra*, and *PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS*, 1990, Innis *et al.*, eds. Academic Press, Inc., New York).

Additionally, methods can be employed which result in the simultaneous identification of interacting target genes. One method which detects protein interactions *in vivo*, the two-hybrid system, is described in detail for illustration purposes only and not by way of limitation. One version of this system has been described (Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, 88: 9578-9582 (1991)) and is commercially available from Clontech (Palo Alto, CA).

Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to a known protein, in this case an inventive protein, and the other contains the activator protein's activation domain fused to an unknown protein (a putative GAP, for instance) that is encoded by a cDNA which has been recombined into this plasmid as part of a cDNA library. The plasmids are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (*e.g.*, *lacZ*) whose regulatory region contains the transcription activator's binding sites. Either hybrid protein alone cannot activate transcription of the reporter gene, the DNA-binding domain hybrid cannot because it does not provide activation function, and the activation domain hybrid cannot because it cannot localize to the activator's binding sites. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or related methodology can be used to screen activation domain libraries for proteins that interact with a known "bait" gene product. By way of example, and not by way of limitation, gene products known to be involved in TH cell subpopulation-related disorders and/or differentiation, maintenance, and/or effector function of the subpopulations can be used as the bait gene products. Total genomic or cDNA sequences are fused to the DNA encoding on activation domain. This library and a plasmid encoding a hybrid of the bait gene product fused to the DNA-binding domain are cotransformed into a yeast reporter strain, and the resulting transformants are screened for those that express the reporter gene. For example, and not by way of limitation, the bait gene can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. These colonies are purified and the library plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the library plasmids.

The present invention, thus generally described, will be understood more readily by reference to the following examples, which are provided by way of illustration and are not intended to be limiting of the present invention.

The examples below are provided to illustrate the subject invention. These examples are provided by way of illustration and are not included for the purpose of limiting the invention.

EXAMPLES

EXAMPLE I: cDNA Library Construction

cDNA library plates and clones originated from five cDNA libraries that were constructed by directional cloning. These are available through the Resource Center (<http://www.rzpd.de>) of the German Genome Project. In particular, the hfbr2 (human fetal brain; RZPD number DKFZp564) and hfkd2 (human fetal kidney; DKFZp566) libraries were generated using the Smart kit (Clontech), except that PCR was carried out with primers that contained uracil residues to permit directional cloning without restriction digestion and ligation, and were complementary with the pAMP1 (LifeTechnologies) cloning sites for directional cloning. The htes3 (human testes; DKFZp434), hute1 (human uterus; DKFZp586) and hmcfl (human mammary carcinoma; DKFZp727) libraries are conventional (Gubler, U., Hoffman, B.J., (1983), A simple and very efficient method for generating cDNA libraries. Gene 25, 263-269), size-selected cDNA libraries. They are cloned into pSPORT1 (LifeTechnologies) via a NotI site which is introduced during reverse transcription downstream of the oligo dT primer and a SalI site that is introduced by the ligation of a adapters. The human mammary carcinoma library was constructed from MCF7 cells.

The cDNA sequences of this application were first identified among the sequences comprising various libraries. Technology has advanced considerably since the first cDNA libraries were made. Many small variations in both chemicals and machinery have been instituted over time, and these have improved both the efficiency and safety of the process. Although the cDNAs could be obtained using an older procedure, the procedure presented in this application is exemplary of one currently being used by persons skilled in the art. For the

purpose of providing an exemplary method, the mRNA isolation and cDNA library construction described here is for the MCF-7 library (DKFZp727) from which the clones named DKFZphmcfl_xxyyxx were obtained.

The human cell line MCF-7 was grown in DMEM supplemented with 10% fetal calf serum until confluency. 3×10^8 cells were harvested with a cell scraper in PBS. Cells were lysed in buffer containing 0.5 % NP-40 to leave the nuclei intact. The debris was pelleted by centrifugation at $15\,000 \times g$ for 10 minutes at 4 degrees Celsius. Proteins in the supernatant were degraded in presence of SDS and Proteinase K (30 minutes at 56 degrees Celsius). Precipitation of proteins was done in a Phenol/Chloroform extraction, RNA was precipitated from the aqueous phase with Na-acetate and Ethanol. Polyadenylated messages were isolated using Qiagen Oligotex (QIAGEN, Hilden Germany).

First strand cDNA synthesis was accomplished using an oligo (dT) primer which also contained an NotI restriction site. Second strand synthesis was performed using a combination of DNA polymerase I, *E. coli* ligase and RNase H, followed by the addition of a SalI adaptor to the blunt ended cDNA. The SalI adapted, double-stranded cDNA was then digested with NotI restriction enzyme, and fractionated by size on an agarose gel. DNA of the appropriate size was cut from the gel and cast into a second gel in a 90° angle. After electrophoresis in the second dimension, cDNA of the appropriate size was cut from the gel. The agarose block was broken down with help of gelase. The cDNA was purified with help of two phenol extractions and an ethanol precipitation. The cDNA was ligated into SalI/NotI pre-digested pSport1 vector (LifeTechnologies) and transformed into DH10B bacteria.

The libraries were arrayed into 384-well microtiter plates and spotted on high density nylon membranes for hybridization analysis. Filters and clones are available through the Resource Center. Whole plates were distributed to the sequencing partners of the consortium for systematic sequencing.

EXAMPLE II: Sequencing of cDNA Clones

All clones in the 384-well microtiter plates were sequenced from the 5' end. Sequencing was done preferentially using dye terminator chemistry (ABD or Amersham) on

ABI automated DNA sequencers (ABI 377, Applied Biosystems), one partner used EMBL prototype instruments (Arakis) mainly with dye primer chemistry.

The resulting expressed sequence tag (EST) sequences ("r1 ESTs" = sequenced from 5'-end) were analysed for:

- a) the lack of identical matches with known genes.

For this, the EST-sequence was blasted against the cDNA consortiums own database and after that against public databases and (with BLASTn and BLASTx against EMBL/EMBLNEW and assembled ESTs, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings). ESTs which were identical to known genes in more than 100 bp, with less than 2 mismatches, were excluded from further analysis.

- b) the presence of an open reading frame

Open reading frames (ORFs) were detected with an tool developed by Munich Information Center for Protein Sequences (MIPS) called ORF-map. ORF-map visualises potential start and stop-codons. If an ORF without a stop codon was detected in a r1-EST, the sequence was processed further.

- c) the presence of GC rich sequences

A script developed by MIPS computed the GC-content of the r1-sequence, which should be >40%. Writing similar scripts is within the ordinary skill of one in bioinformatics.

- d) the lack of repeat structures

Repeats such as Alu, Line or CA-repeats were detected by blasting (BLASTn and BLASTx, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings) against a repeat-database compiled by MIPS. If a repeat was present within the r1-sequence, the sequence were not processed further.

Novel clones that met all criteria were identified to the sequencers, who then performed 3'-end sequencing of these clones. The resulting 3' ESTs ("s1 ESTs" = sequenced from 3'-end) were checked for

a) the lack of matches with known genes in public databases, and sequences already generated by us.

This was done by blasting against EMBL/EMBLNEW and assembled EST (BLASTn and BLASTx, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings).

b) the presence of polyadenylation signals.

Again only clones matching the selection criteria were chosen to be sequenced completely by the sequencers. Clones were selected after the following criteria:

A very good ORF had at least one BLASTx match to other proteins. A "good ORF" should extend to the 3' end and be longer than ~40 codons. If the ORF started in the r1 sequence, in front of the potential start codon, there should not exist too many competing start codons in frame with the ORF start codon and the start should match the Kozak consensus ATG. If the EST sequence was too short to decide according to the potential ORF, and there were only a few or no start codons in the sequence the GC content of the Sequence should be greater than 40%. The r1 sequences needed not contain an polyA-tail at the 3' end. In addition, the results of the blasting against the assembled human ESTs could help in questionable cases to decide whether to stop or to continue. A hit against these ESTs was an indication to go further.

Clones passing the above-described screening were sequenced in full. Sequencing was done preferentially using dye terminator chemistry (ABD or Amersham) on ABI automated DNA sequencers (ABI 377, Applied Biosystems), one partner used EMBL prototype instruments (Arakis) mainly with dye primer chemistry. Primer walking (Strauss et al., 1986, Specific-primer-directed DNA sequencing. *Anal Biochem.* 154, 353-360) was the preferred sequencing strategy because of the lower redundancy possible compared to random shotgun (Messing, J., Crea, R., Seeburg, H.P. (1981) A system for shotgun DNA sequencing. *Nucleic Acids Res.* 9, 32-39) methods. Walking primers were generally designed using software (e.g. Haas, S., Vingron, M., Poustka, A., Wiemann, S. (1998) Primer design in large-scale sequencing. *Nucleic Acids Res.* 26, 3006-3012, Schwager, C., Wiemann, S., Ansorge, W. (1995) GeneSkipper: integrated software environment for DNA sequence assembly and

alignment. HUGO Genome Digest 2, 8-9) that permitted complete automation of this usually time consuming process and helped in the parallel processing of large numbers of clones.

EXAMPLE III: Bioinformatics analysis of full length cDNAs

Each sequence obtained was compared on nucleotide level in a stepwise manner to sequences in EMBL/EMBLNEW, EMBL-EST, EMBL-STS using the BLASTn algorithm. Basic Local Alignment Search Tool (BLAST, Altschul S. F. (1993) J Mol Evol 36:290-300; Altschul, S. F. et al (1990) J Mol Biol 215:403-10) is used to search for local sequence alignments. BLAST produces alignments of both nucleotide (BLASTn) and amino acid sequences (BLASTp or BLASTx) to determine sequence similarity. BLAST is especially useful in determining exact matches or in identifying homologs, because of the local nature of the alignments. While it is useful for matches which do not contain gaps, it is inappropriate for performing motif-style searching. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP).

An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment BLAST approach is to look threshold or cut off score set by the user. BLAST looks for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output. Parameter settings for the BLAST-operations (BLASTN 2.0a19MP-WashU) described were: EMBL-EMBLNEW: H=0 V=5 B=5 -filter seg; EMBL-EST: H=0 E=1e-10 B=500 V=500 -filter seg; EMBL-STS: H=0 V=5 B=5.

Search against EMBL/EMBLNEW was done to determine whether the cDNAs are already known, and also to find out whether the cDNAs are encoded by genomic sequences already sequenced and published/submitted to these databases.

Search against EMBL-EST was performed to get a first impression how abundant a particular cDNA would be and to get information on tissue specificity (so-called "electronic Northern-Blot", e.g. some of the cDNAs derived of the testis library show only hits to ESTs also derived of testis libraries).

The cDNA-sequences were blasted against EMBL-STS to determine STS-sequence-match to the cDNA, thus providing a mapping information to the new cDNA.

The potential protein-sequences were generated automatically by a script searching for the longest open reading frame (ORF) in each of the three forward frames with a minimum length of 90 codons. Next, the automatically generated ORFs were translated into protein sequences. These protein sequences were searched against the non redundant protein data set of PIR/SwissProt/Trembel/Tremblnew (BLASTP 2.0a19MP-WashU, parameter setting: V=7 B=7 H=0 -filter seg). If the script generated more than one ORF, one ORF was chosen manually by the annotater according to the degree of similarity to known proteins, the location of the ORF in the cDNA, the length, the amino acid composition and the content of Prosite-Motifs.

Additionally there was a BLASTx (BLASTX 2.0a19MP-WashU against non redundant protein database comprising PIR/SWISSPROT/TREMBL/TREMBLNEW; parameter-settings were: matrix/home/data/blast/matrix/aa/BLOSUM62 H=0 V=5 B=5 -filter seg) search to find potential frame shift in the complementary cds of the cDNAs and to identify unspliced or partly spliced cDNAs. The protein sequence was then transferred to the PEDANT system, in order to generate additional information on the new proteins. PEDANT (Protein Extraction, Description, and ANalysis Tool, Frishman, D. & Mewes, H.-W. (1997) PEDANTic genome analysis. Trends in Genetics , 13, 415-416) is a platform developed at the Munich Information Center for Protein Sequences (MIPS, Munich, Germany), which incorporates practically all bioinformatics methods important for the functional and structural characterisation of protein sequences. Computational methods used by PEDANT are:

FASTA

Very sensitive protein sequence database searches with estimates of statistical significance. Pearson W.R. (1990) Rapid and sensitive sequence comparison with FASTP and FASTA. *Methods Enzymol.* 183, 63-98.

BLAST2

Very sensitive protein sequence database searches with estimates of statistical significance. Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. Basic local alignment search tool. *Journal of Molecular Biology* 215, 403-10.

PREDATOR

High-accuracy secondary structure prediction from single and multiple sequences. Frishman, D. and Argos, P. (1997) 75% accuracy in protein secondary structure prediction. *Proteins*, 27, 329-335. Frishman, D. and Argos, P. (1996) Incorporation of long-distance interactions in a secondary structure prediction algorithm. *Prot. Eng.* 9, 133-142.

STRIDE

Secondary structure assignment from atomic coordinates. Frishman, D. and Argos, P. (1995) Knowledge-based secondary structure assignment. *Proteins* 23, 566-579.

CLUSTALW

Multiple sequence alignment. Thompson, J.D., Higgins, D.G. and Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. *Nucleic Acids Research*, 22:4673-4680.

TMAP

Transmembrane region prediction from multiply aligned sequences. Persson, B. and Argos, P. (1994) Prediction of transmembrane segments in proteins utilising multiple sequence alignments. *J. Mol. Biol.* 237, 182-192.

ALOM2

Transmembrane region prediction from single sequences. Klein, P., Kanehisa, M., and DeLisi, C. Prediction of protein function from sequence properties: A discriminant analysis of a database. *Biochim. Biophys. Acta* 787, 221-226 (1984). Version 2 by Dr. K. Nakai.

SIGNALP

Signal peptide prediction Nielsen, H., Engelbrecht, J., Brunak, S., and von Heijne, G (1997). Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering* 10, 1-6.

SEG

Detection of low complexity regions in protein sequences. Wootton, J.C., Federhen, S. (1993) Statistics of local complexity in amino acid sequences and sequence databases. *Computers & Chemistry* 17, 149-163.

COILS

Detection of coiled coils. Lupas, A., M. Van Dyke, and J. Stock, "Predicting Coiled Coils from Protein Sequences." *Science* (1991) 252, 1162-1164.

PROSEARCH

Detection of PROSITE protein sequence patterns. Kolakowski L.F. Jr., Leunissen J.A.M., Smith J.E. (1992) ProSearch: fast searching of protein sequences with regular expression patterns related to protein structure and function. *Biotechniques* 13, 919-921.

BLIMPS

Similarity searches against a database of ungapped blocks. J.C. Wallace and Henikoff S., (1992) PATMAT: a searching and extraction program for sequence, pattern and block queries and databases, *CABIOS* 8, 249-254. Written by Bill Alford.

HMMER

Hidden Markov model software . Sonnhammer E.L.L., Eddy S.R., Durbin R. (1997) Pfam: A Comprehensive Database of Protein Families Based on Seed Alignments. *Proteins* 28, 405-420.

pI

Perl script that returns the amino acid composition, molecular weight, theoretical pI, and expected extinction coefficient of an amino acid sequence. By Fred Lindberg. The parameter-settings were as follows: known3d: score > 100; BLAST: E-value < 10; SCOP: <= 50 Alignments, E-Value < 0.0001; signalp: Y=0.7; untersucht vom N-Terminus her: 50 aa; funcat: E-value < 0.001; BLOCKS: <= 10 hits; BLIMPS: threshold 1100.0; COILS: threshold 0.95; SEG: threshold 20.0; BLAST in report: E-value < 0.001; PIR-KW, superfamilies, EC-Nummern in report: E-value < 0.00001; known3d in report: score > 120

The results of PEDANT analysis, together with the results of the similarity searches, constitute the basis for the structural and functional annotation of the cDNAs and the encoded proteins, as specified below.

EXAMPLE III: CELLULAR LOCALIZATIONS OF GFP-FUSION PROTEINS

Plasmids of cDNA-GFP fusions were transfected into mammalian tissue culture cells and allowed to express the proteins for up to 48 hours. Live cells were imaged at 24 hours and 48 hours after transfection and the localisations recorded. The chart, below, depicts the apparent final cellular localisations of 107 cDNA-GFP fusions.

In order to minimize the possibility of the GFP interfering with protein function and/or localization, two separate populations of cDNAs were generated encoding N-terminal or C-terminal GFP fusions. Clearly this appears to be a crucial strategy, since overall only 56% of the proteins localised to a specific compartment irrespective of the position of the GFP. In the instances where only one fusion localized, the complementary fusion either gave no expression or a nuclear and cytosolic staining - characteristic for GFP alone expression.

Each cDNA in turn was subjected to bioinformatic analysis. Where possible, the potential subcellular localisations of the expressed proteins were determined. This

information was then compared to the actual localisations determined from expression of the GFP-fusion proteins in mammalian cells.

DKFZphfbr2_16c16

group: Cell structure and motility

DKFZphfbr2_16c16.3 encodes a novel 586 amino acid protein with similarity to the human actin binding protein MAYVEN and Drosophila Kelch.

MAVEN is a novel actin binding protein predominantly expressed in brain. Drosophila kelch is involved in the maintenance of ring canal organization during oogenesis. The amino half of the protein including the BTB domain mediates dimerization, while the amino half might allow cross-linking of ring canal actin filaments, thus organising the inner rim cytoskeleton. The kelch repeat domain is necessary for ring canal localisation and believed to mediate an additional interaction, possibly with actin. The new protein shares the features of both proteins and therefore should be involved in the organisation of cyto skeleton binding to membrane proteins.

The new protein can find application in modulating/blocking of cyto skeleton-membrane protein interaction.

similarity to Drosophila kelch

complete cDNA, complete cds, EST hits.

on genomic level partly encoded by AC005082 and AC006039

Sequenced by Qiagen

Locus: unknown

Insert length: 3028 bp

Poly A stretch at pos. 3004, polyadenylation signal at pos. 2984

```

1  GGGGGCCCCG  GGACGCAGCC  CAGTTGGTAG  CGTCGCTCCC  TGAGCGTTTC
51  TAAGGGGGCC  GCCCGGCCCT  GTCTTTCGGC  AGTGGCCGAG  CCACCGCCGC
101 CTGCCGCGCG  TTCCAGAGCT  GGGCGCTGCA  GCTGCACTGC  CGATCGCCGT
151 GTTTGGTTCG  TAGAATCCCC  AGTGTGCCCA  GAGAGTGCGA  CQCCTCGCCC
201 GGCCCGGGCG  GCCCGGGGCG  TGAACCGAGC  TGAGGGAGGA  TGGCAGCCTC
251 TGGGGTGGAG  AAGAGCAGCA  AGAAGAAGAC  CGAGAAGAAA  CTGCTGCTC
301 GGAAGAAGC  TAAATTGTTG  GCGGGTTTCA  TGGGCGTCAT  GAATAACATG
351 CGGAAACAGA  AAACGTTGTG  TGACGTGATC  CTCATGGTCC  AGGAAAGAAA
401 GATACCTGCT  CATCGTGTG  TTCTTGCTGC  AGCCAGTCAT  TTTTTAACT
451 TAAATGTTCA  AACTAACATG  CTGAATCAA  AGTCCTTGA  AGTAGAATC
501 AAAGATGCTG  AACCTGATAT  TATTGAACAA  CTGGTGGAAT  TTGCTTATAC
551 TGCTAGAATT  TCCGTGAATA  GCAACAATGT  TCAGTCTTTG  TTGGATGCAG
601 CAAACCAATA  TCAGATTGAA  CCTGTGAAGA  AAATGTGTGT  TGATTTTTTG
651 AAAGAACAAG  TGATGCTTTC  AAATTGCTTT  GGTATAAGTG  TGCTAGCGGA
701 GTGTCTAGAT  TGTCTGAAT  TGAAGCAAC  TGCAGATGAC  TTTATTCATC
751 AGCACTTTAC  TGAAGTTTAC  AAAACTGATG  AATTTCTTCA  ACTTGATGTC
801 AAGCGAGTAA  CACATCTTCT  CAACCAAGAC  ACTCTGACTG  TGAGAGCAGA
851 GGATCAGGTT  TATGATGCTG  CAGTCAGGTG  GTTGAAATAC  GATGAGCCTA
901 ATCGCCAGCC  ATTTATGGTT  GATATCCTTG  CTAAAGTCAG  GTTTCCTCTT
951 ATATCAAAGA  ATTTCTTAAG  TAAAACGGTA  CAAGCTGAAC  CACTTATTCA
1001 AGACAATCCT  GAATGCCTTA  AGATGGTGAT  AAGTGGAATG  AGGTACCATC
1051 TACTGTCTCC  AGAGGACCGA  GAAGAAGTTC  TAGATGGCAC  AAGACCTAGA
1101 AGAAAGAAAC  ATGACTACCG  CATAGCCCTA  TTTGGAGGCT  CTCAACCACA
1151 GTCTTGTAAG  TATTTTAACC  CAAAGGATTA  TAGCTGGACA  GACATCCGCT
1201 GCCCCTTTGA  AAAACGAAGA  GATGCAGCAT  GCGTGTTTTC  GGACAATGTA
1251 GTATACATTT  TGGGAGGCTC  TCAGCTTTTC  CCAATAAAGC  GAATGGACTG
1301 CTATAATGTA  GTGAAGGATA  GCTGGTATTC  GAAACTGGGT  CCTCCGACAC
1351 CTCGAGACAG  CCTTGCTGCA  TGTGCTGCAG  AAGGCCAAAT  TTATACATCT
1401 GGAGGTTTCA  AAGTAGGAAA  CTCAGCTCTG  TATTTATTTG  AGTGCTATGA
1451 TACGAGAAGT  GAAAGCTGGC  ACACAAAGCC  CAGCATGCTG  ACCCAGCGCT
1501 GCAGCCATGG  GATGGTGGAA  GCCAATGGCC  TAATCTATGT  TTGTGGTGGA
1551 AGTTTAGGAA  ACAATGTTTC  AGGGAGAGTG  CTTAATTCCT  GTGAAGTTTA
1601 TGATCCTGTC  ACAGAAACAT  GGAAGTGGCT  GTGTCCAATG  ATTGAAGCCA
1651 GGAAGAATCA  TGGGCTGGTA  TTTGTAAAAG  ACAAGATATT  TGCTGTGGGT
1701 GGTGCAATAT  GTTTAGGTGG  TCTGGACAAT  GTGGAATATT  ACGATATTAA
1751 GTTGAACGAA  TGGAAGATGG  TCTACCAAT  GCCATGGAAG  GGTGTAACAG
1801 TGAAATGTGC  AGCAGTTGGC  TCTATAGTTT  ATGCTTTGGC  TGGTTTTTCAG

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2301 AGAAGATTGG CTCATCAGTG AAGCGCAGTA TCTTAGCTCT AGATTCTATT
2351 TTCATGCATC ACAGAAAGTG TATACGGTTA GGTCTGTTTG TGCTCAGTCA
2401 AGAACTAAGA AATAGTATGA ATTGTAAGTC AAGATGGGCA ACTCAGATGG
2451 AGCAGCTTAG TCTCACAGTT TGCTTGTCTA TTTATTTTAT TTAGTGCCAA
2501 ATGTATTCCA TTTTAAAAGT AAGCCAGAGT GAGTCAAGGC ATATACACAC
2551 TTTCTCACAA AACTTCCTAA ACAGATTTGG GGGTTAATA TGTCCAACCTC
2601 CTCATGAAAT ATATTCAATC CACTTAAATA TATTCCATCT TTTTAACATA
2651 AAATGTAAAG CTTAGCACCC ATCATTAAAT TATGTCTCTG TTTTATCCAG
2701 TGGTTAAAAA AGGATTCTGC CTCTTTAGTC CTCACTGTGA AATAAAACCC
2751 AATCATAGTA AGTGATTAAC TAGCAAAAAG TAAAGCTATT TATAGCAAAT
2801 TTCTAGATCA TTAGAAAAGC ACTGGTAGTT GTACAATATC AGTGTGACT
2851 TTGAACCTCT TTAACGAGAT CATGAATTCT TTTCCCTTAG CCAAAACATG
2901 AAATATTTAA CCTAGTTGTC TCTAAAAGTT TTGTAATCAT GAGTTAGATA
2951 TATGTCATCT CCTATTCTT GCTTTTATGT GATCAATAAA TCTTTTACAA
3001 ACCCAAAAGA AAAAAAAAAA AAAAAAAA

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BLAST Results

Entry AC005082 from database EMBL:
Homo sapiens clone RG271G13; HTGS phase 1, 7 unordered pieces.
Score = 6460, P = 0.0e+00, identities = 1292/1292
4 exons matching Bp 1180-3007

Entry AC006039 from database EMBL:
*** SEQUENCING IN PROGRESS *** Homo sapiens clone NH0319F03; HTGS phase 1, 3 unordered pieces.
Score = 1780, P = 2.0e-117, identities = 368/377
5 exons matching Bp 6-860

Entry HSG20603 from database EMBL:
human STS A005Y34.
Score = 670, P = 1.0e-23, identities = 134/134

Medline entries

93201592:
kelch encodes a component of intercellular bridges in Drosophila egg chambers.

97412177:
Drosophila kelch is an oligomeric ring canal actin organizer.

Peptide information for frame 3

ORF from 240 bp to 1997 bp; peptide length: 586
Category: strong similarity to known protein

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1 MAASGVEKSS KKKTEKKLAA REEAKLLAGF MGVMNNMRKQ KTLCDVILMV
51 QERKIPAHRV VLAAASHFFN LMFTTNMLES KSFEVELKDA EPDIIEQLVE
101 FAYTARISVN SNNVQSLDDA ANQYQIEPVK KMCVDFLKEQ VDASNCLGIS
151 VLAECCLDCE LKATADDFIH QHFTEVYKTD EFLQLDVKRV THLLNQDTLT
201 VRAEDQVYDA AVRWLKYDEP NRQPEMVDIL AKVRFPLISK NFLSKTVQAE
251 PLIQDNPECL KMVISCMRYH LLSPEDEREL VDCTRPRRKK HDYRIALFGG
301 SQPQSCRYFN PKDYSWTDIR CPFKEKRRDAA CVFWDNVVYI LGGSQLFPIK
351 RMDCYNVVKD SWYSKLGPPPT PRDSLAAACAA EGKIYTSGGG EVGNSALYLF
401 ECYDTRTESW HTKPSMLTQR CSHGMVEANG LIYVCGGSLG NNVSGRVLNS
451 CEVYDPATET WTELCPMIEA RKNHGLVFVK DKIFAVGGQN GLGGLDNVEY
-501 YDIKLEWKM VSPMPWKGVT VKCAAVGSIV YVLAGFQGVG RLGHILEYNT
551 ETDKWVANSK VRAFPVTSCL ICVVDTCGAN EETLET

```

BLASTP hits

Entry KELC_DROME from database SWISSPROT:
RING CANAL PROTEIN (KELCH PROTEIN).
Length = 689
Score = 816 (287.2 bits), Expect = 1.9e-81, P = 1.9e-81
Identities = 187/542 (34%), Positives = 290/542 (53%)

Entry AC004021_1 from database TREMBL:
WUGSC:H_DJ0186K10.1"; Human PAC clone DJ0186K10 from 5q31,
complete sequence. Homo sapiens (human)
Length = 497

Score = 704 (247.8 bits), Expect = 1.4e-69, P = 1.4e-69
Identities = 163/483 (33%), Positives = 253/483 (52%)

Entry HSDKG12_1 from database TREMBL:
"KIAA0132": Human mRNA for KIAA0132 gene, complete cds. Homo sapiens (human)
Length = 624
Score = 692 (243.6 bits), Expect = 2.6e-68, P = 2.6e-68
Identities = 175/527 (33%), Positives = 272/527 (51%)

Entry A45773 from database PIR:
kelch protein, long form - fruit fly (Drosophila melanogaster)
Length = 1476
Score = 817 (287.6 bits), Expect = 1.7e-80, P = 1.7e-80
Identities = 189/549 (34%), Positives = 292/549 (53%)

Alert BLASTP hits for DKFZphfbr2_16c16, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_16c16, frame 3

Report for DKFZphfbr2_16c16.3

[LENGTH] 586
[MW] 65992.06
[pI] 6.08
[HOMOL] PIR:A45773 kelch protein, long form - fruit fly (Drosophila melanogaster) 5e-85

[BLOCKS] BL00075D Dihydrofolate reductase proteins
[SCOP] dlgo3 2.46.1.1.1 (151-537) Galactose oxidase, central domain 6e-36
[PIRKW] zinc finger 2e-11
[PIRKW] DNA binding 9e-10
[PIRKW] transcription factor 1e-06
[SUFFAM] A55R protein middle region homology 1e-35
[SUFFAM] POZ domain homology 1e-35
[SUFFAM] vaccinia virus 59K HindIII-C protein 5e-15
[SUFFAM] A55R protein 1e-35
[SUFFAM] myxoma virus M9-R protein 2e-11
[SUFFAM] A55R protein carboxyl-terminal homology 1e-35
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] MYRISTYL 8
[PROSITE] CK2_PHOSPHO_SITE 10
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] PKC_PHOSPHO_SITE 11
[PROSITE] ASN_GLYCOSYLATION 1
[KW] Alpha_Beta
[KW] LOW_COMPLEXITY 3.75 %

SEQ MAASGVKSSKKKTEKKLAAREEAKLLAGFMGMNMRKQKTLCDVILMVQERKIPAHRV
SEGXXXXXXXXXXXXXXXXXXXXXXXXX.....
PRD ccccecc

SEQ VLAAASHFFNLMFTTNMLESKSFVELKDAEPDIIIEQLVEFAYTARISVNSNNVQSL LDA
SEG
PRD ecc

SEQ ANQYQIEPVKKMCVDLKEQVDASNCLGISVLAECDCPELKATADDFIHQHFTEVYKTD
SEG
PRD hhh

SEQ EFLQLDVKRVTHLLNQDTLTVRAEDQVYDAAVRWLKYDEPNRQPFMVDILAKVRFPLISK
SEG
PRD hhh

SEQ NFLSKTVQAEPLIQDNPECLKMVISGMRHYLLSPEDREELVDGTRPRRKKHDYRIALFGG
SEG
PRD hhh

SEQ SQPQSCRYFNP KDYSWTDIRCPFEKRRDAACVFDWNVVYILGGSQLFPIKRMDCYNVVKD
SEG
PRD ccc

SEQ SWYSKLGPPTPRDSLAAACAEKGKIYTSGGSEVGNSALYLFECYDTRTESWHTKPSMLTQR
SEG
PRD ccc

```

SEQ      CSHGMVEANGLIYVCGGSLGNNVSGRVLNSCEVYDPATETWTELCPMIEARKNHGLVFK
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      DKIFAVGGQNLGLGDLNVEYYDIKLNEWKMVSPMPWKGVTVKCAAVGSIVYVLAGFQGVG
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      RLGHILEYNTETDKWVANSKVRAPVTSCLICVVDTCGANEETLET
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

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Prosites for DKFZphfbr2_16c16.3

PS00001	442->446	ASN_GLYCOSYLATION	PDOC00001
PS00004	11->15	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	188->192	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	9->12	PKC_PHOSPHO_SITE	PDOC00005
PS00005	10->13	PKC_PHOSPHO_SITE	PDOC00005
PS00005	14->17	PKC_PHOSPHO_SITE	PDOC00005
PS00005	104->107	PKC_PHOSPHO_SITE	PDOC00005
PS00005	200->203	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005
PS00005	370->373	PKC_PHOSPHO_SITE	PDOC00005
PS00005	418->421	PKC_PHOSPHO_SITE	PDOC00005
PS00005	444->447	PKC_PHOSPHO_SITE	PDOC00005
PS00005	520->523	PKC_PHOSPHO_SITE	PDOC00005
PS00005	552->555	PKC_PHOSPHO_SITE	PDOC00005
PS00006	4->8	CK2_PHOSPHO_SITE	PDOC00006
PS00006	42->46	CK2_PHOSPHO_SITE	PDOC00006
PS00006	116->120	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	315->319	CK2_PHOSPHO_SITE	PDOC00006
PS00006	370->374	CK2_PHOSPHO_SITE	PDOC00006
PS00006	405->409	CK2_PHOSPHO_SITE	PDOC00006
PS00006	460->464	CK2_PHOSPHO_SITE	PDOC00006
PS00006	550->554	CK2_PHOSPHO_SITE	PDOC00006
PS00007	202->209	TYR_PHOSPHO_SITE	PDOC00007
PS00008	5->11	MYRISTYL	PDOC00008
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	389->395	MYRISTYL	PDOC00008
PS00008	424->430	MYRISTYL	PDOC00008
PS00008	436->442	MYRISTYL	PDOC00008
PS00008	440->446	MYRISTYL	PDOC00008
PS00008	487->493	MYRISTYL	PDOC00008
PS00008	493->499	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16c16.3)

DKFZphfbr2_16f21

group: brain derived

DKFZphfbr2_16f21 encodes a novel 208 amino acid protein with strong similarity to human zinc finger protein 216.

The novel protein shows strong similarity to the human zinc finger protein 216, but has no Zn finger.

PROSITE: Contains no Zinc finger; No informative BLAST results; no predictive prosite, pfam or SCOP motif

The new protein can find application in studying the expression profile of brain-specific genes.

strong similarity to zinc finger protein 216

complete cDNA, complete cds, EST hits
start matches Kozak consensus ANNatgG,

Sequenced by Qiagen

Locus: unknown

Insert length: 1512 bp

Poly A stretch at pos. 1490, polyadenylation signal at pos. 1474

```
1 GGGAGCAAGC AGGGGTTCGG CGGCATTACC TGTACCCATT CACCGGCGGC
51 TACCGGCGGC GGC GCGTAGC GTGTCAGGCG GAGAGACCCG CCGCCAGGTG
101 TGCAACTGAG GAACATGGCT CAAGAAACTA ATCAGAGCCA AGTGCCTATG
151 CTTTGTTCCT CTGGCTGTGG ATTTTATGGA AACCCCTCGTA CAAATGGCAT
201 GTGTTTCAGTA TGCTATAAAG AACATCTTCA AAGACAGAAT AGTAGTAATG
251 GTAGAATAAG CCCACCTGCA ACCTCTGTCA GTAGTCTGTC TGAATCTTTA
301 CCAGTTCAAT GCACAGATGG CAGTGTGCCA GAAGCCCACT CAGCATTAGA
351 CTCTACATCT TCATCTATGC AGCCCAGCCC TGTATCAAAT CAGTCACTTT
401 TATCAGAATC TGTAGCATCT TCTCAATTGG ACAGTACATC TGTGGACAAA
451 GCAGTACCTG AACAGAGAAG TGTGCAGGCT TCAGTATCAG ACACAGCACA
501 GCAGCCATCT GAAGAGCAAA GCAAGCCTCT TGAAAAACCG AAACAAAAAA
551 AGAATCGCTG TTTTCATGTG AGGAAGAAAG TGGGACTTAC TGGGTTTGAA
601 TGCCGCTGTG GAAATGTTTA CTGTGGTGTA CACCGTTACT CAGATGTACT
651 CAATTGCTCT TACAATTACA AAGCCGATGC TGCTGAGAAA ATCAGAAAAG
701 AAAATCCAGT AGTTGTTGGT GAAAAGATCC AAAAGATTTG AACTCCTGCT
751 GGAATACAAA ATTCTTGAGC ATCTGCAAAAC TAAAAATTGA CTTGAGGTTT
801 TTTTTCCTCT AGTCATTGGG AATGTACAGC ACTGTATCTT GCATGTCATC
851 GGAAGAATAG ATTTTGTGTT TGGTTTGTGTT TTGAAAATGA CTCTGAACAT
901 TTATTTCCAT TGCAATTTCT GTGGCTGAGG AGACTTAAAC TTTACAAGTA
951 TTATCCTTTT AAGATCATTT TAATTTTAGT TGAGTGCAGA GGGCTTTTAT
1001 AACAAACGTG CAGAAATTTT GGAGGGCTGT GATTTTTCCT GTATTAAACA
1051 TGCATGCATT AATCTTGCGC TTTATTTTCT CATTATGTAT GTATATATCG
1101 CTTTCTCTCG CAGCAGGATT TCTCTTTTGA TAATGCCCTT TAGGGCACA
1151 CTAGTTATCA GTAAGTGAAT GTATCTTAAT CATTATGGCT GCTTCTGTTT
1201 TTTTCAATTA AAAGGTTATT CATATGTTAG CATATAGTTT CTTTGACCCC
1251 ACTATTTATG TCTGAATCAT TTGTCACAAG AGAGTGTGTG CTGATGAGAT
1301 TGTAAGTTTC TGTGTTTAAA CTTTTTTTTC AGCGAGGGAA GAAAAASCTG
1351 TATGCATTTT ATTGCTGTCT ACAGGTTTCT TTCAGATTAT GTTCATGGGT
1401 TTGTGTGTAT ACAATATGAA GAATGATCTG AAGTAATTGT GCTGTATTTA
1451 TGTATTATCA CCAGTCTTTG ATTAAATAAA AAGGAAAACC AGAAAAAAA
1501 AAAAAAAA AA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 115 bp to 738 bp; peptide length: 208
Category: strong similarity to known protein

```

1 MAQETNHSQV PMLCSTGCGF YGNPRTNGMC SVCYKEHLQR QNSSNGRISP
51 PATSVSSLSE SLPVQCTDGS VPEAQSALDS TSSSMQPSPV SNQSLLESV
101 ASSQLDSTSV DKAVPETEDV QASVSDTAQQ PSEEQSKPLE KPKQKKNRCF
151 MCRKKVGLTG FECRCGNVYC GVHRYSDVLN CSYNYKADAA EKIRKENPVV
201 VGEKIQKI

```

BLASTP hits

Entry ATF7H19_1 from database TREMBLNEW:
gene: "F7H19.10"; product: "putative protein"; Arabidopsis thaliana DNA
chromosome 4, BAC clone F7H19 (ESSAII project) >TREMBL:ATT12H17_21
gene: "T12H17.210"; product: "predicted protein"; Arabidopsis thaliana
DNA chromosome 4, BAC clone T12H17 (ESSAII project)
Score = 206, P = 2.1e-24, identities = 51/146, positives = 77/146

Entry PVPVPR3A_1 from database TREMBL:
gene: "PVPVPR3"; P.vulgaris PVPVPR3 protein mRNA, complete cds.
Score = 237, P = 4.9e-20, identities = 50/136, positives = 73/136

Entry AF062072_1 from database TREMBL:
gene: "ZNF216"; product: "zinc finger protein 216"; Homo sapiens zinc
finger protein 216 (ZNF216) gene, complete cds.
Score = 591, P = 1.6e-57, identities = 124/215, positives = 147/215

Alert BLASTP hits for DKFZphfbr2_16f21, frame 1

TREMBL:AF062071_1 product: "zinc finger protein ZNF216"; Mus musculus
zinc finger protein ZNF216 mRNA, complete cds., N = 1, Score = 590, P =
2.1e-57

TREMBLNEW:AB001773_1 gene: "pem-6"; product: "PEM-6"; Ciona savignyi
pem-6 (posterior end mark 6) mRNA, complete cds., N = 1, Score = 421, P
= 1.7e-39

>TREMBL:AF062071_1 product: "zinc finger protein ZNF216"; Mus musculus zinc
finger protein ZNF216 mRNA, complete cds.
Length = 213

HSPs:

Score = 590 (88.5 bits), Expect = 2.1e-57, P = 2.1e-57
Identities = 123/213 (57%), Positives = 146/213 (68%)

```

Query:      1 MAQETNHSQV PMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQNSSNGRISPPAT---SVSS 57
             MAQETN + PMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQ +S GR+SP T S S
Sbjct:      1 MAQETNQTG PMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQNS-GRMSPMGTASGSNSP 59

Query:      58 LSESLPVQCTDGSVPEAQSALDSTSSSMQPSPVSNQSLLE--SVASSQLDSTSVDKAVP 115
             S+S VQ D + + A STS + PV+ + + ++ S+ D + K
Sbjct:      60 TSDSASVQRADAGLNNCEGAAGSTSEKSRNVPAALPVTQQMTEMSISREDKITPKT-E 118

Query:      116 ETEDVQASVSDTAQQPSEEQS--KPLEKPKQKKNRCFCMCRKKVGLTGFECCRCGNVYCGVH 173
             +E V S + QPS QS K E PK KKNRCFCMCRKKVGLTGF+CRCGN++CG+H
Sbjct:      119 VSEPVTTPSPSPSVSQSSSQSEEKAPELPKPKKNRCFCMCRKKVGLTGFDRCGNLFCGLH 178

Query:      174 RYSDVLNCSYNYKADAAEKIRKENPVVVGEKIQKI 208
             RYSD NC Y+YKA+AA KIRKENPVVV EKIQ+I
Sbjct:      179 RYSDKHNCPPDYKAEAAAKIRKENPVVVAEKIQRI 213

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Pedant information for DKFZphfbr2_16f21, frame 1

Report for DKFZphfbr2_16f21.1

```

[LENGTH]      208
[MW]           22541.23
[pI]           6.80
[HOMOL]        TREMBL:AF062072_1 gene: "ZNF216"; product: "zinc finger protein 216"; Homo
sapiens zinc finger protein 216 (ZNF216) gene, complete cds. 9e-57
[PIRKW]        zinc 8e-13
[PIRKW]        zinc finger 8e-13

```

[PIRKW] fusion-protein 8e-13
 [SUPFAM] unassigned ubiquitin-related proteins 8e-13
 [SUPFAM] ubiquitin homology 8e-13
 [PROSITE] MYRISTYL 2
 [PROSITE] CK2_PHOSPHO_SITE 7
 [PROSITE] ASN_GLYCOSYLATION 4
 [KW] Irregular
 [KW] LOW_COMPLEXITY 7.21 %

SEQ MAQETNHSQVPMCLSTGCGFYGNPRTNGMCSVCYKEHLQRQNSSNGRISPPATSVSSLSE
 SEG
 PRD ccc

SEQ SLPVQCTDGSVPEAQSALDSTSSSMQSPVSNQSLLESVASSQLDSTSVDKAVPETEDV
 SEGXXXXXXXXXXXXXXXXXXXX.....
 PRD ccc

SEQ QASVSDTAQQPSEEQSKPLEKPKQKKNRCFMCRKKVGLTGFECCGCVNYCGVHRYSDVLN
 SEG
 PRD ccc

SEQ CSYNYKADAAEKIRKENPVVVGEKIQKI
 SEG
 PRD ccchhh

Prosites for DKFZphfbr2_16f21.1

PS00001	6->10	ASN_GLYCOSYLATION	PDOC00001
PS00001	42->46	ASN_GLYCOSYLATION	PDOC00001
PS00001	92->96	ASN_GLYCOSYLATION	PDOC00001
PS00001	180->184	ASN_GLYCOSYLATION	PDOC00001
PS00006	57->61	CK2_PHOSPHO_SITE	PDOC00006
PS00006	70->74	CK2_PHOSPHO_SITE	PDOC00006
PS00006	76->80	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	108->112	CK2_PHOSPHO_SITE	PDOC00006
PS00006	123->127	CK2_PHOSPHO_SITE	PDOC00006
PS00006	159->163	CK2_PHOSPHO_SITE	PDOC00006
PS00008	22->28	MYRISTYL	PDOC00008
PS00008	166->172	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16f21.1)

DKFZphfbr2_16g18

group: cell cycle

DKFZphfbr2_16g18.3 encodes a novel 984 amino acid protein with similarity to centromeric proteins of yeasts.

The novel protein shows similarity to *S. pombe* SPAC17A5.07c and the *S. cerevisiae* Smt4p suppressor of MIF2 gene. MIF2 encodes a centromeric protein with homology to the mammalian centromeric protein CENP-C. Mutations in MIF2 stabilise dicentric minichromosomes and confer high instability to chromosomes that bear a cis-acting mutation in element I of the yeast centromeric DNA (CDEI). Therefore the new protein should be involved in centromer organisation, too.

The new protein can find application in modulating/blocking the cell cycle and influencing the behavior of chromosomes, both natural and artificial in eukaryotic cells.

similarity to KIAA0797 and yeast Smt4p

complete cDNA, complete cds, EST hits
the yeast Smt4 protein seems to be involved in centromer function
and microtubule organisation

Sequenced by Qiagen

Locus: unknown

Insert length: 4826 bp

Poly A stretch at pos. 4756, polyadenylation signal at pos. 4736

```
1 GGGTCGAGGT CGACGGTATC GATAAGTTTT TTTTTTTTTT TTTTTTTTTT
51 TTTTCCTTTC CCCTCCCTCC CCGGAGGGG TCCTGAGGTG
101 ACAGCGCCTC CAACTGAAAT TTCAGCAGCG GGAGAAGATG GACAAGAGAA
151 AGCTCGGGCG ACCGCCATCT TCATCCGAAA TCATCACAGA AGGAAAAAAGG
201 AAAAAAGTCAT CTCTGATTT ATCGGAGATA AGAAAGATGT TAAATGCAAA
251 ACCAGAGGAT GTCCATGTTC AATCACCCT GTCCAAATTC AGAAGCTCAG
301 AACGCTGGAC TCTCCCTTTG CAGTGGGAAA GAAGCCTAAG GAATAAAGTC
351 ATCTCTCTAG ACCATAAAAA TAAAAAACAT ATCCGAGGGT GTCCTGTTAC
401 TTCCAGGTCA TCACCAGAAA GGATACCCAG AGTTATATTG ACGAATGTCC
451 TGGGAACGGA GTTAGGAAGA AAATACATAA GGACCCACCC TGTAACTGAG
501 GGAAGTTTGA GTGATACAGA CAACTTGCAA TCAGAGCAAC TTTCTTCATC
551 ATCTGATGGC AGCCTAGAAT CTTATCAAAA TCTAAACCCT CACAAGAGCT
601 GTTATTTTATC TGAAGGGGGC TCACAACGAA GTAAGACAGT AGATGACAA
651 TCTGCAAAAGC AGACTGCGCA CAATAAAGAA AAACGAAGAA AGGATGATGG
701 CATTTCTCTT TTAATATCTG ATACTCAGCC TGAAGACCTT AACAGTGCAA
751 GTAGAGGTTG TGATCATCTC GAACAGGAAA GCAGAAACAA GGATGTTAAA
801 TATTCTGATT CAAAAGTGA ACTCACTCTG ATTTCCAGGA AGACAAAGAG
851 AAGGCTTAGA AATAATTTAC CTGATTCTCA ATATTGTACT TCTTTGGATA
901 AGTCAACAGA ACAGACAAAA AAACAAGAAG ATGACTCAAC AATATCCACT
951 GAGTTTGAAA GGCCAAGTGA AAATATCAT CAGGATCCAA AACTGCCTGA
1001 AGAAATTACA ACTAAACCTA CAAAAGTGA TTTACTAAG CTATCCTCAC
1051 TTAACAGTCA GGAGTTGACT TTGAGTAATG CCACCAAAAG TGCCTCTGCC
1101 GGTTCACACA CTGAAACCGT TGAGTACTCT AATTCCATTG ATATTGTGGG
1151 GATTTCTTCC CTGGTTGAGA AGGATGAGAA TGAGTTGAAT ACCATAGAAA
1201 AGCCTATTCT AAGAGGACAT AATGAAGGGA ACCAATCACT GATCTCAGCT
1251 GAACCAATTG TTGTTTCCAG TGATGAAGAA GGACCTGTTG AACATAAAAG
1301 TTCAGAAATT CTTAAGTTAC AATCTAAGCA AGACCGTGAG ACAACTAATG
1351 AAAATGAGAG TACTTCTGAA TCAGCATTTG TAGAATACC ATTGATTACA
1401 TGTGAATCTG TACAGATGTC ATCTGAATTA TGCCCATATA ATCCTGTCAT
1451 GGAGAACATT TCCAGTATTA TGCCTAGTAA TGAGATGGAT CTACAACCTG
1501 ATTTTATATT TACTTCTGTT TATATTGGTA AAATAAAGG AGCTTCTAAA
1551 GGTGTGTGTTA CAATCACAAA AAAATATATT AAGATCCCAT TTCAAGTGTC
1601 CCTGAATGAG ATTTCATTGC TAGTGGATAC CACACATTTA AAGCGGTTTG
1651 GGTATTGGAA AAGTAAGGAT GATAATCACA GTAAAAGGAG TCATGCTATT
1701 CTTTTCTTCT GGGTCTCTTC AGATTATCTT CAAGAGATTC AGACCAATT
1751 AGAACAATCT GTATTAAAGC AGCAATCAAA ATCTAGTGAA TTCATTTTCC
1801 TTGAACCTCA CAATCCTGTT TCACAGAGAG AAGAAATGAA GCTGAAAGAT
1851 ATTATGACGG AAATAAGTAT AATCAGTGGA GAATTAGAGC TTTCTTACCC
1901 GTTGTCTTGG GTTCAGGCAT TTCTTTGTT TCAGAACCTC TCTTCAAAG
1951 AAAGTTCTTT TATTCAATT TACTGTGTTT CAACTTGTTT TTTCCCTGCT
2001 GGTGTTGCTG TTGCTGAAGA AATGAAGCTG AAATCAGTAT CTCAGCCCTC
2051 AAACACAGAT GCGGCCAAGC CTACTTACAC CTTCTGTCAG AAGCAAAGTA
2101 GCGGTTGCTA TCCCTTTCT ATTACATCTA ATCCAGATGA AGAATGGCGG
2151 GAAGTCAGGC AACTGGGACT TGTTCAAGAG TTGATTGTAT ATCCTCCACC
2201 ACCTACTAAG GGGGGATTGG GAGTAACTAA TGAAGATCTG GAGTGTTTAG
2251 AAGAAGGAGA GTTCTTAAT GATGTAATCA TTGATTITTA CCTTAAGTAT
2301 CTTATATTGG AGAAGGCATC AGATGAACCT GTTGAACGAA GTCACATTTT
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2351 TAGTAGCTTT TTCTATAAAT GETTGACAAG AAAGGAAAAA AATTTAACAG
2401 AAGATAATCC AAATCTTTCA ATGGCACAGA GAAGACATAA AAGAGTAAGA
2451 ACATGGACTC GTCACATAAA CATTTTTAAT AAAGATTACA TCTTTGTACC
2501 TGTAATAGAG TCGTCTCACT GGTATCTCGC AGTCATTTGT TTTCCATGGT
2551 TAGAAGAAGC TGTGTATGAA GATTTTCCAC AAACGTGTATC CCAGCAGTCC
2601 CAGGCTCAGC AGTCCCAAAG TGACAACAAA ACAATAGATA ATGATCTACG
2651 TACTACTTCG ACACGTGCTT TGAGTGCAGA GGATTCCCAA AGTACCGAGT
2701 CGAATATGTC AGTACCAAAG AAAATGTGTA AAAGGCCATG TATTCTTATA
2751 CTAGACTCCT TGAAAGCTGC TTCTGTACGA AACACAGTTC AGAATTACG
2801 AGAGTATTTA GAGGTAGAGT GGGAAGTTAA ACTAAAAACT CATCGTCAAT
2851 TCAGCAAAAAC AAACATGGTG GATCTATGCC CTAAGTTCC TAAACAGGAC
2901 AATAGCAGTG ATTGTGGAGT ATATTATTG CAGTATGTGG AAAGCTTCTT
2951 CAAGGATCCT ATTGTTAACT TTGAACCTCC AATTCAATTG GAGAAGTGGT
3001 TTCTCTGTCG TGAATAAAG ACCAAACGGG AAGATATTCC AGAGCTCATC
3051 TTGAAACTTC ATTTACAGCA ACAGAAGGGC AGCAGTAGCT AGTTAATCTG
3101 TACAAACATG ACACAGATGT TCTCTAAGAT TACTGGAAG CCCCTTACCA
3151 GCATTTGTGT TAGCCAGCTC ACAGAGAAGA AAATAACTTG CAGTAGTTTT
3201 ATAATAAGTC ATTGGAACAT TATTTAAAT ATGTAGGACA CATTATTAGA
3251 ATTGTTGGGA TCTCATAGAT GGAATGGGAA TGGGGGTGAT ATAGATAAAC
3301 TTACTAGATA TAAATTAAAA TTTTATAAAT ATTTTCATATT TTTCTGAGTA
3351 AATATGATTG GATTATGCAA CAGCATATGT AATATGGGAA TGTTTGTAG
3401 ATAATAAAGC TTACATGATC TGTACTTCCA CGTGACTGGG TGCTGAGGGG
3451 AGTTAAAGCC TCCCTGGTGC CAGCCCCAGT GCTTGTCAA TTTGCTGACA
3501 GGTCAACATCA TATTGTAATT CTATCTTTTG CAGCTCAAGC ATGCAGTATG
3551 AATACTGTGT ATTTTAAAT AAAATAATTT AGTATCAAGC CTTTCAGAAA
3601 TGCCATTTAC GGCATCCCTT CTGTATGTAA CAAAAGACA TTCATAATGT
3651 TAGGAAGATG ATAAAAATTC GCTCTTTTAA AGTGCAGCTT ATTATTCTCA
3701 ATTGCTAAAT ACGATTACTC TGCTTTTTTT TTTTCATTTC TTTTGATGTC
3751 ATATGTGAGT ATCTTATAAT TTAGTTCATT TGTTCAGGGT AAAATTGAA
3801 ACAAATAATTT TTACCTGTGC AAAATAGTTT TTTAAAAAT ATACATGTAG
3851 CTCAACTTGA GGTACTGCTA TATAAATATT CACTCACATT ATCACGGAAT
3901 TTATGTATAG TTTCTCTAAT ATAGAAGATA AAATGGGTGT CCTCATAACT
3951 TTAACAAAGA AAACCTCAG TCCTATTTAT TAATGGGTAG AATTAAATAT
4001 ATAATTTTAT AGCTCAGTTT ACCCAGTATT CATCTGCAA GCCAGATTGC
4051 TCTCATTGCT TTTATATTTT TAAATGTAG CTTTTAGAGA CCTATGATCC
4101 TCATGGAAC TAAATTTTTA TTAATATTC AGGTAACAGT TCTGAATTCA
4151 TGTGATAATG GTGGCATTAT ATATGATTAA ACACCTCAGA ACTTTCTAAT
4201 GTTATCAGGA GTATTTTGAG GGAGATATGA TTATATTGTA TTTTCTCAGA
4251 TAAGAAAAAT GTTTTTTAA AATATTATTT TAATCTGTTT TAAGCATCTC
4301 TTAGATTTAC ATTATAACTA CATAAAGCAG TGAAGCAAAG GCAAATTAAG
4351 ATAAAGCTAG AAAGCTGAA CATTTTATTT CAAAATCATA CGAATCGGGG
4401 TCAGTTAAGC CTCAGTATTC TTAGCTTTTG TTGATTTTGG CACTATCTTT
4451 ATATTATTAA ATATATTTGT TGTGTTGATA TTTTCATATA AGATGGCTAT
4501 AATTACATAT TTCATTCCCA ATTTGTGTGT GTTGGGGGGT ACTTTTAAAG
4551 GTGACTATTG TTTTGTACAT CTAATTTTGG GAAACCAAGT CTATAAGACA
4601 TCTTGTGATT TCTTAATGTT TTTGTTTGTA TGTTTTTCAA AGATATCACT
4651 GTCCTTTATC ATGTTTGA GATTGTTTAA AATTCAATTT CCTAAATTA
4701 TGTGCAAGTA ATGTTTGA GATATCGGTG TTTTATATTA AACATATTTT
4751 CAATTCAAAA AAAAAAATAA AAAAAGTTAT CGATACCGTC GACCTCGATG
4801 ATGATGATGA TGATGATGAT GTCGAC
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 138 bp to 3089 bp; peptide length: 984
Category: similarity to known protein

```
1 MDKRLGRRP SSSEIITEGK RKKSSDLS EIRKMLNAKPE DVHVQSPLSK
51 FRSSERWTLF LQWERSLRNK VISLDHKNKK HIRGCPVTSR SSPERIPRVI
101 LTNVLGTELG RKYIRTPPVT EGSLSDDTDL QSEQLSSSSD GSLESYQNLN
151 PHKSCYLSESR GSQSKTVDD NSAKQTAHNE EKRKDDGIS LLISDTQPED
201 LNSGSRGCDH LEQESRKNKV KYSDSKVELT LISRKTKRRL RNNLPDSQYC
251 TSLDKSTEQT KKOEDDSTIS TEFERPSYNY HQDPKLPEEI TTKPTKSDFT
301 KLSSNSQEL TLSNATKSAS AGSTTETVEY SNSIDIVGIS SLVEKDENEL
351 NTIEKPILRG HNEGNSQLIS AEPIVVSSDE EGPVEHKSSE ILKLQSKQDR
401 ETTNENESTS ESALLEPLI TCESVQMSSE LCPYNPMVEN ISSIMPSNEM
451 DLQLDFIFTS VYIGIKIGAS KGCVTITKKY IKIPQVSLN EISLVDTH
```

```

501 LKRFGWLKSK DDNHSKRSHA ILFFWVSSDY LQEIQTQLEH SVLSQSKSS
551 EFIFLELHNP VSQREELKLLK DIMTEISIIS GELELSYPLS WVQAFPLFQN
601 LSSKESSEFIH YYCVSTCSFP AGVAVAEEMK LKSVSQPSNT DAAKPTYTFL
651 QKQSSGCYSL SITSNPDEEW REVRHTGLVQ KLIVYPPPT KGG LGVTNED
701 LECLEEGEFL NDVIIDFYLYL YLILEKASDE LVERSHIFSS FFYKCLTRKE
751 NNLTEDNPNL SMAQRRHKRV RTWTRHINIF NKDYIFVPVN ESSHWYLAVI
801 CFPWLEEA VY EDFFQTVSQQ SQAQOSQSDN KTIDNLRIT STLSLSAEDS
851 QSTESNMSVP KKMCKRPCIL ILDSLKAASV RNTVQNLREY LEVEWEVKLK
901 THROFSKTNM VDLCPKVPKQ DNSSDCGVYL LQYVESFFKD PIVNFELPIH
951 LEKWFPRHVI KTKREDIREL ILKLHLQQQK GSSS

```

BLASTP hits

Entry SPAC17A5_7 from database TREMBL:
 "SPAC17A5.07c"; product: "hypothetical protein"; S.pombe
 chromosome I cosmid c17A5. Schizosaccharomyces pombe (fission
 yeast)
 Length = 652
 Score = 275 (96.8 bits), Expect = 1.9e-29, Sum P(3) = 1.9e-29
 Identities = 56/120 (46%), Positives = 78/120 (65%)

Entry S49947 from database PIR:
 SMT4 protein - yeast (Saccharomyces cerevisiae)
 Length = 1034
 Score = 163 (57.4 bits), Expect = 4.6e-16, Sum P(3) = 4.6e-16
 Identities = 46/159 (28%), Positives = 76/159 (47%)

Entry YQG6_CAEEL from database SWISSPROT:
 HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.
 Length = 342
 Score = 162 (57.0 bits), Expect = 6.1e-13, Sum P(3) = 6.1e-13
 Identities = 37/119 (31%), Positives = 62/119 (52%)

Entry AB018340_1 from database TREMBL:
 gene: "KIAA0797"; product: "KIAA0797 protein"; Homo sapiens mRNA for
 KIAA0797 protein, partial cds.
 Score = 540, P = 1.9e-50, identities = 120/243, positives = 155/243

Alert BLASTP hits for DKFZphfbr2_16g18, frame 3

TREMBL:ATT16L1_11 gene: "T16L1.110"; product: "putative protein";
 Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII
 project), N = 2, Score = 239, P = 2.1e-18

>TREMBL:ATT16L1_11 gene: "T16L1.110"; product: "putative protein";
 Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)
 Length = 710

HSPs:

Score = 239 (35.9 bits), Expect = 2.1e-18, Sum P(2) = 2.1e-18
 Identities = 51/135 (37%), Positives = 78/135 (57%)

Query: 683 IVYPPPTKGG LGVTNEDLECEEGEFLNDVIIDFYLYLKY LILEKASDELVERSHIFSSFF 742
 +VYP + V +D+E L+ F+ND IIDFY+KYL + S + R H F+ FF
 Sbjct: 176 LVYPQGE PDVV-VRKQDIELLKPRRFINDTIIDFYIKYL-KNRISP KERG RHFHFNCF 233

Query: 743 YKCLTRKENNLTEDNPNLSMAQRRHKRVRTWTRHINIFNKDYIFVPVN ESSHWYLAVICF 802
 + RK NL + P+ + +RV+ WT++++F KDYIF+P+N S HW L +IC
 Sbjct: 234 F----RKLANLDKGTPTSCG GREAYQ RVQKWTKNVDLFEKDYIFIPINCSFHWLSLVIICH 289

Query: 803 PWLEEA VYEDFPQTV 817
 P + + PQ V
 Sbjct: 290 PGELVPSHVENPQ RV 304

Score = 70 (10.5 bits), Expect = 2.1e-18, Sum P(2) = 2.1e-18
 Identities = 13/28 (46%), Positives = 15/28 (53%)

Query: 948 PIHLEKWFPRHVIKTKREDIRELILKLH 975
 P HL WFP KR +I EL+ LH
 Sbjct: 403 PSHLRNWFPAKEASLKRRNILELLYNLH 430

Pedant information for DKFZphfbr2_16g18, frame 3

Report for DKFZphfbr2_16g18.3

{LENGTH} 984
 {MW} 112265.80
 {PI} 6.13
 {HOMOL} TREMBL:AB018340_1 gene: "KIAA0797"; product: "KIAA0797 protein"; Homo sapiens
 mRNA for KIAA0797 protein, partial cds. 8e-53
 {FUNCAT} 03.22 cell cycle control and mitosis [S. cerevisiae, YIL031w] 9e-17
 {FUNCAT} 99 unclassified proteins [S. cerevisiae, YPL020c] 4e-06
 {BLOCKS} BL00494C Bacterial luciferase subunits proteins
 {PROSITE} AMIDATION 3
 {PROSITE} MYRISTYL 9
 {PROSITE} CAMP_PHOSPHO_SITE 2
 {PROSITE} CK2_PHOSPHO_SITE 30
 {PROSITE} TYR_PHOSPHO_SITE 1
 {PROSITE} PKC_PHOSPHO_SITE 19
 {PROSITE} ASN_GLYCOSYLATION 12
 {KW} Alpha_Beta
 {KW} LOW_COMPLEXITY 4.47 %

SEQ MDKRKLGRPPSSSEIITEGKRKSSSSDLSEIRKMLNAKPEDVHVQSPLSKFRSSERWTLP
 SEG
 PRD cccccceccccceeeccccccccccccchhhhhhhhhccccccccccccccccccccchh

 SEQ LQWERSLRNKVISLDHKNKKHIRGCPVTSRSSPERIPRVILTNLGTTELGRKYIRTPPVT
 SEG
 PRD hhhhhhhhhheeeccccceeeccccccccccccceeeeeeecccccecccccccc

 SEQ EGSLSDTDNLQSEQLSSSSDGSLSEYQNLNPHKSCYLSESGRSQRSKTVDDNSAKQTAHNK
 SEGxxxxxxxxxxxxxxxx.....
 PRD cchhhhhhh

 SEQ EKRRKDDGISLLISDTQPEDLNSGSRGCDHLEQESRNKDKVYSDSKVELTLISRKTKRRL
 SEG
 PRD hhhccccceeeccccccccccccccccccccccccccccccccccccceeeehhhhhhh

 SEQ RNNLPDSQYCTSLDKSTEQTKQEDDSTISTEFERPSSENYHQDKPLPEEITTKPTKSDFT
 SEG
 PRD hccccccccccccccccchhhhhcccccccccccccccccccccccccccccccccccc

 SEQ KLSSLNSQELTSLNATKSASAGSTTETVEYSNSIDIVGISSLVEKDENELNTIEKPILRG
 SEG
 PRD cccccccccceehhhhhhhccccceeeccccceeeccccchhhhhhhhhhhcccccccc

 SEQ HNEGQSLISAEPVIVSSDEEGPVEHKSSEILKLSKQDRETTNENESTSESALLELPLI
 SEGxxxxxxxxxxxxxxxx.....
 PRD cccccceeeccccceccccccccchhhhhhhhhhhhhccccccccchhhhhccccce

 SEQ TCESVQMSSELCYPNPMENISSIMPSNEMDLQDFITSVYIGKIKGASKGCVTITKKY
 SEG
 PRD eccccccccccccccccccccceccccchhhhhhhheeeeeeeeeccccceeeeeee

 SEQ IKIPFQVSLNEISLLVDTHLKRFLGWSKDDNHSKRSHAILFFWSSDYLQEIQTQLEH
 SEG
 PRD eeeccccceeeccccccccccccccccccccccccccccccccccccchhhhhhhhhhh

 SEQ SVLSQSKSSEFIFLELHNPVSQREELKLDIMTEISISGELELSYPLSWQAFPLFQN
 SEG
 PRD hhhccccceeeccccccccchhhhhhhhhheeeccccceeeccccceeeccccceec

 SEQ LSSKESFIHYVCSTCSFPAGVAEEMKLKSVSQPSNTDAAKPTYTFLQKQSSGCYSL
 SEG
 PRD cccccccccceeeccccccccchhhhhhhhhhhccccccccccccccccceccccccccce

 SEQ SITSNPDEEWREVHTGLVQKLIYPPPTKGGLGVTNEDLECLEEGEFLNDVIIDFYLK
 SEG
 PRD eccccccccceeeccccccccccccccccccccchhhhhhhhhccchhhhhhhhhhh

 SEQ YLILEKASDELVERSHIFSSFFYKCLTRKENNLTEDNPNLSMAQRRHRKRVTRWTRHINIF
 SEG
 PRD hhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhc

 SEQ NKDYIFVPVNESSHWYLAVICFPWLEEAVYEDFPQTVSQSQSQSQSDNKTIDNLRRTT
 SEGxxxxxxxx.....
 PRD cceeeccccccccceeeccccchhhhhhhccccchhhhhhhhhcccccccccccccc

 SEQ STLSSLASDSQSTESNMSVPKKMKRIPCILIDSLKAASVRNTVQNLREYLEVEWEVKLK
 SEG
 PRD cceeeccccccccceccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhh

 SEQ THRQFSKTNMVDLCPKVPKODNSSDCGVYLLQYVESFFKDPVNFELPIHLEKWFPRHVI

```

SEG .....
PRD hhhhhccccccccccccccccccccceeeehhhhhhhccccceccccccccccccchhh

SEQ KTKREDIRELILKLHLQQQKGSSS
SEG .....
PRD hhhhhhhhhhhhhhhhhhhhhcccccc

```

Prosites for DKFZphfbr2_16gl8.3

PS00001	314->318	ASN_GLYCOSYLATION	PDOC00001
PS00001	365->369	ASN_GLYCOSYLATION	PDOC00001
PS00001	406->410	ASN_GLYCOSYLATION	PDOC00001
PS00001	440->444	ASN_GLYCOSYLATION	PDOC00001
PS00001	513->517	ASN_GLYCOSYLATION	PDOC00001
PS00001	600->604	ASN_GLYCOSYLATION	PDOC00001
PS00001	752->756	ASN_GLYCOSYLATION	PDOC00001
PS00001	759->763	ASN_GLYCOSYLATION	PDOC00001
PS00001	790->794	ASN_GLYCOSYLATION	PDOC00001
PS00001	830->834	ASN_GLYCOSYLATION	PDOC00001
PS00001	856->860	ASN_GLYCOSYLATION	PDOC00001
PS00001	922->926	ASN_GLYCOSYLATION	PDOC00001
PS00004	8->12	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	21->25	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	54->57	PKC_PHOSPHO_SITE	PDOC00005
PS00005	66->69	PKC_PHOSPHO_SITE	PDOC00005
PS00005	88->91	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00005	162->165	PKC_PHOSPHO_SITE	PDOC00005
PS00005	172->175	PKC_PHOSPHO_SITE	PDOC00005
PS00005	233->236	PKC_PHOSPHO_SITE	PDOC00005
PS00005	236->239	PKC_PHOSPHO_SITE	PDOC00005
PS00005	260->263	PKC_PHOSPHO_SITE	PDOC00005
PS00005	291->294	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	515->518	PKC_PHOSPHO_SITE	PDOC00005
PS00005	562->565	PKC_PHOSPHO_SITE	PDOC00005
PS00005	602->605	PKC_PHOSPHO_SITE	PDOC00005
PS00005	747->750	PKC_PHOSPHO_SITE	PDOC00005
PS00005	874->877	PKC_PHOSPHO_SITE	PDOC00005
PS00005	879->882	PKC_PHOSPHO_SITE	PDOC00005
PS00005	901->904	PKC_PHOSPHO_SITE	PDOC00005
PS00005	962->965	PKC_PHOSPHO_SITE	PDOC00005
PS00006	11->15	CK2_PHOSPHO_SITE	PDOC00006
PS00006	24->28	CK2_PHOSPHO_SITE	PDOC00006
PS00006	91->95	CK2_PHOSPHO_SITE	PDOC00006
PS00006	123->127	CK2_PHOSPHO_SITE	PDOC00006
PS00006	125->129	CK2_PHOSPHO_SITE	PDOC00006
PS00006	137->141	CK2_PHOSPHO_SITE	PDOC00006
PS00006	167->171	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00006	225->229	CK2_PHOSPHO_SITE	PDOC00006
PS00006	251->255	CK2_PHOSPHO_SITE	PDOC00006
PS00006	271->275	CK2_PHOSPHO_SITE	PDOC00006
PS00006	295->299	CK2_PHOSPHO_SITE	PDOC00006
PS00006	323->327	CK2_PHOSPHO_SITE	PDOC00006
PS00006	341->345	CK2_PHOSPHO_SITE	PDOC00006
PS00006	377->381	CK2_PHOSPHO_SITE	PDOC00006
PS00006	396->400	CK2_PHOSPHO_SITE	PDOC00006
PS00006	402->406	CK2_PHOSPHO_SITE	PDOC00006
PS00006	408->412	CK2_PHOSPHO_SITE	PDOC00006
PS00006	488->492	CK2_PHOSPHO_SITE	PDOC00006
PS00006	509->513	CK2_PHOSPHO_SITE	PDOC00006
PS00006	536->540	CK2_PHOSPHO_SITE	PDOC00006
PS00006	562->566	CK2_PHOSPHO_SITE	PDOC00006
PS00006	602->606	CK2_PHOSPHO_SITE	PDOC00006
PS00006	638->642	CK2_PHOSPHO_SITE	PDOC00006
PS00006	664->668	CK2_PHOSPHO_SITE	PDOC00006
PS00006	697->701	CK2_PHOSPHO_SITE	PDOC00006
PS00006	747->751	CK2_PHOSPHO_SITE	PDOC00006
PS00006	826->830	CK2_PHOSPHO_SITE	PDOC00006
PS00006	846->850	CK2_PHOSPHO_SITE	PDOC00006
PS00006	962->966	CK2_PHOSPHO_SITE	PDOC00006
PS00007	216->223	TYR_PHOSPHO_SITE	PDOC00007
PS00008	84->90	MYRISTYL	PDOC00008
PS00008	106->112	MYRISTYL	PDOC00008
PS00008	141->147	MYRISTYL	PDOC00008
PS00008	161->167	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008
PS00008	468->474	MYRISTYL	PDOC00008

PS00008	505->511	MYRISTYL	PDOC00008
PS00008	622->628	MYRISTYL	PDOC00008
PS00008	693->699	MYRISTYL	PDOC00008
PS00009	6->10	AMIDATION	PDOC00009
PS00009	18->22	AMIDATION	PDOC00009
PS00009	109->113	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_16g18.3)

DKFZphfbr2_16i12

group: transmembrane protein

DKFZphfbr2_16i12 encodes a novel 185 amino acid protein, with strong similarity to PUT2 protein of Fugu rubripes.

The novel protein contains 1 transmembrane region.

PUT 2 is a Fugu rubripes protein similar to the neural cell adhesion molecule L1 (L1-CAM) a mitosis-specific chromosome segregation protein (SMC1) and the calcium channel alpha-1 subunit homolog (CCA1).

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

strong similarity to Fugu rubripes PUT2

complete cDNA, complete cds, EST hits,
TRANSMEMBRANE 1

Sequenced by LMU

Locus: /map="873.3/875.1 cR from top of Chr1 linkage group"

Insert length: 1552 bp

Poly A stretch at pos. 1528, polyadenylation signal at pos. 1506

```
1 GGGGGGGGAC AACTGGGTCT TTTGCGGCTG CAGCGGGCTT GTAGGCGTCC
51 GGCTTTGCTG GCCCAGCAAG CCTGATAAGC ATGAAGCTCT TATCTTTGGT
101 GGCTGTGGTC GGGTGTTTGC TGGTGCCCCC AGCTGAAGCC AACAAGAGTT
151 CTGAAGATAT CCGGTGCAAA TGCATCTGTC CACCTTATAG AAACATCAGT
201 GGGCACATTT ACAACCAAGAA TGTATCCCAG AAGGACTGTT GTAGCAACTG
251 CCTGCACGTG GTGGAGCCCA TGCCAGTGCC TGGCCATGAC GTGGAGGCCT
301 ACTGCCTGCT GTGCGAGTGC AGGTACGAGG AGCGCAGCAC CACCACCATC
351 AAGGTCATCA TTGTCATCTA CCTGTCCGTG GTGGGTGCCC TGTGCTCTA
401 CATGGCCTTC CTGATGCTGG TGGACCCTCT GATCCGAAAG CCGGATGCAT
451 ACACTGAGCA ACTGCACAAT GAGGAGGAGA ATGAGGATGC TCGCTCTATG
501 GCAGCAGCTG CTGCATCCCT CGGGGGACCC CGAGCAAACA CAGTCCTGGA
551 GCGTGTGGAA GGTGCCCAGC AGCGGTGGAA GCTGCAGGTG GAGGAGCAGC
601 GGAAGACAGT CTTGATCGG CACAAGATGC TCAGCTAGAT GGGCTGGTGT
651 GGTGGGTGCA AGGCCCCAAC ACCATGGCTG CCAGCTTCCA GGCTGGACAA
701 AGCAGGGGGC TACTTCTCCC TTCCCTCGGT TCCAGTCTTC CCTTTAAAG
751 CCTGTGGCAT TTTTCTCCTT TCTCCCTAAC TTTAGAAATG TTGTACTTGG
801 CTATTTTGAT TAGGGAAGAC GGATGTGCTC TCTGATCTCT GTTCTCTCT
851 TGGGTCTTTG GGGTTGAAGG GAGGGGGAAG GCAGGCCAGA AGGGAATGGA
901 GACATTCGAG GCGGCCTCAG GAGTGGATGC GATCTGTCTC TCCTGGCTCC
951 ACTCTTGCCG CCTTCCAGCT CTGAGTCTTG GGAATGTTGT TACCCTTGGA
1001 AGATAAAGCT GGGTCTTCAG GAACTCAGTG TTTGGGAGGA AAGCATGGCC
1051 CAGCATTCAG CATGTGTTCC TTTCTGCAGT GGTCTTATC ACCACCTCCC
1101 TCCCAGCCCC AGCGCCTCAG CCCCAGCCCC AGCTCCAGCC CTGAGGACAG
1151 CTCTGATGGG AGAGCTGGGC CCCCTGAGCC CACTGGGTCT TCAGGGTGCA
1201 CTGGAAGCTG GTGTTGCTG TCCCCTGTGC ACTTCTCGCA CTGGGGCATG
1251 GAGTGCCCAT GCATACTCTG CTGCCGGTCC CCTCACCTGC ACTTGAGGGG
1301 TCTGGGCAGT CCCTCCTCTC CCCAGTGTCC ACAGTCACTG AGCCAGACGG
1351 TCGGTGGAA CATGAGACTC GAGGCTGAGC GTGGATCTGA ACACCACAGC
1401 CCCTGTACTT GGGTTGCCTC TTGTCCCTGA ACTTCGTTGT ACCAGTGCAT
1451 GGAGAGAAAA TTTTGTCCCT TTGTCTTAGA GTTGTGTGTA AATCAAGGAA
1501 GCCATCATT AATTGTTTTA TTTCTCTCAA AAAAAAAAAA AAAAAAATA
1551 TC
```

BLAST Results

Entry HS808349 from database EMBL:
human STS WI-11986.
Score = 1716, P = 5.7e-73, identities = 364/378

Entry HS487355 from database EMBL:
human STS WI-13088.
Score = 1358, P = 1.3e-56, identities = 274/277

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 81 bp to 635 bp; peptide length: 185
Category: similarity to unknown protein

```

1 MKLLSLVAVV GCLLVPPAEA NKSSDIRCK CICPPYRNIS GHIYNQNVSO
51 KDCCSNCLHV VEPMPVPGHD VEAYCLLCEC RYEERSTTTI KVIVYILSV
101 VGALLLYMAF LMLVDPLIRK PDAYTEQLHN EEENEDARSM AAAASLGGP
151 RANTVLERVE GAQQRWKLOV QEQRKTVFDR HKMLS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_16i12, frame 3

TREMBL:AF026198_5 gene: "PUT2"; product: "putative protein 2"; Fugu
rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene,
complete cds; putative protein 1 (PUT1) gene, partial cds;
mitosis-specific chromosome segregation protein SMC1 homolog (SMC1)
gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1)
and putative protein 2 (PUT2) genes, partial cds, complete sequence., N
= 1, Score = 655, P = 2.8e-64

TREMBL:CER12C12_5 gene: "R12C12.6"; Caenorhabditis elegans cosmid
R12C12., N = 1, Score = 225, P = 1e-18

>TREMBL:AF026198_5 gene: "PUT2"; product: "putative protein 2"; Fugu
rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete
cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific
chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and
calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2
(PUT2) genes, partial cds, complete sequence.
Length = 187

HSPs:

Score = 655 (98.3 bits), Expect = 2.8e-64, P = 2.8e-64
Identities = 124/163 (76%), Positives = 140/163 (85%)

```

Query:   22 KSSDIRCKCICPPYRNISGHIYNQNVSQKDCCSNCLHVVEPMPVPGHDVEAYCLLCECR 81
          KS +D+RCKCICPPYRNISGHIYN+N +QKDC NCLHVV+PMPVPG+DVEAYCLLCEC+
Sbjct:   31 KSFDVVRCKCICPPYRNISGHIYRNFTQKDC--NCLHVVDPMPVPGNDVEAYCLLCECK 88

Query:   82 YEERSTTTIKVIVYILSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMA 141
          YEERST TI+V I+I+LSVVGALLYM FL+LVDPLIRKPD + LHNEE++ED +
Sbjct:   89 YEERSTNTIRVTIIIFLSVVGALLLYMLFLLLVDPLIRKPDPLAQLHNEEEDSIDIQPM 148

Query:   142 AAAASLGGP-RANTVLERVEGAQQRWKLOVQEQRKTVFDRHKML 184
          + G P R NTVLERVEGAQQRWK QVQEQRKTVFDRHKML
Sbjct:   149 S-----GDPARGNTVLERVEGAQQRWKQVQEQRKTVFDRHKML 187

```

Pedant information for DKFZphfbr2_16i12, frame 3

Report for DKFZphfbr2_16i12.3

```

[LENGTH]      185
[MW]           20764.29
[pI]           6.21
[HOMOL]        TREMBL:AF026198_5 gene: "PUT2"; product: "putative protein 2"; Fugu rubripes
neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1
(PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1)
gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2
(PUT2) genes, partial cds, complete sequence. 3e-68
[PROSITE]      MYRISTYL 1
[PROSITE]      CK2_PHOSPHO_SITE 4
[PROSITE]      PKC_PHOSPHO_SITE 2
[PROSITE]      ASN_GLYCOSYLATION 3
[KW]           SIGNAL_PEPTIDE 21

```


[KW] TRANSMEMBRANE 1
[KW] LOW_COMPLEXITY 2.70 %

```

SEQ  MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCCSNCLHV
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  VEPMPVPGHDVEAYCLLCECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRK
SEG  .....
PRD  eccccccccccchhhhhhhhhhhcccccccccccccccccccccccccccccccccccc
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM...

SEQ  PDAYTEQLHNEEENEDARSMAAAAASLGGRANTVLERVEGAQQRWKLQVQEQRKTVFDR
SEG  .....xxxxx.....
PRD  cccchhhhhhhhhccccchhhhhhhhhhhccccccccchhhhhhhhhchhhhhhhhhhhhhhhhh
MEM  .....

SEQ  HKMLS
SEG  .....
PRD  hhccc
MEM  .....

```

Prosites for DKF2phfbr2_16i12.3

PS00001	21->25	ASN_GLYCOSYLATION	PDOC00001
PS00001	38->42	ASN_GLYCOSYLATION	PDOC00001
PS00001	47->51	ASN_GLYCOSYLATION	PDOC00001
PS00005	49->52	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00006	23->27	CK2_PHOSPHO_SITE	PDOC00006
PS00006	49->53	CK2_PHOSPHO_SITE	PDOC00006
PS00006	154->158	CK2_PHOSPHO_SITE	PDOC00006
PS00006	176->180	CK2_PHOSPHO_SITE	PDOC00006
PS00008	148->154	MYRISTYL	PDOC00008

(No Pfam data available for DKF2phfbr2_16i12.3)

DKFZphfbr2_16k22

group: brain derived

DKFZphfbr2_16k22 encodes a novel 108 amino acid protein with very weak similarity to thioredoxin of *Bacillus subtilis*.

No informative BLAST results: No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to thioredoxin

complete cDNA, complete cds, genomic DNA?
no EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 2088 bp

Poly A stretch at pos. 2065, no polyadenylation signal found

```
1 AAAAGGAAGA AGGAAATAAG GATATTTCAA GGGTTACCAA AGTCGAGGAA
51 AACTATTTTA AGAAGAAATC TGAATTATTT GTGCACATAG GTTGTAATAA
101 TAGCATCTTG CATTAAATGG TGTCTTCTAG CTTACAAAGT GGATTTCATAT
151 ACACATATTGT AACTGACTCT CTACAAACTT GCAAGGTTAG CAAGACAAAT
201 GGTATTTTAA GATAACAAAC TGAGACTCAA AAAAGGCAAG TAACTCGTTC
251 TACTTCCCAA AGCCAGAAAG TGGCAAAATA GAAAATGGAT CCTGAATCTC
301 CAACACCATG CAAACTAAGA GAGGGAATCC TCTGTAGAGG GAATGGAAGT
351 AAAAAGGCAC AAGTCGTGAT GTCACCTTCT GAACAGAGAT GGAACCTTTC
401 TTCCTCTGAG AAAAAGAGA AAAGATAGTT TTAAGTGGCA AAAGAACATG
451 AAGCAATGTG AGGTGAAGAA ACAGAAAGA CTATGGATGG AATTCCTAGA
501 TGTGAGATAC ACAAAGTTCC ATTTCAAAGA GAAATATCTA TAGATAGGCA
551 TAAAGTTACA CACCTGAACCT ACCAACTCTG AACCAGTAAC TCAAGAGATA
601 TTTTGTGTGT CCCACAAGCC ATATGGCTCT GGGGACAAAT TATCTGAAAG
651 TGCCCAATAA GAAAAATATT TGAGGAAGGG GAGTTGGTGA GTGAATGAAT
701 TAAAGGACAT CAGAAAGATA CATTGACTGT TCTCCTTCCC AGGAAACAAA
751 GTGGCTAAGT CAAAACAACG GGCAGCTGTG GGATAGCAAA GAAAAAATAA
801 CTTCCAGGCC CAGGTTCTAG TGAAAGCTAC TATGGAGTT AGCCACTCAA
851 CTTTAGAACC AGAGGCTTCT TTTCTCTCTC CCTTCTTATC TTTTCTAGTT
901 TATAGCAAAT TTATATTGAG CCACCTATTC TTTCTGAATG CTAGTTCCCC
951 TTTAGCATTT CTTTTTCTTC ATTCCCTTTG GACTGGCCCA ATGCTTTGGC
1001 CCCTTATCAA AGCATTCTCT AAGAAACAGT CTCACAGCTC TAATTTGCAT
1051 CTGGTTATGC AAGATGTGGT TAAGAACATG GACTCTGGAG GTAAATACAC
1101 CTTGATTCCA ATTCATTCTC TCATTATTTC ATTCAGCAAA TATTTAGTGA
1151 ACATCTAACA TGTGCTAGGC ACTGTTCTAG TTGCTGAGGA TACAGCTTCA
1201 AACAAAATAA GGTCTCTGCA AGGATGCCTT CTCTTACCAC TCCTATTCAG
1251 CGTAGTATTG GAAGTCCTGG CCAGGGCAAT CAGGCAAGAA AAAGAAATCA
1301 AGGTATCCA AATAGGAAGA GAGGAAGTCA AACTATCCCT GTTTACAGAC
1351 AACATGATCC TACATCTAGA AAAAAACCCA TTGCTCTAGC CCAAAGCTT
1401 CTTAGGCTGA TAAACAACCT CAGCAAAGTC TTAGGATACA AAATCCATGT
1451 GCAAAAAACA CTAGCATTCT TATACACCAA CAACAGTCAA GCCGAGATCC
1501 AAATCAGGAA CAACTCCTA TTCACAATTG CCACAAAAAC AATAGAACAG
1551 GAAAACAGCT AACTAGGAAG GTGAAAGATC TCTACAAGGA GAACTACAAA
1601 CCACTGCTCA CAGAAATCAG AGATGACACA TATAAATGGA AAAACATTCC
1651 ATGATCATGG ATAGGAAGAA TGAATATTAC TGAAATGGCT ATACTGTCCA
1701 AAGCAATTTA TAGATTCAAT GCTATTCCTA GTAAACTACC ATTGAGATTT
1751 TTTACAGAAC TAGAAAAAAL AAAAATATT TTAAGGCTGG GCGCAGTGGC
1801 TCTCACCTGT AATCCAGCA CTTTGGGAGG CCGAGATGGG TGGATCAGCA
1851 GGTCAGGAGA TGGAAAACAT CCTGGCTAAC ATGGTGAAAC CCCGTCTCTA
1901 CTAATAATAC AAAAAATTAG CCAGGCGTGG TGGTGGGCGC CTGTAATCCC
1951 AGCTGCTCGG GAGGCTGAGG CAGGATAATG GTGTGAACCC GGGAGGCAGA
2001 GCTTGCACTG AGCTGAGATT GCACCACTGC ACTCCAGCCT GAGGGACAGA
2051 GTGAGACTCC ATCTCAAAAA AAAAAAATAA AAAAAAATAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 832 bp to 1155 bp; peptide length: 108
Category: putative protein

1 MEVSHSTLEP EASFPPFPLS FLVYSKFILS HLFFLNASSP LAFLFLHSLW
51 TGPMLWPLIK AFSKKQSDSS NLHLVMQDVV KNMDSGGKYT LIPIHSLIYS
101 FSKYLVNI

BLASTP hits

Entry B37192 from database PIR:
thioredoxin - Bacillus subtilis Score = 71 (25.0 bits), Expect = 0.040,
P = 0.039
Identities = 16/49 (32%), Positives = 30/49 (61%)

Alert BLASTP hits for DKFZphfbr2_16k22, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_16k22, frame 1

Report for DKFZphfbr2_16k22.1

[LENGTH] 108
[MW] 12281.47
[pI] 8.06
[PROSITE] MYRISTYL 1
[PROSITE] CAMP_PHOSPHO_SITE 1
[PROSITE] CK2_PHOSPHO_SITE 1
[PROSITE] PKC_PHOSPHO_SITE 1
[PROSITE] ASN_GLYCOSYLATION 1
[KW] Alpha_Beta

SEQ MEVSHSTLEPEASFPPFPLSFLVYSKFILSHLFFLNASSPLAFLFLHSLWTGPMLWPLIK
PRD cccccccccccccccccchhhhhhhhhhhhhhhccccchhhhhhhhhccccccccchhhh
SEQ AFSKKQSDSSNLHLVMQDVVKNMDSGGKYTLIPIHSLIYSFSKYLVINI
PRD hhhccccccccceehhhhhhhccccccccceeecccccccccccccccc

Prosite for DKFZphfbr2_16k22.1

PS00001	36->40	ASN_GLYCOSYLATION	PDOC00001
PS00004	64->68	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	63->66	PKC_PHOSPHO_SITE	PDOC00005
PS00006	6->10	CK2_PHOSPHO_SITE	PDOC00006
PS00008	86->92	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16k22.1)

DKF2phfbr2_16112

group: transmembrane protein

DKF2phfbr2_16112 encodes a novel 267 amino acid protein with similarity to gallus gallus putative transmembrane protein E3-16

The novel protein contains one putative transmembrane domain. In chicken, E3-16 is expressed specifically in the inner ear.

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neurons involved in perception of hearing.

similarity to gallus putative transmembrane protein E3-16

complete cDNA, complete cds, EST hits
potential start at Bp 73 matches kozak consensus PyCCataG
TRANSMEMBRANE 1

Sequenced by Qiagen

Locus: unknown

Insert length: 2042 bp

Poly A stretch at pos. 2024, polyadenylation signal at pos. 2003

```
1  GGGGGCGGGC  GAGGCAGAGA  CCGAGGCTGC  ACCGGCAGAG  GCTGCGGGGC
51  GGACGCGCGG  GCCGGCGCAG  CCATGGTGAA  GATTAGCTTC  CAGCCCGCCG
101  TGGCTGGCAT  CAAGGGCGAC  AAGGCTGACA  AGGCGTCGGC  GTCGGCCCTT
151  CCGCCGGCCT  CGGCCACCGA  GATCCTGCTG  ACGCCGGCTA  GGGAGGAGCA
201  GCCCCACAAA  CATCGATCCA  AGAGGGGGGG  CTCAGTGGGC  GGCCTGTGCT
251  ACCTGTCGAT  GGGCATGGTC  GTGCTGCTCA  TGGGCCCTCG  GTTCGCCTCT
301  GTCTACATCT  ACAGATACTT  CTTCTTGCG  CAGCTGGCCC  GAGATAACTT
351  CTTCCGCTGT  GGTGTGCTGT  ATGAGGACTC  CCTGTCTCTC  CAGGTCCGGA
401  CTCAGATGGA  GCTGGAAGAG  GATGTGAAAA  TCTACCTCGA  CGAGAACTAC
451  GAGCGCATCA  ACGTGCCTGT  GCCCCAGTTT  GCGGGCGGTG  ACCCTGCAGA
501  CATCATCCAT  GACTTCCAGC  GGGGTCTGAC  TGCGTACCAT  GATATCTCCC
551  TGGACAAGTG  CTATGTGATC  GAACTCAACA  CCACCATTTG  GCTGCCCCCT
601  CGCAACTTCT  GGGAGTCTCT  CATGAACGTG  AAGAGGGGGA  CCTACTGCCC
651  GCAGACGTAC  ATCATCCAGG  AGGAGATGGT  GGTCACGGAG  CATGTCAGTG
701  ACAAGGAGGC  CCTGGGGTCC  TTCATCTACC  ACCTGTGCAA  CGGGAAAGAC
751  ACCTACCGGC  TCCGGCGCCG  GGCAACGCGG  AGGCGGATCA  ACAAGCGTGG
801  GGCCAAGAAC  TGCAATGCCA  TCCGCCACTT  CGACAACACC  TTCGTGGTGG
851  AGACGCTCAT  CTGCGGGGTG  GTGTGAGGCC  CTCCTCCCCC  AGAACCCCTT
901  GCCGTGTTCC  TCTTTTCTTC  TTTCCGGCTG  CTCTCTGGCC  CTCTCTCTTC
951  CCCCTGCTTA  GCTTGTACTT  TGGACGCGTT  TCTATAGAGG  TGACATGTCT
1001  CTCCATTCTT  CTCCAACCCT  GCCCACCTCC  CTGTACCAGA  GCTGTGATCT
1051  CTCGGTGGGG  GGCCCATCTC  TGCTGACCTG  GGTGTGGCGG  AGGGAGAGGC
1101  GATGCTGCAA  AGTGTCTTCT  GTGTCCCACT  GTCTTGAAGC  TGGGCCTGCC
1151  AAAGCCTGGG  CCCACAGCTG  CACCGGCAGC  CCAAGGGGAA  GGACCGGTTG
1201  GGGGAGCCGG  GCATGTGAGG  CCCTGGGCAA  GGGGATGGGG  CTGTGGGGGC
1251  GGGGCGGCAT  GGGCTTCAGA  AGTATCTGCA  CAATTAGAAA  AGTCCTCAGA
1301  AGCTTTTCTT  TGGAGGGTAC  ACTTTCTTCA  CTGTCCCTAT  TCCTAGACCT
1351  GGGGCTTGAG  CTGAGGATGG  GACGATGTGC  CCAGGGAGGG  ACCCACCAGA
1401  GCACAAGAGA  AGGTGGCTAC  CTGGGGGTGT  CCCAGGGAAT  CTGTCACTGC
1451  CTTACGCCCC  CCAGCAGGAG  CTTGGAGTTT  GGGGAGTGGG  GATGAGTCCG
1501  TCAAGCACAA  CTGTTCTCTG  AGTGGAAACA  AAGAAGCAAG  GAGCTAGGAC
1551  CCCCAGTCTT  GCGCCCAAGC  AGCACAAGCA  GGGTCCCTCT  AGTCAAGGCA
1601  GTGGGATGGG  CGGCTGAGGA  ACGGGGCAGG  CAAGGTCACT  GCTCAGTCAC
1651  GTCCACGGGG  GACGAGCCGT  GGGTTCTGCT  GAGTAGGTGG  AGCTCATTGC
1701  TTTTCTCAAG  CTTGGAAGTG  TTTTGAAGA  TAACACAGAG  GGAAGGGGAG
1751  AGCCACCTGG  TACTTGTCCA  CCCTGCCTCC  TCTGTTCTGA  AATTCCATCC
1801  CCCTCAGCTT  AGGGGAATGC  ACCTTTTCTC  CTTTCTTCTT  CACTTTTGCA
1851  TGTTTTTACT  GATCATTCGA  TATGCTAACC  GTTCTCAGCC  CTGAGCCTTG
1901  GAGAGGAGGG  CTGTAACGCC  TTCAGTCAGT  CTCTGGGGAT  GAAACTCTTA
1951  AATGCTTTGT  ATATTTTCTC  AATTAGATCT  CTTTTCAGAA  GTGTCTATAG
2001  AACATAAAAA  ATCTTTTACT  TCTGAAAAAA  AAAAAAAAAA  AA
```

BLAST Results

No BLAST result

Medline entries

96325063:

Isolation of markers for chondro-osteogenic differentiation using cDNA library subtraction. Molecular cloning and characterization of a gene belonging to a novel multigene family of integral membrane proteins.

Peptide information for frame 1

ORF from 73 bp to 873 bp; peptide length: 267
Category: similarity to known protein

```

1 MVKISFQPAV AGIKGDKADK ASASAPAPAS ATEILLTPAR EEQPPQHRSK
51 RGGSVGGVCY LSMGMVVLLM GLVFASVYIY RYFFLAQLAR DNFFRCGVLY
101 EDSLSSQVRT QMELEEDVKI YLDENYERIN VPVPQEGGGD PADIHDFQR
151 GLTAYHDISL DKCYVIELNT TIVLPPRNFW ELLMNVKRGY YLPQTYIIQE
201 EMVVTEHVSD KEALGSFIYH LCNGKDTYRL RRRATRRRIN KRGAKNCNAI
251 RHFENTFVVE TLICGVV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_16112, frame 1

SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16)., N = 1, Score = 573, P = 1.4e-55

SWISSNEW:ITMB_MOUSE INTEGRAL MEMBRANE PROTEIN 2B (E25B PROTEIN)., N = 1, Score = 559, P = 4.2e-54

SWISSNEW:ITMA_HUMAN INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN)., N = 1, Score = 452, P = 9.1e-43

>SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16).
Length = 262

HSPs:

Score = 573 (86.0 bits), Expect = 1.4e-55, P = 1.4e-55
Identities = 118/264 (44%), Positives = 175/264 (66%)

```

Query:      1 MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGGSVGGVCY 60
             MVK+SF A+A  + A+K  ++          ++L+ P  + + P+      G  C+
Sbjct:      1 MVKVSFNSALA--HKEAANKEEENS-----QVLILPP-DAKEPEDVVVPAGHKRAWCW 50

Query:     61 -LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSL-----SQVRTQM- 112
             +  G+  +L G++  Y+Y+YF  Q          + CG+ Y ED LS      +Q+++
Sbjct:     51 CMCFLAFMLAGVILGGAYLYKYFAFQQ---GGVYFCGIKIEDGLSLPESGAQLKSARY 107

Query:     113 -ELEDVKIYLDENYERINVPVPQEGGGDPADIHDFORGLTAYHDISLDKCYVIELNTT 171
             +E++++I  +E+ E I+VPVP+F  DPADI+HDF R LTAY D+SLDKCYVI LNT+
Sbjct:     108 HTIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRLTAYLDLSLDKCYVIPLNTS 167

Query:     172 IVLPPRNFWELLNMVVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLR 231
             +V+PP+NF ELL+N+K GTYLPQ+Y+I E+M+VT+ + + + LG FIY LC GK+TY+L+
Sbjct:     168 VVMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVVDQLGFFIYRLCRGKETYKLO 227

Query:     232 RRATRRRINKRGAKNCNAIRHFENTFVVETLIC 264
             R+  + I KR A NC  IRHFEN F +ETLIC
Sbjct:     228 RKEAMKGIQKREAVNCRKIRHFENRFAMETLIC 260

```

Pedant information for DKFZphfbr2_16112, frame 1

Report for DKFZphfbr2_16112.1

[LENGTH] 267
[MW] 30223.94

```

[pI]          8.16
[MOLECULAR WEIGHT]  100.0
[ISoelectric point]  8.16
[PROSITE]        PRENYLATION      1
[PROSITE]        MYRISTYL         5
[PROSITE]        CAMP_PHOSPHO_SITE 2
[PROSITE]        CK2_PHOSPHO_SITE  3
[PROSITE]        TYR_PHOSPHO_SITE  1
[PROSITE]        PKC_PHOSPHO_SITE  4
[PROSITE]        ASN_GLYCOSYLATION 1
[DOMAIN]          TRANSMEMBRANE    1
[DOMAIN]          LOW COMPLEXITY    15.36 %

```

```
SEQ      MVKISFQPAVAGIKGDKADKASAPAPASATEIILLTPAREEQPPQHRSKRGSSVGGVCY
SEG      .....xxxxxxxxxxxxxxxx.....
PRD      ccccccccchhhhhhhhhhhhhhhhhcccccceeeccccccccccccccccccccchh
MEM      MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM
```

```
SEQ      LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLYEDSLSSQVRTQMEELEDVKI  
SEG      . . xxxxxxxxxxxx .  
PRD      hhhhhhccccccccccchhhhhhhcccceeeeeeccccccccchhhhhhhhhhhhhhh  
MEM      mmmmmmmmmmmmmmmmmmmmmm
```

```

SEQ      YLDENYERINVPVPQFGGGDPADIIHDFORGLTAYHDISLDKCYVIELNTTIVLPPRNFW
SEG      .....
PRD      hhccccceeeccccccccccccchhhhhhhhhhhhhhhhhccceeeeeeccccecccchhh
MEM

```

```
SEQ      ELLMNVKRGTYLPQTYIIQEEMVVTEHVSDEKALGSFIYHLCNGKDTYFLRRRATRRRIN
SEG      .....xxxxxxxxxxxxx
PRD      hhhhhhccccccccceeehhhhhhccccchhhhhheeeccccchhhhhhhhhhhhhhhhh
MEM
```

```
SEQ      KRGAKNCNAIRHFENTFVVETLICGVV
SEG      xx.....
PRD      hhhhccceeeccchhhhhheeeccc
MEM
```

Prosites for DKFZphfbr2_16112.1

PS000001	169->173	ASN_GLYCOSYLATION	PDOC000001
PS000004	187->191	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	232->236	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	49->52	PKC_PHOSPHO_SITE	PDOC000005
PS000005	209->212	PKC_PHOSPHO_SITE	PDOC000005
PS000005	227->230	PKC_PHOSPHO_SITE	PDOC000005
PS000005	235->238	PKC_PHOSPHO_SITE	PDOC000005
PS000006	30->34	CK2_PHOSPHO_SITE	PDOC000006
PS000006	110->114	CK2_PHOSPHO_SITE	PDOC000006
PS000006	209->213	CK2_PHOSPHO_SITE	PDOC000006
PS000007	119->127	TYR_PHOSPHO_SITE	PDOC000007
PS000008	52->58	MYRISTYL	PDOC000008
PS000008	53->59	MYRISTYL	PDOC000008
PS000008	71->77	MYRISTYL	PDOC000008
PS000008	138->144	MYRISTYL	PDOC000008
PS000008	243->249	MYRISTYL	PDOC000008
PS00294	264->268	PRENYLATION	PDOC00268

(No Pfam data available for DKF2phfbr2_16112.1)

DKFZphfbr2_22f21

group: brain derived

DKFZphfbr2_22f21 encodes a novel 567 amino acid protein with weak similarity to C. elegans cosmid C18C4.5

No informative BLAST results; no predictive prosite, pfam or SCOP motif

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to C.elegans C18C4.5

EST HSAA6531/HSAA5273/ defines splice variant, or unspliced cDNA additional -180 Bp at position 250

Sequenced by AGOWA

Locus: /map="311.4 cR from top of Chr14 linkage group".

Insert length: 1910 bp

Poly A stretch at pos. 1887, polyadenylation signal at pos. 1867

```
1 TGGGCCCTTA GCAACGGCCT GGCACGGTT TCCTTGCTGC TGCAGCCCCC
51 GTCGGCTCCT CTTTTCAGT CCTCCACTGC CGGGCTGGG CCCGGCCGCG
101 GGAAGGACCG AAGGGGATAC AGCGTGTCCC TCGGCGGGCT GCAAGAGGAC
151 TAAGCATGGA TGGCAGCCGG AGAGTCAGAG CAACCTCTGT CCTTCCCAGA
201 TATGGTCCAC CGTGCCTATT TAAAGGACAC TTGAGCACCA AAAGTAATGC
251 TGCAGTAGAC TGCTCGGTTC CAGTAAGCAT GAGTACCAGC ATAAAGTATG
301 CAGACCAACA ACGAAGAGAG AAACCTCAAAA AGGAATTAGC ACAATGTGAA
351 AAAGAGTTCA AATTAACATA AACTGCAATG CGAGCCAATT ATAAAAATAA
401 TTCCAAGTCA CTTTTAATA CCTTACAAGA GCCCTCAGGC GAACCGCAAA
451 TTGAGGATGA CATGTTAAAA GAAGAAATGA ATGGATTTTC ATCCTTTGCA
501 AGGTCACTAG TACCCTCTTC AGAGAGACTA CACCTAAGTC TACATAAATC
551 CAGTAAAGTC ATCACAATG GTCTGAGAA GAACTCCAGT TCCTCCCCGT
601 CCAGTGTGGA TTATGCAGCC TCCGGGCCCC GGAAGTGAAG CTCTGGAGCC
651 CTGTATGGGA GAAGGCCCGA AAGCACATTC CCAAATTCCC ACCGGTTTCA
701 GTTAGTCATT TCGAAAGCAC CCAGTGGGGA TCTTTGGAT AAACATTCTG
751 AACTCTTTTC TAACAAACAA TTGCCATTCA CTCCTCGCAC TTTAAAAACA
801 GAAGCAAAAT CTTTCTGTG ACAGTATCGT TATTATACAC CTGCCAAAAG
851 AAAAAAGGAT TTTACAGATC AACGGATAGA AGCTGAAACC CAGACTGAAT
901 TAAGCTTTAA ATCTGAGTTG GGGACAGCTG AACTTAAAAA CATGACAGAT
951 TCAGAAATGA ACATAAAGCA GGCATCTAAT TGTGTGACAT ATGATGCCAA
1001 AGAAAAATA GCTCCTTTAC CTTTAGAAGG GCATGACTCA ACATGGGATG
1051 AGATTAAGGA TGATGCTCTT CAGCATTCTT CACCAAGGGC AATGTGTCTG
1101 TATTCCCTGA AGCCCCCTTC AACTCGTAAA ATCTACTCTG ATGAAGAAGA
1151 ACTGTTGTAT CTGAGTTTCA TTGAAGATGT AACAGATGAA ATTTTGAAC
1201 TTGGTTTATT TTCAAACAGG TTTTGTAGAA GACTGTTTGA GCGACATATA
1251 AAACAAAATA AACATTGGGA GGGGGAAAAA ATGCGCCACC TGCTGCATGT
1301 CCTGAAAGTA GACTTAGGCT GCACATCGGA GGAAACTCG GTAAAGCAAA
1351 ATGATGTTGA TATGTTGAAT GTATTGATT TTGAAAAGGC TGGGAATTCA
1401 GAACCAATAA AATTAAAAAA TGAAAGTGAA GTAACAATTC AGCAGGAACG
1451 TCAACAATAC CAAAAGGCTT TGGATATGTT ATTGTCGGCA CCAAAGGATG
1501 AGAACGAGAT ATTCCCTTCA CCAACTGAAT TTTTCATGCC TATTATAAAA
1551 TCAAGCATT CAGAAGGGGT TATAATTCAA CAGGTGAATG ATGAAACAAA
1601 TCTTGAAACT TCAACTTTGG ATGAAAATCA TCCAAGTATT TCAGACAGTT
1651 TAACAGATCG GGAACTTCT GTGAATGTCA TTGAAGGTGA TAGTGACCCT
1701 GAAAAGGTTG AGATTTCAAA TGGATTATGT GGTCTTAACA CATCACCTTC
1751 CCAATCTGTT CAGTTCTCCA GTGTCAAAG CGACAATAAT CATGACATGG
1801 AGTTATCAAC TCTTAAATC ATGGAATGA GCATTGAGGA CTGCCCTTTG
1851 GATGTTTAAAT TTTCATTAAT AAATACCTCA AATGGCCAGT AAAAAAAA
1901 AAAAAAAA
```

BLAST Results

Entry HS477360 from database EMBL:

human STS WI-14643.

Length = 418

Minus Strand HSPs:

Score = 1850 (277.6 bits), Expect = 2.5e-77, P = 2.5e-77

Identities = 392/405 (96%), Positives = 392/405 (96%), Strand = Minus / Plus

Peptide information for frame 3

1	MDGSRVRVRAT	SVLPRYGPPC	LFKGHLSTKS	NAAVDCSVPV	SMSTSICYAD
51	QQQREKLKKE	LAQCEKEFKL	TKTAMRANYX	NNSKSLFNTL	QEPSGEPQIE
101	DDRLKEEMNG	FSSFARSLVP	SESTRHLHSLH	KSKSVITNGP	KEQNSSSPSS
151	VDYAASGPRK	LSSGALYGRR	PRSTFPNSHR	FQLVISKAPS	GDLLDKHSEL
201	FSNKQLFPTP	RTLKTEAKFS	LSQYRYTTPA	KRKKDFDQDR	IEAETQTELS
251	FKSELGTAET	KNMTDSEMMI	QOASNCVTYD	AEKIAFPLD	EGHDSWTDEI
301	KDDALQHSSP	RAMCQYSLKP	PSTRKIYSDE	EELLYLSFIE	DVTDEILKLG
351	LFSNRFLERL	FERHIQKNKH	LEGEKMRHLH	HYLVKVDLGT	SEENSQVQND
401	VDMLNVFDEL	KAGNSEPNKL	KNSEVITIQQ	ERQQYQALD	MLLSAPKDND
451	EIFPSPTEFF	MPYIKSKHSE	GVIIQQVND	TNLETSTLDE	NHPSISDLSL
501	DRETSNVNIE	GDSDPKEVEI	SNGLCGLNTS	PSQSVQFSSV	KGDNNHOMEL
551	STLKIMEMSI	EDCPDLV			

Entry CEC18C4_3 from database TREMBL:
"C18C4.5"; *Caenorhabditis elegans* cosmid C18C4.
Length = 1091
Score = 98 (34.5 bits), Expect = 0.29, P = 0.25
Identities = 105/470 (22%), Positives = 192/470 (40%)

No Alert BLASTP hits found

Pedant information for DKFZphfbr2 22f21, frame 3

Report for DKFZphfbr2 22f21.3

```

[LENGTH]          567
[MW]               64120.02
[pI]               5.68
{PROSITE}          AMIDATION          1
{PROSITE}          MYRISTYL          3
{PROSITE}          CAMP_PHOSPHO_SITE  1
{PROSITE}          CK2_PHOSPHO_SITE  16
{PROSITE}          PKC_PHOSPHO_SITE  18
{PROSITE}          ASN_GLYCOSYLATION  4
[KW]               All Alpha
[KW]               LOW_COMPLEXITY      1.23 %

```

```
SEQ      MDGSRVRVATSVLPTRYGPCLFKGHLSSTKSNAAVDCSVPVSMSTSIIKYADQQRREKLKKE  
SEC      .....  
PRD      cccccceeeeeeccccccccccgcgccccccccceeeccccccccchhhhhhbbbbbbbbb
```

SEQ LAQCEKEFKLTKTAMRANYKNSKSLFNTLQEPSGEPQIEDMLKEEMNGFSSFARSLVP
SEG
PRD hhhhhhhhhhhhhhhhhhhhhccccccceeecccccccchhhhhhhhhhccccccceeecc

```
SEQ      SSERLHLSLHKSSKVITNGPEKNSSSPSSVDYAAAGPRKLSSGALYGRRPSTFPNSHR
SEG                                     .XXXXXXXXX.
PRD      ccchhhhhhhhhhceeeccccccccccccccccccccccccccccccccccccccccc
```

[illegible]

```
SEQ      IEAETQTELSFKSELGTAETKNMTDSEMNIQASNCVTDYAKEKIAPLPLEGHDSTWDEI
SEG      .....
PRD      hhhhhhhhhhhhhhhcccccccccccccchhhhhhccccceehhhhhhhccccccccccccccccc
```



```

SEQ      KDDALQHSSPRAMCQYSLKPPSTRKIYSDEEELLYLSFIEDVTDEILKGLFSNRFLERL
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ      FERHIKQKNHLEGEKMRHLLHVLKVDLGCTSEENSVKQNDVDMNLNVDFEKGAGNSEPNKL
SEG      .....
PRD      hhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ      KNESEVTIQQERQQYQKALDMLLSAPKDENEIFPSPTEFFMPIYKSKHSEGVIIQQVNDE
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

```

```

SEQ      TNLETSTLDENHPSISDSLTDRETSVNVIEGOSDPEKVEISNGLCGLNTSPSQSVQFSSV
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ      KGDNNHDMELSTLKIMEMSIEDCPLDV
SEG      .....
PRD      cccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

```

Prosites for DKFZphfbr2_22f21.3

PS00001	81->85	ASN_GLYCOSYLATION	PDOC00001
PS00001	143->147	ASN_GLYCOSYLATION	PDOC00001
PS00001	262->266	ASN_GLYCOSYLATION	PDOC00001
PS00001	422->426	ASN_GLYCOSYLATION	PDOC00001
PS00004	159->163	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	4->7	PKC_PHOSPHO_SITE	PDOC00005
PS00005	27->30	PKC_PHOSPHO_SITE	PDOC00005
PS00005	45->48	PKC_PHOSPHO_SITE	PDOC00005
PS00005	122->125	PKC_PHOSPHO_SITE	PDOC00005
PS00005	132->135	PKC_PHOSPHO_SITE	PDOC00005
PS00005	178->181	PKC_PHOSPHO_SITE	PDOC00005
PS00005	202->205	PKC_PHOSPHO_SITE	PDOC00005
PS00005	209->212	PKC_PHOSPHO_SITE	PDOC00005
PS00005	212->215	PKC_PHOSPHO_SITE	PDOC00005
PS00005	250->253	PKC_PHOSPHO_SITE	PDOC00005
PS00005	309->312	PKC_PHOSPHO_SITE	PDOC00005
PS00005	317->320	PKC_PHOSPHO_SITE	PDOC00005
PS00005	322->325	PKC_PHOSPHO_SITE	PDOC00005
PS00005	353->356	PKC_PHOSPHO_SITE	PDOC00005
PS00005	395->398	PKC_PHOSPHO_SITE	PDOC00005
PS00005	500->503	PKC_PHOSPHO_SITE	PDOC00005
PS00005	539->542	PKC_PHOSPHO_SITE	PDOC00005
PS00005	552->555	PKC_PHOSPHO_SITE	PDOC00005
PS00006	89->93	CK2_PHOSPHO_SITE	PDOC00006
PS00006	149->153	CK2_PHOSPHO_SITE	PDOC00006
PS00006	245->249	CK2_PHOSPHO_SITE	PDOC00006
PS00006	264->268	CK2_PHOSPHO_SITE	PDOC00006
PS00006	295->299	CK2_PHOSPHO_SITE	PDOC00006
PS00006	328->332	CK2_PHOSPHO_SITE	PDOC00006
PS00006	337->341	CK2_PHOSPHO_SITE	PDOC00006
PS00006	390->394	CK2_PHOSPHO_SITE	PDOC00006
PS00006	455->459	CK2_PHOSPHO_SITE	PDOC00006
PS00006	481->485	CK2_PHOSPHO_SITE	PDOC00006
PS00006	486->490	CK2_PHOSPHO_SITE	PDOC00006
PS00006	494->498	CK2_PHOSPHO_SITE	PDOC00006
PS00006	498->502	CK2_PHOSPHO_SITE	PDOC00006
PS00006	500->504	CK2_PHOSPHO_SITE	PDOC00006
PS00006	513->517	CK2_PHOSPHO_SITE	PDOC00006
PS00006	559->563	CK2_PHOSPHO_SITE	PDOC00006
PS00008	164->170	MYRISTYL	PDOC00008
PS00008	256->262	MYRISTYL	PDOC00008
PS00008	350->356	MYRISTYL	PDOC00008
PS00009	167->171	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_22f21.3)

DKFZphfbr2_22h13

group: transmembrane protein

DKFZphfbr2_22h13 encodes a novel 520 amino acid protein, with similarity to *Drosophila melanogaster* EG:39E1.3.

The protein contains an ATP/GTP A Prosite pattern (P-loop). This loop interacts with one of the phosphate groups of a A or G nucleotide. It is found in numerous ATP- or GTP-binding proteins, such as ATP synthase alpha and beta subunits, Myosin heavy chains, Kinesin heavy chains and kinesin-like proteins, Dynamins and dynamin-like proteins, several kinases, DNA and RNA helicases, GTP-binding elongation factors and the Ras family of GTP-binding proteins. Additionally, the novel protein contains one putative transmembran domain.

No informative BLAST results; no predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

AC004780_1, differences to predicted genmodel

membrane regions: 1

AC004780_1, differences to predicted genmodel

complete cDNA, complete cds, EST hits
on genomic level encoded by AC004780,
differences to predicted genmodel!
TRANSMEMBRANE 1

Sequenced by AGOWA

Locus: unknown

Insert length: 2292 bp

Poly A stretch at pos. 2272, polyadenylation signal at pos. 2255

```
1 GGGGGAGGGA ACTGATCTCA GCTCGGGCCC GCGTTACATC CTCCTCCTCT
51 TCTTCCTTCG GCCCAGCTTT CTTAGGGGCG TGCAACCCGG ACGCCGAGGC
101 CGGTTTCGGA GTGGGGAGTG CCCATTTTCT CTCCTTCCCA CGTTCCTGGC
151 CCCCAGACGC CATTTGCAGG CGGGTGGCTT GGGTCAGCCT CCCC GCCCCC
201 ACCCGACTCC CGTCACGGGA GAGCGCACAC CGCGCCCGCA GAACCAATCA
251 GCAGCCGCGT TAGGTAACCA GTCTGAGTC TGGACACAGT CAGCCTGGAC
301 TCTATGGGAT AGAGCGGCGG CGACGGTGGA AGGAGCCTGG CTCTGGTGCC
351 CCCCAGAAATC TCTCTGGGCC TGGTGGTCGG GAGAGGGACT ACATTGCACC
401 ATGGGAAAGA GAGAGAAGGG ATGCCAGCGA AGAGACAAGC ACTTCCGTCA
451 TGCAGAAAC CCCCATCATC CTCTCAAAAC CTCCAGCAGA GCGGTCAAAA
501 CAGCCACACG CTCCAACAGC CCCTGCTGCC CCGCCTGCTC CAGCCCTCT
551 GGAGAAGCCC ATCGTTCTCA TGAAGCCACG GGAGGAGGGG AAGGGGCCCTG
601 TGGCCGTGAC AGGTGCTCTT ACCCTGAGG GCACCGCCCC ACCACCCCT
651 GCAGCCCTGT CGCCACCCAA GGGGGAGAAG GAGGGGCAGA GACCCACACA
701 CCCTGTGTAC CAGATCCAGA ACCGGGGCAT GGGCACTGCC GCACCAAGCAG
751 CCATGGACCC GTCTGTGGGT CAGGCCAAAC TACTGCCCCC AGAGCGCATG
801 AAGCACAGCA TCAAGTTGGT GGATGACCAG ATGAATTGGT GTGACAGTGC
851 CATCGAGTAC CTGTTGGATC AGACTGATGT GTTGGTGGTT GGTGTCTTGG
901 GCCTCCAGGG GACAGGCAAG TCCATGGTCA TGTCATTGTT GTCAGCCAAC
951 ACTCCAGAGG AGGACCAGAG GACTTATGTT TTCCGGGCCC AGAGCGCTGA
1001 AATGAAGGAA CGAGGGGGCA ACCAGACCAG TGGCATCGAC TTCTTTATTA
1051 CCAAGAACG GATTGTTTTC CTGGACACAC AGCCCATCCT GAGCCCTTCT
1101 ATCTAGACC ATCTCATCAA TAATGACCGC AAACCTGCCTC CAGAGTACAA
1151 CCTTCCCCAC ACTTACGTTG AAATGCAGTC ACTCCAGATT GCTGCCTTCC
1201 TTTTACCGCT CTGCCATGTG GTGATTGTTG TCCAGGACTG GTTCACAGAC
1251 CTCAGTCTCT ACAGGTTTCT GCAGACAGCA GAGATGTTGA AGCCCTCCAC
1301 CCCATCCCCC AGCCACGAGT CCAGCAGCTC ATCGGGCTCC GATGAAGGCA
1351 CCGAGTACTA CCCCCACCTA GTCTTCTTGC AGAACAAGC TCGCCGAGAG
1401 GACTTCTGTC CTCGGAAGCT GCGGCAGATG CACCTGATGA TTGACCAGCT
1451 CATGGCCCCC TCCCACCTGC GTTACAAGGG AACTCTGTCC ATGTTACAAT
1501 GCAATGTCTT CCGGGGGCTT CCACCTGACT TCCTGGACTC TGAGGTCAAC
1551 TTATTCCTGG TACCCTTCAT GGACAGTGAA GCAGAGAGTG AAAACCCACC
1601 AAGAGCAGGA CCTGGTTCCA GCCCCTCTT CTCCCTGCTG CCTGGGTATC
1651 TTGGCCACCC CAGTTTCCAG TCCTTGGTGA GCAAGCTCCG GAGCCAAGTG
1701 ATGTCCATGG CCCGGCCACA GCTGTCACAC ACGATCTCA CCGAGAAGAA
1751 CTGGTTCCAC TACGCTGCCC GGATCTGGGA TGGGGTGAGA AAGTCTCTG
1801 CTCTGGCAGA GTACAGCCGC CTGCTGGCCT GAGGCCAAGG AGAGGAATGT
1851 CATGCAGGGG ACCTCCTGGG TCCGCAAGTG ACTGCGAGGG AGCACAGATG
1901 TCCATCCCCC GCTGGGGTGG AGAGCGGCAG CAGGCCTGAT GGATGAGGGA
1951 TCGTGGCTTC CCGGCCAGA GACATGAGGT GTCCAGGGCC AGGCCCCCA
```

```

2001 CCCTCAGTTG GGGCTGTTCC GGGGGTGA CTGTGCGATC CCACCCCAAA
2051 CCTGAGATGG GGTAGCCCGT CCTGTGTCCT CCACAGGGAC AAGCAGTGGG
2101 AGGAGTCTGA ATGGTCACCA GGAAGCCCGG GCTCCATCTT GACCTCCTTT
2151 TTCAGGGACA GGAGCAACAG GCCCTCTTTC CCTGACTCTA AGCCCTTCCC
2201 TGTAAGGTGA GGCAGGGTCT GGAGAGCTCT TTATTGGAAC AGATCTGGTG
2251 GTTCAATAA ACACAGTCAT GCAAAAAA AA

```

BLAST Results

Entry AC004780 from database EMBL:
Homo sapiens chromosome 19, cosmid F17127, complete sequence.
Score = 2616, P = 0.0e+00, identities = 524/525
15 exons Bp 8031-31789

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 270 bp to 1829 bp; peptide length: 520
Category: similarity to unknown protein
Prosites motifs: ATP_GTP_A (211-219)

```

1 MSESCHSQPG LYGIERRRRW KEPGSGCPON LSGPGGRERD YIAPWERERR
51 DASEETSTSV MQKTPPIILSK PPAERSKQPP PPTAPAAPPA PAPLEKPIVL
101 MKPREEGKGP VAVTGASTPE GTAPPPPAAP APPKGEKEGQ RPTQPVYQIQ
151 NRGMGTAAPA AMDPVVGQAK LLPPERMKHS IKLVDDQMNW CDSAIEYLLD
201 QTDVLVVGVL GLQGTGKSMV MSLLSANTPE EDQRTYVFRA QSAEMKERGG
251 NQTSGLDFFI TQERIVFLDT QPILSPSILD HLINNDKLP PEYNLPHTYV
301 EMQSLQIAAF LFTVCHVVIV VQDWFTDLSL YRFLQTAEMV KPSTSPSPHE
351 SSSSSGSGDEG TEYYPHLVFL QNKARREDFC PRKLRQMHLM IDQLMAHSHL
401 RYKGTLSMLQ CNVFPGLPPD FLDSEVNLFV VPFMDSEAES ENPPRAGPGS
451 SPLFSLPGY RGHPFSQSLV SKLRSQVMSM ARPQLSHTIL TEKNWFHYAA
501 RIWDGVRKSS ALAEYSRLLA

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_22h13, frame 3

TREMBL:AC004780_1 product: "F17127_1"; Homo sapiens chromosome 19,
cosmid F17127, Complete sequence., N = 2, Score = 1264, P = 1.3e-231

TREMBL:CEY54E2A_1 gene: "Y54E2A.2"; Caenorhabditis elegans cosmid
Y54E2A, N = 2, Score = 219, P = 1.4e-15

>TREMBL:AC004780_1 product: "F17127_1"; Homo sapiens chromosome 19, cosmid
F17127, complete sequence.
Length = 528

HSPs:

Score = 1264 (189.6 bits), Expect = 1.3e-231, Sum-P(2) = 1.3e-231
Identities = 254/302 (84%), Positives = 264/302 (87%)

```

Query: 46 ERERRDASEETSTSVMQKTPPIILSKPPAERSKQPPPTAPAAPPAPAPLEKPIVLMPKPRE 105
      E+ER D+ + S +Q+T + R + P + A APLEKPIVLMPKPRE
Sbjct: 39 EKER-DSDSDFSP--LQQTGECQRDRKHFRHAENPHHPLKTSSRA-APLEKPIVLMPKPRE 94

Query: 106 EGKGPVAVTGASTPEGTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAAPAAMPDV 165
      EGKGPVAVTGASTPEGTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAAPAAMPDV
Sbjct: 95 EGKGPVAVTGASTPEGTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAAPAAMPDV 154

Query: 166 VGQAKLLPPERMKHSIKLVDDQMNWCDISAIEYLLDQTDVLVVGVLGLQGTGKSMVMVSLLS 225
      VGQAKLLPPERMKHSIKLVDDQMNWCDISAIEYLLDQTDVLVVGVLGLQGTGKSMVMVSLLS
Sbjct: 155 VGQAKLLPPERMKHSIKLVDDQMNWCDISAIEYLLDQTDVLVVGVLGLQGTGKSMVMVSLLS 214

```

Query:	226	ANTPEEDQRTYVVFRAQSAEMKERGGNQTSgidffITQERIVFLDTQPILSPSILDHLINN	285
		ANTPEEDQRTYVVFRAQSAEMKERGGNQTSgidffITQERIVFLDTQPILSPSILDHLINN	
Sbjct:	215	ANTPEEDQRTYVVFRAQSAEMKERGGNQTSgidffITQERIVFLDTQPILSPSILDHLINN	274
Query:	286	DRKLPEEYNLPHTYVEMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYRFLQTAEMVKPSTP	345
		DRKLPEEYNLPHTYVEMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYR	K ++
Sbjct:	275	DRKLPEEYNLPHTYVEMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYRLWDLGCKCKSNSH	334
Query:	346	SP 347	
		SP	
Sbjct:	335	SP 336	
Score = 993 (149.0 bits), Expect = 1.3e-231, Sum P(2) = 1.3e-231			
Identities = 189/189 (100%), Positives = 189/189 (100%)			
Query:	332	RFLQTAEMVKPSTPSPSHESSSSSGSDegTEYYPHLVFLQNkarredFCPrKLrQMHLMI	391
		RFLQTAEMVKPSTPSPSHESSSSSGSDegTEYYPHLVFLQNkarredFCPrKLrQMHLMI	
Sbjct:	340	RFLQTAEMVKPSTPSPSHESSSSSGSDegTEYYPHLVFLQNkarredFCPrKLrQMHLMI	399
Query:	392	DQLMAHSHLRYKGTLSMLQCNVFPGLPPDFLDSEVNFLVFPFMDSEAESENPPRAGPGSS	451
		DQLMAHSHLRYKGTLSMLQCNVFPGLPPDFLDSEVNFLVFPFMDSEAESENPPRAGPGSS	
Sbjct:	400	DQLMAHSHLRYKGTLSMLQCNVFPGLPPDFLDSEVNFLVFPFMDSEAESENPPRAGPGSS	459
Query:	452	PLFSLLPGYRGHPSFQSLVSKLRsQVMSMARPQLSHTILTEKNWFHYAARIWDGVRKSSA	511
		PLFSLLPGYRGHPSFQSLVSKLRsQVMSMARPQLSHTILTEKNWFHYAARIWDGVRKSSA	
Sbjct:	460	PLFSLLPGYRGHPSFQSLVSKLRsQVMSMARPQLSHTILTEKNWFHYAARIWDGVRKSSA	519
Query:	512	LAEYSRLLA 520	
		LAEYSRLLA	
Sbjct:	520	LAEYSRLLA 528	

Pedant information for DKFZphfbr2 22h13, frame 3

Report for DKFZphfbr2 22h13.3

```
[LENGTH]          520
[MW]              57650.81
[pI]              6.52
[HOMOL]           TREMBL:AC004780_1 product: "F17127_1"; Homo sapiens chromosome 19, cosmid
F17127, complete sequence. 0.0
[PROSITE]         ATP_GTP_A             1
[PROSITE]         MYRISTYL              8
[PROSITE]         CAMP_PHOSPHO_SITE     1
[PROSITE]         CK2_PHOSPHO_SITE      8
[PROSITE]         GLYCOSAMINOGLYCAN    1
[PROSITE]         PKC_PHOSPHO_SITE      3
[PROSITE]         ASN_GLYCOSYLATION     2
[KW]              TRANSMEMBRANE         1
[KW]              LOW COMPLEXITY        11.73 %
```

```

SEQ      MSESQHSQPGLYGIERRRRWKEPGSGGPQNLSGPGGRERDYIAPWERERRDASEETSTSV
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM      .....

SEQ      MQKTPIILSKPPAERSKQPPPTAPAAPAPAPLEKPIVLMPREEGKGPVAVTGASTPE
SEG      .....xxxxxxxxxxxxxxxxxxxx
PRD      ecccccecccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM      .....

SEQ      GTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAPAAMD PVVGAKLLPPERMKHS
SEG      .....xxxxxxxxxxxx
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM      .....

SEQ      IKLVDDQMNWCDSAIEYLLDQTDVLVVGVLGLQGTGKSMVMSLLSANTPEEDQRTYVFRA
SEG      .....xxxxxxxxxxxxxxxxxxxxxx
PRD      hhhhccccchhhhhhhhhhhccccccccccccccccccccccccccccccccccccccccch
MEM      .....

SEQ      QSAEMKERGGNQTSIGIDFFITQERIVFLDTQPILSPSILDHLINNRKLPPEYNLPHTYV
SEG      .....
PRD      hhhhhhhccccccccccccccccccccccccccccccccccccccccccccccccccccch
MEM      .....

SEQ      EMQSLQIAAFLFTVCHVVIVVQDWFDTLSLYRFLQTAEMVKPSTPSPSHSSSSSSSGSDEG
SEG      .....xxxxxxxxxxxxxxxxxxxxxx

```

```

PRD      hhhhhhhhhhhhhhhheeeeeeeccchhhhhhhhhhhhhcccccccccccccccccc
MEM      MMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ      TEYYPHLVFLQNKARREDFCPRKLRQMHLMIDQLMAHSHLRYKGTLSMLQCNVFPGLPPD
SEG      .....
PRD      cccccceeehhhhhhccccccchhhhhhhhhhhhhhhcccccccccccccccccc
MEM      .....

SEQ      FLDSEVNLFLVPFMDSEAESENPPRAGPGSSPLFSLPGYRGHPSPFQSLVSKLRSQVMSM
SEG      .....
PRD      chhhhhheeeccccccccccccccccccccceccccccccchhhhhhhhhhhhhh
MEM      .....

SEQ      ARPQLSHTILTEKNWFHYAARIWDGVRKSSALAEYSRLLA
SEG      .....
PRD      hhhhhhhheeeccchhhhhhhhhhhcchhhhhhhhhccc
MEM      .....

```

Prosites for DKFZphfbr2_22h13.3

PS00001	30->34	ASN_GLYCOSYLATION	PDOC00001
PS00001	251->255	ASN_GLYCOSYLATION	PDOC00001
PS00002	32->36	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	507->511	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	180->183	PKC_PHOSPHO_SITE	PDOC00005
PS00005	215->218	PKC_PHOSPHO_SITE	PDOC00005
PS00005	491->494	PKC_PHOSPHO_SITE	PDOC00005
PS00006	117->121	CK2_PHOSPHO_SITE	PDOC00006
PS00006	193->197	CK2_PHOSPHO_SITE	PDOC00006
PS00006	228->232	CK2_PHOSPHO_SITE	PDOC00006
PS00006	254->258	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	298->302	CK2_PHOSPHO_SITE	PDOC00006
PS00006	355->359	CK2_PHOSPHO_SITE	PDOC00006
PS00006	436->440	CK2_PHOSPHO_SITE	PDOC00006
PS00008	26->32	MYRISTYL	PDOC00008
PS00008	139->145	MYRISTYL	PDOC00008
PS00008	153->159	MYRISTYL	PDOC00008
PS00008	211->217	MYRISTYL	PDOC00008
PS00008	214->220	MYRISTYL	PDOC00008
PS00008	249->255	MYRISTYL	PDOC00008
PS00008	356->362	MYRISTYL	PDOC00008
PS00008	505->511	MYRISTYL	PDOC00008
PS00017	211->219	ATP_GTP_A	PDOC00017

(No Pfam data available for DKFZphfbr2_22h13.3)

DKF2phfbr2_22i4

group: brain derived

DKF2phfbr2_22i4.1 encodes a novel 228 amino acid protein with similarity to the N-terminus of human p52rIPK.

No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to Human P52rIPK N-terminus

complete cDNA, complete cds, few EST hits

function of P52rIPK, repressor of p58IPK protein kinase inhibitor
upstream regulator of interferon induced proteins

Sequenced by AGOWA

Locus: unknown

Insert length: 4748 bp

Poly A stretch at pos. 4726, polyadenylation signal at pos. 4709

```
1 TGGGTCCGGT CCTAGGGTCA CACCCACCGC AGGGTCTGGC TTGGTACAGT
51 TGGGTGCATG CAGAAGTAGG TGGAGCTGCT GTTGACGCT TGAGAGAGTT
101 TTATTGTAAA ACTCTGTGTA TTTATAGTAA TCGGAGGGGA AAACACCTCT
151 TCCTTTTAAT TGCTCTGAGG ACCGCTGCCA AAGAAACGCA GTAGATCCGC
201 TCCCTCTTGG GGGCGGGGAG AAAGAACGGG TTGTGTCCGC CATGTTGGTG
251 AAGTCAAGCG AAGGCGACTA GAGCTCCAGG AGGGCCAGTT CTGTGGGCTC
301 TAGTCGGCCA TATTAATAAA GAGAAAGGGA AGGCTGACCG TCCTTCGCCT
351 CCGCCCCCAC ATACACACCC CTTCTTCCCA CTCGCTCTC ACGACTAAGC
401 TCTACGATT AAGGCACGCC TGCCTCGATT GTCCAGCCTC TGCCAGAAGA
451 AAGCTTAGCA GCCAGCGCCT CAGTAGAGAC CTAAGGGCGC TGAATGAGTG
501 GGAAAGGGAA ATGCCGACCA ATTGCGCTGC GCGGGGCTGT GCCACTACCT
551 ACAACAAGCA CATTAAACATC AGCTTCCACA GGTTCCTTTT GGATCCTAAA
601 AGAAGAAAAG AATGGGTTCC CTTGGTTAGG CGCAAAAATT TTGTGCCAGG
651 AAAACACACT TTTCTTTGTT CAAAGCACTT TGAAGCCTCC TGTTTTGACC
701 TAACAGGACA AACTCGACGA CTTAAATGG ATGCTGTTCC AACCATTTTT
751 GATTTTGTGA CCCATATAAA GTCTATGAAA CTCAAGTCAA GGAATCTTTT
801 GAAGAAAAAC AACAGTTGTT CTCCAGCTGG ACCATCTAAT TTAATTCAA
851 ACATTAGTAG TCAGCAAGTA CTACTGTAAC ACAGCTATGC CTTTAGGAAT
901 CCTATGGAGG CAAAAAAGAG GATCATTAAA CTGGAATAAG AAATAGCAAG
951 CTTAAGAAGA AAAATGAAAA CTTGCCTACA AAAGGAACGC AGAGCAACTC
1001 GAAGATGGAT CAAAGCCACG TGTTCGTGTA AGAATTAGA AGCAATAGT
1051 GTATTACCTA AAGGTACATC AGAACACATG TTACCAACTG CCTTAAGCAG
1101 TCTTCCCTTG GAAGATTTTA AGATCCTTGA ACAAGATCAA CAAGATAAAA
1151 CACTGCTAAG TCTAAATCTA AAACAGACCA AGAGTACCTT CATTTAAATT
1201 TAGCTTGAC AGAGCTTGAT GCCTATCCTT CATTCTTTTC AGAAGTAAAG
1251 ATAATTATGG CACTTATGCC AAAATTCATT ATTTAATAAA GTTTTACTTG
1301 AAGTAACATT ACTGAATTG TGAAGACTTG ATTACAAAAG AATAAAAAAC
1351 TTCCATATGA AATTTTATT GAAAATGAGT GGAAGTGCTT CATTATAGAA
1401 TTACGGACTT AAAAATTTTG CTAATAAATT GTGTGTTTGA AAGGTGTTT
1451 TTGTTTTTGT CTTTTTAAAC TACTGTAAA AGAACAGCTT ATGATAAGTA
1501 ATATGTTTAA CTTAGAGAAG AATTTTTC TGTACCAAAG TTGGCATATT
1551 GCATTCTAAA TAAGATGCTA AATAAGAGTT AACCACATT CAACATGACC
1601 TTAAGACTGC TGGGTTTTGT ATTAATTAAT TTATAATTGG CACTGTGATT
1651 TGAAAAATTT ATAGAAAAAA AGGTACAGGG CAAGTTTTTA AATTAAAACT
1701 TTCTATATTT TGTTTTACCA GTAAAAGTGA CCTTATCATG GCCTCTCTCA
1751 TCAAGATGAT TTTAAATAG GTTGTAATAT ATTTTGAAA TATTTGAATG
1801 TGAAGTACCA TTGAGTCATC CAAACTAGGT AAGGCCTCAA GTACTTTAAA
1851 CTAGTAAAAA CTAGTAGCTG ATAATATTCA CCTAAGTAAG TGTTGTAAAA
1901 TAATTCAGAG TTCAGGACCT AGCTTAGATA AATGTATACT ACTCTTTTC
1951 TCATAGTAAA AATCTTACAT TTCCAACCTC AAAATTGGTG CTTCCATATT
2001 TGTGATAAAC CAAACTCCT AAGGTTTTT GTTTTCTTTT TAACTACTTT
2051 CCAATGCAT ACTATACCT AGAAATAGTG TATCAATATA GTGGGCTTTT
2101 TTTTCTCTCT TCATAAACCC ACAGTAAAT TTAATCACAG GAACTACTT
2151 ATATCTTAC ACTTTGTATT GATACTTAA AATGGCATCA GTTTATCTTA
2201 TCCAGCAGCT TGCTTTTAT CTCCTTTTT AGTGAGTGA ATAGAGCAAC
2251 TAGCATGCCT GTGTCCCAG CTACTGGGA GGCTAAGGTG GGAAGATCAA
2301 TTGAACCTAG GAGGTGAGG CTATAGTGAG CTGTGATTGC ACGACTGCAC
2351 TCCAGCCTAG GCAATGGAGT GAGACTCCTG TCTCTAAAAC AGCAACAACA
2401 AAAATAAAGC AACCATAGTG CATAAGGGAA ATTAATGTT CCCTATAGAA
2451 ATATGTGTAT GTCTGTGATA GTGGTATGCA AATGCTAATT ATTTTATAAA
2501 ATAAAAGTTC AGAATATTTC TTATCATTGC CACTTGAACA ATTAAGGGT
2551 TTGCTTTATT TCACTAATGT TTAATAGGAA CCCTTTGCTT CAAACAGCTT
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2601 TGTGAAATC ATGTAAAAAT TTGTTAATAG AGAATCAAGT TATTTAACTC
2651 AACTTATTTA ATTCAGGCTT GTGATACTAA CATACAAAGG TAGCATAAAC
2701 CAAGTCATAA ATTGCTGTAA TCTTTCCTGT AGAGTAATAG CTACTTCATG
2751 ATTTTITTTAA AAATTTTCATT TTTTGTCTAT TTAGGATTGC ATTTGCTTGG
2801 CTCCTAGTAA CAATTCTTTT ACAGTATTAG CACTCTCTTT ACTAAGGAAT
2851 GCCTCCCAAG GAAATGCAAA GGTAGGAAAA GTCTCTTAGA ATGCCCATGA
2901 GGTATTTAAA ACAGATATTT ATGAAATCT TTTTGTGAAT GTTATAAATC
2951 TTGCTAGTTA TTTTATCTTT ATCTTAAGTA TTAGATGTAG TTCCTTGGA
3001 TTGTCATTAC ATATTATTTT TTTTCTAGTG TGGTTTCAAA TAACTTTTGG
3051 CCAACATATA ATCATCATCA AACATTCCT GACCATATCT ATTTTATAAC
3101 TCAAAATAAG TTGGACAAAT AATCATTTTA ATAAAACTA TTTTTCCTCA
3151 GTATAACCAAC TGTCATGTGG TTCACCTTTC ACCCCAGATA CAAAACACTT
3201 ATTTGTGTAG CCCAGTTCCC ATCTACAGTA ATACCTGAA ACCTTAATAA
3251 ATTTTAAAAA TCATAAAAAA AAAATATTGT AAAATACAAC AAATTTTGG
3301 CAAGGTACT TCATCTTCAT TCATTATTAC CTGACAGTAT TAACTACTA
3351 CTCAATAATT TTAGASTAAA CTTTCTGTG TTTTCCCGT GATTTTCATT
3401 GTGCTGTCTT GACAACATGC TCCAACTCT TTGCATCAAA TTGTTTTATT
3451 AACATACATT TGTCTACCTT AAAACTAGCT TTATTACAG AGAAAGACCT
3501 AAAAGGAGTC TATTAATAATG CTGCTTCAG TTGATAGTT TTTTITTA
3551 TCACCTGTGAC CATAAACTAA CTGAAATTAT AATGGATTTT TTTTCTCTC
3601 CCGGTCACAA CACAGATCTT CTGTTTCAAT GTTCTCTGTC TACTGGGCAC
3651 CAACCTCTAC AAAGAACCAG CCAAAGGCTA GGTACTTGAT ATAAAAAGGA
3701 ATATTACATT ATTTTCTGCC CTCAAGTTGC TCTATCTCCT GAAAGAAACA
3751 AGTAATATTT ATAATACAAT ATGATAAATG CTACAAAGA AATAGCTGTA
3801 AAGTCCTTTG GTAAATGCTG TTGAATTGGA ATTCAGTAAG AACTATAAAC
3851 TGTAGACCTT TTTATAATCA AATGCTTTTG TCTTGAAACA AAACAGATTC
3901 CTCCTTATAT TGACTTAGCA AAGGAGGTAC AAGGACATTG GCATTTGACC
3951 TGAATTATGG TGTTTTATTG AATGAGCTAT AAGACAACAT TTTTACCCTT
4001 TAAAAATGAAC ACTGAACAAA TGTGTTAATG GTATCTTGT TAAAAGGAAA
4051 ACATAGCTAT AAATAAAATA CTACATCGAA ATCCAGCACT GGAGTTCATT
4101 TGAAATTTGA TATTTTGTGT AAAGTAACAA ACCTATTAAC ACAGATTTT
4151 AAAATAAATC AGAATCGTAT AAAGCACTT GGTACTTATT TGTCTCTTT
4201 TCCCTTACAT TCTGTGTGGT AGGTGGTATT ATCTCTGATT TACACATGAA
4251 GACATCCTTG TTAATGCAAT TTATTTATTC ATTCGGGCAT TTAATGTGTG
4301 CCAACTTGCA AAAGGAATAG AAATGTCTGT GATCTAGATA GTTCTAGATT
4351 GAACATAGAT TTTCTGCCAA CAAATCCTCT CTGCTGTTCA CATTATCCTT
4401 TGTTTAACGT ATGAACCAGG TTAATAAAAT AGGATAAATC ATGTGTCTTA
4451 GAATATGAAA ATAGTAAGGT CTTTGAGGTC ACTTGATCTT CTCTAAGTAG
4501 ACTTTATAAT ATTGTGTTTT ATCTCATTTC TCAATATTAG AATACGGGTA
4551 GATTTTAATT TTGCTATAAT ATAGGAAATG GTTCATCTTT GTACCAAAAT
4601 ATTGCATTCT TCTGATATTT AGACAGTTGG AAACCTTCTA AAATTGAGGA
4651 TTTTGTAGTG TATACTAAAT AATTGCATAT TCAAAAAAAT GTATTCTGAG
4701 TATGGTGATA TTAACATTT TTCCCCAAAA AAAAAAATAA AAAAAAATAA

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BLAST Results

No BLAST result

Medline entries

98107671:

Regulation of interferon-induced protein kinase PKR:
modulation of P58IPK inhibitory function by a novel protein,
P52rIPK

Peptide information for frame 1

ORF from 511 bp to 1194 bp; peptide length: 228
Category: similarity to known protein

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1 MPTNCAAGC ATTYNKHINI SFHRFPLDPK RRKEWVRLVR RKNFVPGKHT
51 FLCSKHFEAS CFDLTGQTRR LKMDAVPTIF DFCTHIKSMK LKSRNLLKKN
101 NSCSPAGPSN LKSNISSQOV LLEHSYAFRN PMEAKKRIK LEKEIASLRR
151 KMKTCLOKER RATRRWIKAT CLVKNEANS VLPKGTSEHM LPTALSSSLPL
201 EDFKILEQDQ QDKTLLSLNL KQTKSTFI

```

BLASTP hits

Entry AF007393.1 from database TREMBL:
product: "P52rIPK"; Homo sapiens P52rIPK mRNA, complete cds.
Score = 166, P = 2.5e-11, identities = 40/106, positives = 56/106

No Alert BLASTP hits found

Report for DKFZphfbr2 22i4.1

```
SEQ      MPTNCAAGCATTYNKHINISFHRFLDPKRKEWVRLVRKNFVPGKHTFLCSKFHEAS
SEG      .....
PRD      cccccccccccccccccccceeeccccchhhhhhhhhhhhcccccccceehhhhhhhh

SEQ      CFDLTGQTRRLKMDAVPTIFDFCTHIKSMKLKSRNLLKKNNNSCPAGPSNLKSNISSQQV
SEG      .....xxxxxxxxxxxxxxx
PRD      cccccccccccccccccccceeeccccchhhhhhhhhhhccccccccccccccccchhh

SEQ      LLEHSYAFRNPMEAKKRIIKLEKEIASLRKMKTCLOKERRATRRIKATCLVKNLEANS
SEG      .....
PRD      hhhhccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhheeeecccccc

SEQ      VLPKGTSEHMLPTALSSLPLEDFKILEQDQDKTLLSLNLKQTSTFI
SEG      .....
PRD      cccccccccccccccccccchhhhhhhcccccccccccccccccccc
```

PS000001	19->23	ASN_GLYCOSYLATION	PDOC000001
PS000001	100->104	ASN_GLYCOSYLATION	PDOC000001
PS000001	114->118	ASN_GLYCOSYLATION	PDOC000001
PS000004	160->164	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	68->71	PKC_PHOSPHO_SITE	PDOC000005
PS000005	88->91	PKC_PHOSPHO_SITE	PDOC000005
PS000005	147->150	PKC_PHOSPHO_SITE	PDOC000005
PS000005	163->166	PKC_PHOSPHO_SITE	PDOC000005
PS000006	60->64	CK2_PHOSPHO_SITE	PDOC000006
PS000006	78->82	CK2_PHOSPHO_SITE	PDOC000006
PS000008	9->15	MYRISTYL	PDOC000008

161

DKFZphfbr2_22k3

group: brain derived

DKFZphfbr2_22k3 encodes a novel 538 amino acid protein with weak similarity to extensins.

No informative BLAST results; no predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to extensins

complete cDNA, complete cds, few EST hits
CpG Island in 5' UTR complete cDNA

Sequenced by AGOWA

Locus: unknown

Insert length: 2775 bp

Poly A stretch at pos. 2755, polyadenylation signal at pos. 2718

```
1 GGGGCTGCCC GCGCGCTCCA CGGTGCAGAG CTCTAAGCGC GCGGGCTGGC
51 AGGCTGCGGC GCGTCAAGGT CAGCCTGGAG CTGGGTGGCG GCCTGCCTGG
101 GGGCGGGGGA CCCTACTGGA GGCCCGGGCT GGGGCTCCCG AGCGCCTCGG
151 CCATATTGAA TAGCTTCGAC TGGACCGTCT TTGTCTGCGA AGTCCTGTCC
201 CAAGTTCCAG CCGCGTCCCT GGGGCTGGG GCAGGAAGAG TCGCTGGCAG
251 CCCGCGCGCC CCAACTTGGA GCTGGGACAC CACGTTTCCA GCTTGGAGTG
301 GGCCTTGAGC CTTGGGACTG ACCTCGCCCC CGGCTCACGT AGGCATCCTG
351 GAAATTGATT CCCCCAAGTC CTGGTGGGG GAGCCGACT TGGTCAAGAC
401 TGTACTTGTT GCAGGCGAAG AGATTGGAGG CGTTTGGCTC GTCCCTGGCT
451 AGGGAGGTGA GACTCTCCGG TCAGCGTTGC TGGAACTCCC CCCATCCAGT
501 CCCTCCCTCA AGACTAAGGG CTACAGTAGT TTGTTGGGGC TCATTGCCCC
551 CTCACCCAG ATATCACCCCT GGAGATCTTA AAGACTCTCG AGAAAAGCCA
601 CGTGGGGGGC TGGTTCCCTT GGGGCTTCCT GCCGTCCCC GACTGCCTCA
651 TTCTTTGGAG CGTCCCGAT GTCTGCAAAG ATGTGGATTT GGACGTCTC
701 GTGGAAGCCC TAAAGCCCGT GGGGACATTT AAGAAGATCG GCAAGGTGTT
751 CCGCAAGGAG GAGGACTCCA CGGTGGGGAT GCTGCAGATC GGGGAGGACG
801 TCGACTATTT GCTCATCCCC CGGGAGGTCA GGCTGGCTGG GGGCGTCTGG
851 AGAGTCATCT CTAAGCCCGC CACCAAGGAA GCAGAATTTC GGGAGCGGCT
901 GAGGAGTTCT CTGGAAGAAG AGGGCCGCAC CCTGGAGGAC GTGGCCCGCA
951 TCATGGAGAA GAGCACCOCG CACCCGCCCC AGCCCCCAA AAAGCCCAAG
1001 GAGCCCGGAG TGAGGAGGAG AGTGCAGCAG ATGGTGACTC CTCCGCCCGG
1051 GCTGGTCGTG GGCACGTACG ACAGCAGCAA CGCCAGCGAC AGCGAGTTCA
1101 GCGACTTCGA GACCTCCAGA GACAAGAGCC GCCAGGGCCC GCGGCGGGGC
1151 AAGAAGGTGC GCAAAATGCC CGTCAGCTAC CTGGGCAGCA AGTTCTCTGG
1201 AAGCGACCTG GAGAGTGAGG ATGATGAGGA ACTGGTCGAG GCCTTCCTCC
1251 GCGGACAGGA GAAGCAGCCC AGCGCGCCGC CTGCCCCCGG CCGCGTCAAC
1301 CTGCCAGTGC CCATGTTGA GGACAACCTG GGGCCTCAGC TGTCCAAGC
1351 GGACAGGTGG CGGGAGTATG TCAGCCAGGT GTCCTGGGGG AAGCTGAAGC
1401 GGAGGGTGAA GGGTTGGGCG CCGAGGGCGG GCCCCGGGGT GGGCGAGGCC
1451 CCGCTGGCCT CCACCGCAGT GGAGAGCGCA GGGGTATCAT CGGCAGCAGA
1501 GGGCACCAGC CCGGGGGATC GCTTGGGAAA CGCGGGAGAT GTTTGTGTGC
1551 CCCAGGCTTC CCCTAGGCGA TGGAGGCCCA AGATCAACTG GGCCTCCTTT
1601 CCGCGCCGCA GGAAGGAGCA GACAGCACCC ACAGGTCAGG GGGCAGACAT
1651 CGAGGCTGAT CAGGGGGGAG AGGCTGCAGA TAGTCAAAGG GAAGAGGCCA
1701 TAGCTGACCA GCGGGGAAGG GCTGCAGGTA ATCAGAGGGC TGGGGCCCCA
1751 GCTGACCAGG GGGCAGAGGC TGCAGATAAT CAGAGGGAAG AGGCTGCAGA
1801 TAATCAGAGG GCAGGGGCCC CAGCTGAGGA GGGGGCAGAG GCTGCAGATA
1851 ACCAGAGGGA AGAGGCTGCA GATAATCAGA GGGCAGAGGC CCCAGCTGAC
1901 CAGAGGTCAC AGGGCACAGA TAACCACAGG GAAGAGGCTG CAGATAATCA
1951 GAGGGCGGAG GCCCAGCTG ACCAGGGGTC AGAGGTTACA GATAATCAAA
2001 GGGAAGAGGC CGTACATGAC CAGAGGGAAA GGGCCCCAGC TGTCCAGGGT
2051 GCAGATAATC AAGGGGCACA GGCCCGGGCT GGCCAGAGGG CAGAGGCTGC
2101 ACATAATCAG AGGGCAGGGG CCCCAGGTAT CCAGGAAGCT GAAGTCTCAG
2151 CTGCCCCAAG GACCACAGGA ACAGCTCCAG GAGCCAGGGC CCGGAACAG
2201 CTCAAGACAG TGAGGTTCCA GACCCCTGGA CGCTTTTCGT GGTTTTGCAA
2251 GCGCCGGAGA GCCTTCTGGC ACACTCCCCG GTTGCCAACC CTGCCCCAGA
2301 GAGTCCCCAG GGCAGGAGAG GTCAGGAACC TCAGGGTGCT GAGGGCCGAG
2351 GCCAGATGAG AAGCTGAGCA GGGAGAGCAA GAAGACCAGC TGTGAGGTGA
2401 GGGCTAGAGA CAGCCCACGG GCCCTCCCTC CAAGTGTGGG AGGGAGAGAT
2451 GCTCTGCCTC TGAACCTCAA AGTGGAGGTG GAGTGCTGGC CACGCTCCA
2501 CCTAACAAAC CTCTTTATTC TCTTGTTAAA GTTTTGTTCA TGCTTTGATT
2551 TTTTTTAAAA TTTTTTAGAG ACAGGGTCTC ACTCTGTGTC CCAGGCTGGA
2601 GTGCACTGGC ATGATCATAA CTCACTGCAG CCTCAAACCT CTGGCCTCAA
2651 GTGATCCTCC TGCCCTCGGC TCCCAAATG CTGGGATTAC AGATGTGAGC
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2701 CACCACACAC ACCATCTGAT TAAAAA AAAAATACTGAT TCCCTGTAGC
 2751 AACCCAAAAA AAAAAA AAAA

BLAST Results

Entry HS164A7F from database EMBL:
 H.sapiens CpG island DNA genomic MseI fragment, clone 164a7, forward
 read cpgl64a7.ft1a
 Score = 740, P = 3.0e-25, identities = 150/151

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 779 bp to 2392 bp; peptide length: 538
 Category: similarity to known protein

1 MLQIGEDVDY LLIPREVRLA GGVWRVISKP ATKEAEFRER LTQFLEEEGR
 51 TLEDVARIME KSTPHPPQPP KKPKEPRVRR RVQOMVTPPP RLTVGTYDSS
 101 NASDSEFSDF ETSRDKSRQG PRRGKKVRKM PVSYLGSKFL GSDLESEDDE
 151 ELVEAFLRRQ EKQPSAPPAR RRVNLPVPMF EDNLGPQLSK ADRWREYVSQ
 201 VSWGKLRVRV KGWAPRAGPG VGEARLASTA VESAGVSSAP EGTSPGDRLG
 251 NAGDVCVPQA SPRRWPKIN WASFRRRRKE QTAPTGGCAD IEADQGGEAA
 301 DSQREEAIAD QREGAAGNQR AGAPADQGAE AADNQREEAA DNQRAGAPAE
 351 EGAEAADNQR EEAADNQR AEAPADQRSQGT DNHREEAADN QRAEAPADQG
 401 SEVTDNQREE AVHDQRRERAP AVQGADNQRA QARAGQRAEA AHNQRAGAPG
 451 IQEAEVSAAQ GTTGTAAPGAR ARKQVKTVRF QTPGRFSWFC KRRRAFWHTP
 501 RLPTLPKRVP RAGEVRNLRV LRAEAREAE OGEQEDQL

BLASTP hits

Entry RNU67136_1 from database TREMBL:
 "A-kinase anchoring protein AKAP150"; Rattus norvegicus
 A-kinase anchoring protein AKAP150 mRNA, complete cds. Rattus
 norvegicus (Norway rat)
 Length = 714
 Score = 182 (64.1 bits), Expect = 1.2e-10, P = 1.2e-10
 Identities = 73/257 (28%), Positives = 104/257 (40%)

Alert BLASTP hits for DKFZphfbr2_22k3, frame 2

TREMBL:PFSANTY_1 product: "S-antigen"; Plasmodium falciparum KF1916
 S-antigen gene, complete cds., N = 1, Score = 178, P = 3.7e-11

>TREMBL:PFSANTY_1 product: "S-antigen"; Plasmodium falciparum KF1916
 S-antigen gene, complete cds.
 Length = 285

HSPs:

Score = 178 (26.7 bits), Expect = 3.7e-11, P = 3.7e-11
 Identities = 60/217 (27%), Positives = 97/217 (44%)

Query: 269 INWASFRRRRKEQTAPTGGQA-DIEADQGGEAADSQRE-EAIADQ---REGAAGNQ RAGA 323
 +N + + + E G+G DE E+D+ EEI Q EA N+ AG+
 Sbjct: 47 LNGKNGKGNKYEDLQEEGEGENDDEEHSNSEESDNDEENEIIVGQGSNEKAGSNEEAGS 106
 Query: 324 PADQGAEEAADNQREEAADNQ RAGAPAEEGA--EAADNQ---EEAADNQRAEAPADQRS 377
 G+ E+A N++AG+ E G+ EA N+ EEA N++A + S
 Sbjct: 107 NEKAGSNEEAGSNEKAGSNEKAGSNEEAGSNEEAGSNEEAGSNEEAGSNEKAGSNEKAGS 166
 Query: 378 QGTDNHREEAADNQRAEAPADQSGSEVTDNQREEAVHDQRRERAPAVQGADNQRAQAR--AG 435
 EEA N++A + + GS E+A +++ + G+ N++A + AG
 Sbjct: 167 NEKAGSNEEAGSNEKAGSNEEAGSNEKAGSNEKAGSNEKAGSNEEAGS-NEKAGSNEEAG 225
 Query: 436 QRAEAAHNQ RAGA---PGIQEAEVSAAQGTGTGA-PGA 469


```

SEQ  EDNLGPQLSKADRWREYVSQVSWGKLRVKGWAPRAGPGVGEARLASTAVESAGVSSAP
SEG  .....
PRD  cccccccchhhhhhhhhheeeccchhhhhhhccccccccchhhhhhhhhhhccccccc

SEQ  EGTSPGDR LGNAGDVCVPQASPRRWRPKINWASFRRRRKEQTAPTGGADIEADQGGEEA
SEG  .....
PRD  cccccccccccccceeeccccccccccccchhhhhhhhhhhhhccccccchhhhhccchhh

SEQ  DSQREEAIADQREGAAGNQ RAGAPADQGA EADNQ REEAADNQ RAGAPAE EGA EADNQ R
SEG  .....xxxxxxxxxxxxx.....xxxxxxxxxxxxx...
PRD  hhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhh

SEQ  EEAADNQRAEAPADQRSQGTDNHREEAADNQRAEAPADQGEVTDNQREEAVHDQRRERAP
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  AVQGADNQRAQARAGQRAEAAHNQ RAGAPGIQEA EVSAAQGTGTAPGARARKQVKT VRF
SEG  .....xxxxxxxxxxxxx.....xxxxxxxxxxxxx...
PRD  hhccccchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhccccccccchhhhhhhhhhh

SEQ  QTPGRFSWFCRRRAFWHTPLPTLPKRVPFRAGEVRNLRVLRAEAREAEQGEQEDQL
SEG  .....xxxxxxxxxxxxx...
PRD  cccccceehhhhhhhccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhcc

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Prosites for DKFZphfbr2_22k3.2

PS00001	101->105	ASN_GLYCOSYLATION	PDOC00001
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	261->264	PKC_PHOSPHO_SITE	PDOC00005
PS00005	273->276	PKC_PHOSPHO_SITE	PDOC00005
PS00005	302->305	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	499->502	PKC_PHOSPHO_SITE	PDOC00005
PS00006	51->55	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	108->112	CK2_PHOSPHO_SITE	PDOC00006
PS00006	112->116	CK2_PHOSPHO_SITE	PDOC00006
PS00006	142->146	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	189->193	CK2_PHOSPHO_SITE	PDOC00006
PS00006	229->233	CK2_PHOSPHO_SITE	PDOC00006
PS00006	238->242	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00006	302->306	CK2_PHOSPHO_SITE	PDOC00006
PS00008	95->101	MYRISTYL	PDOC00008
PS00008	220->226	MYRISTYL	PDOC00008
PS00008	242->248	MYRISTYL	PDOC00008
PS00008	296->302	MYRISTYL	PDOC00008
PS00008	314->320	MYRISTYL	PDOC00008
PS00008	317->323	MYRISTYL	PDOC00008
PS00008	328->334	MYRISTYL	PDOC00008
PS00008	352->358	MYRISTYL	PDOC00008
PS00008	400->406	MYRISTYL	PDOC00008
PS00008	450->456	MYRISTYL	PDOC00008
PS00008	461->467	MYRISTYL	PDOC00008
PS00008	464->470	MYRISTYL	PDOC00008
PS00009	123->127	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_22k3.2)

DKFZphfbr2_22k8

group: brain derived

DKFZphfbr2_22k8 encodes a novel 172 amino acid protein without similarity to known proteins.

No informative BLAST results; no predictive prosite, pfam or SCOP motif

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits.

Sequenced by AGOWA

Locus: /map="7"

Insert length: 2789 bp

Poly A stretch at pos. 2769, polyadenylation signal at pos. 2756

```
1 GGGGGAGCCA TGAGGCGCCA GCCTGCGAAG GTGGCGGCGC TGCTGCTCGG
51 GCTGCTCTTG GAGTGCACAG AAGCCAAAAA GCATTGCTGG TATTTGGAAG
101 GACTCTATCC AACCTATTAT ATATGCCGCT CCTACGAGGA CTGCTGTGGC
151 TCCAGGTGCT GTGTGCGGGC CCTCTCCATA CAGAGGCTGT GGTACTTCTG
201 GTTCCTTCTG ATGATGGGCG TGCTTTTCTG CTGCGGAGCC GGCTTCTTCA
251 TCCGGAGGCG CATGTACCCC CGCCCGCTGA TCGAGGAGCC AGCCTTCAAT
301 GTGTCTTACA CCAGGCAGCC CCCAAATCCC GGGCCAGGAG CCCAGCAGCC
351 GGGGCGGCCC TATTACACTG ACCCAGGAGG ACCGGGGATG AACCTGTGCG
401 GGAATTCCAC GGCATATGGT TTCCAGGTCC CACCCAATC ACCCCAGGGG
451 AGTGTGGCCT GCCCGCCCCC TCCAGCCTAC TGCAACACGC CTCCGCCCCC
501 GTACGAACAG GTAGTGAAGG CCAAGTAGTG GGGTGCCAC GTGCAAGAGG
551 AGAGACAGGA GAGGGCCTTT CCCTGGCCTT TCTGTCTTCG TTGATGTTCA
601 CTTCCAGGAA CGGTCTCGTG GGCTGCTAAG GGCAGTTCCT CTGATATCCT
651 CACAGCAAGC ACAGCTCTCT TTCAGGCTTT CCATGGAGTA CAATATATGA
701 ACTCACACTT TGTCTCTCTT GTTGTCTCTG TTTCTGACGC AGTCTGTGCT
751 CTTCTGTCCC GGGTATTAAT AGGAAGCCCC ATGCCGGGCG GCTCAGCCGA
801 GCGTGACCAG ATCTACAGGA GAGAGACTGA GAGGAAGAAG GCAGTGCTGG
851 AGGTGCAAGT GGCATGTAGA GGGGCCAGGC CGAGCATCCC AGGCAAGCAT
901 CTTCTGTCCC GGGTATTAAT AGGAAGCCCC ATGCCGGGCG GCTCAGCCGA
951 TGAAGCAGCA GCCGACTGAG CTGAGCCCGC CAGGTCATCT GCTCCAGCCT
1001 GTCTCTCTCGT CAGCCTTCCT CTTCCAGAAG CTGTTGGAGA GACATTCAGG
1051 AGAGAGCAAG CCCCTTGTC TGTCTGTGTC TCTGTTCATA TCCTAAAGAT
1101 AGACTTCTCC TGCACCGCCA GGAAGGATA GCACGTGCAG CTCTACCCGC
1151 AGGATGGGGC CTAGAATCAG GCTTGCCCTG GAGGCCTGAC AGTGATCTGA
1201 CATCCACTAA GCAAAATTTT TTAATTCAT GGGAAATCAC TTCTGCCCCC
1251 AAAGTGAGAC ATTGCATTTT GTGAGCTCTT GGTCTGATTT GGAGAAAGGA
1301 CTGTTACCCA TTTTCTTGGT GTGTTTATGG AAGTGCATGT AGAGCGTCTT
1351 GCCCTTTGAA ATCAGACTGG GTGTGTGTCT TCCCTGGACA TCACTGCCTC
1401 TCCAGGGCAT TCTCAGGCCC GGGGGTCTCC TTCCCTCAGG CAGCTCCAGT
1451 GGTGGGTCTT GAAGGGTGCT TTCAAACCGG GGCACATCTG GCCGGGAAGT
1501 CACATGGACT CTTCCAGGGA GAGAGACCAG CTGAGGCGTC TCTCTCTGAG
1551 GTTGTGTTGG GTCTAAGCGG GTGTGTGCTG GGCTCCAAGG AGGAGGAGCT
1601 TGCTGGGAAA AGACAGGAGA AGTACTGACT CAACTGCACT GACCATGTTG
1651 TCATAATTAG AATAAAGAAG AAGTGGTCGG AAATGCACAT TCCTGGATAG
1701 GAATCACAGC TCACCCAGG ATCTCACAGG TAGTCTCCTG AGTAGTTGAC
1751 GGCTAGCGGG GAGCTACTTC CGCCGCATAG TTATAGTGTG GATGTGTGAA
1801 CGCTGACCTG TCCTGTGTGC TAAGAGCTAT GCAGCTTAGC TGAGGCGCCT
1851 AGATTACTAG ATGTGCTGTA TCACGGGGAA TGAGGTGGGG GTGCTTATTT
1901 TTTAATGAAC TAATCAGAGC CTCTTGAGAA ATTGTTACTC ATTGAACTGG
1951 AGCATCAAGA CATCTCATGG AAGTGGATAC GGAGTGATTT GGTGTCCATG
2001 CTTTTCACTC TGAGGACATT TAATCGGAGA ACCTCCTGGG GAATTTTGTG
2051 GGAGACACTT GGAACAAAAA CAGACACCCT GGAATGCAAG TTGCAAGCAC
2101 AGATGCTGCC ACCAGTGTCT CTGACCACCC TGGTGTGACT GCTGACTGCC
2151 AGCGTGGTAC CTCCCATGCT GCAGGCCTCC ATCTAAATGA GACAACAAAG
2201 CACAATGTTT ACTGTTTACA ACCAAGACAA CTGCGTGGGT CCAAACTCCT
2251 CTCTTCTCTC AGGTCATTTG TTTTGCATTT TTAATGTCTT TATTTTGTG
2301 AATGAAAAAG CACACTAAGC TGCCCTGGA ATCGGGTGCA GCTGAATAGG
2351 CACCCAAAAG TCCGTGACTA AATTCCGTTT GTCTTTTGA TAGCAATTA
2401 TGTTAAGAGA CAGTGATGGC TAGGGCTCAA CAATTTTGTA TTCCCATGTT
2451 TGTGTGAGAC AGAGTTTGTG TTCCCTTGAA CTGGTTTGA ATTGTGCTAC
2501 TGTGAACGCT GATCTGCAT ATGGAAGTCC CACTTTGGTG ACATTTCTCG
2551 GGCATTCTTG TTTCCATTGT GTGGATGGTG GGTGTGCCC ACTTCTGGGA
2601 GTGAGACAGC TCCTGGTGTG TAGAATTCCT GAGGCGTCCG TGGTTCCAGG
2651 TAAACTTGAA GCAGATCTGT GCATGCTTTT CCTCTGCAGC AATTGGCTCG
2701 TTTCTCTTTT TTGTTCTCTT TTGATAGGAT CCTGTTTCCT ATGTGTGCAA
```

2751 AATAAAATA AATTGGGCA AAAAAAAAAA AAAAAAAAAA

BLAST Results

Entry HS671255 from database EMBL:

human STS SHGC-11828.

Length = 400

Minus Strand HSPs:

Score = 1822 (273.4 bits), Expect = 4.8e-76, P = 4.8e-76

Identities = 382/397 (96%), Positives = 382/397 (96%),

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 10 bp to 525 bp; peptide length: 172

Category: putative protein

Classification: unset

```

1 MRRQPAKVAA LLLGLLLECT EAKKHCWYFE GLYPTYIICR SYEDCCGSRC
51 CVRALSIQRL WYFWLLMMG VLFCCGAGFF IRRMYPPPL IEEPAFNVSY
101 TROPNPGPG AQOPGPYYT DPGGPGMNPV GNSTAMAFQV PNPSPQGSVA
151 CPPPPAYCNT PPPPYEQVVK AK

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_22k8, frame 1

PIR:S14970 extensin class I (clone w17-1) - tomato, N = 1, Score = 118,
P = 2.3e-07

>PIR:S14970 extensin class I (clone w17-1) - tomato
Length = 132

HSPs:

Score = 118 (17.7 bits), Expect = 2.3e-07, P = 2.3e-07
Identities = 30/82 (36%), Positives = 35/82 (42%)

```

Query: 87 PPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQ 146
      PPP P Y + PP P P P P YY P P +P + P SP
Sbjct: 32 PPPSPSPPP--PYYYKSPPPPSPSP--PPPYYYKSPPPPDPSPPPPYYYKSPPPPSPSP 87

```

```

Query: 147 GSVACPPPPAYCNTPPPP--YEQV 168
      PPPP Y + PPPP YE +
Sbjct: 88 PPSPPPPPTYGSPPPPPPFYENI 111

```

Score = 104 (15.6 bits), Expect = 6.9e-06, P = 6.9e-06
Identities = 28/78 (35%), Positives = 34/78 (43%)

```

Query: 87 PPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQ 146
      PP P + Y + PP P P P P YY P P +P ++ PP P
Sbjct: 1 PPSPPSPPPY---YYKSPPPPSPSP--PPPYYYKSPPPPSPSP---PPPYYYKSPP-PPS 51

```

```

Query: 147 GSVACPPPPAYCNTPPPP 164
      S PPPP Y +PPPP
Sbjct: 52 PS---PPPPYYKSPPPP 66

```

Score = 102 (15.3 bits), Expect = 1.1e-05, P = 1.1e-05
Identities = 30/78 (38%), Positives = 33/78 (42%)

```

Query: 87 PPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQ 146
      PPP P Y + PP P P P P YY P P +P S + PP P
Sbjct: 48 PPSPPSPPP--PYYYKSPPPPDPSP--PPPYYYKSPPPPSPSPPPSPS-----PP-PPT 97

```

BNSDOCID: <WO 0112659A2 | >

(No Pfam data available for DKFZphfbr2_22k8.1)

Pedant information for DKFZphfbr2_22k8, frame 3

Report for DKFZphfbr2_22k8.3

[LENGTH] 122
[MW] 12854.08
[pI] 10.27
[KW] All_Alpha
[KW] LOW_COMPLEXITY 25.41 %

SEQ GSHEAPACEGGGAAARAALGVHRSQKALLVFRRTLSNLLYMPLLRGLLWLQVLCAGPLHT
SEG
PRD cccccccccchhhhhhhccccchhhhhhhhhhhhhccccccccchhhhhhhcccccc

SEQ EAVVLLVPSDDGRAFLRSRLHPEAHVPPAADRGASLQCVLHQAAPKSRPRSPAAGAAL
SEG
PRD cceeeeccccchhhhhhhccccccccccccccccchhhhhhhccccccccchhhhhc

SEQ LH
SEG ..
PRD CC

(No Prosite data available for DKFZphfbr2_22k8.3)

(No Pfam data available for DKFZphfbr2_22k8.3)

DKFZphfbr2_23b10

group: nucleic acid managment

DKFZphfbr2_2b10 encodes a novel 580 amino acid protein with strong similarity to rat RNA helicase HEL117.

HEL117 is a DEAD/H box helicase, which co-localises with a splicing factor and thus seems to be involved in splicing.

The new protein can find application in modulation of splicing.

strong similarity to rat RNA helicase HEL117

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 2905 bp

Poly A stretch at pos. 2885, no polyadenylation signal found

```
1 GGGGGCTCCG CTCCGCACCA CCAACCCCGG GCCGCAGTCC TGACGAGCGG
51 GTCAGGGCTT GTCGGGCGGA AGCCTGGCCT GGAGCCTGGA AGGGGGAGAC
101 GGGCCGAGCG GGAGCGGGAG CGGACGCGGC CTCAGTCCTG CGCGGAATAT
151 TGAAGGATGT TTGTTCCAAG ATCTCTAAAA ATCAAGAGGA ATGCTAATGA
201 TGATGGCAAA AGTTGTGTGG CTAAGATAAT TAAACCAGAC CCAGAAGACC
251 TTCAGTTGGA CAAAAGCAGA GATGTTCCCG TTGATGCTGT AGCTACAGAA
301 GCAGCCACAA TAGACAGGCA CATCAGCGAA TCATGCCCTT TCCCCAGCCC
351 AGGTGGCCAG TTGGCAGAGG TTCATTCACT AAGTCCCGAG CAGGGTGCGA
401 AGGACAGCCA TCCTTCTGAA GAGCCCTTA AGTCATTTTC CAAAACACAG
451 CGCTGGGCGA AACCAAGGGA ACCCATCTGT GTTGTCTGTG GTCGTTATGG
501 AGAGTATATC TGTGATAAGA CAGATGAAGA TGTGTGTAGT TTGGAGTGTA
551 AAGCGAAACA TCTTCTACAA GTTAAGGAAA AGGAAGAGAA ATCAAACTC
601 AGCAATCCAC AGAAGGCTGA TTCTGAGCCA GAGTCTCCAC TGAATGCTTC
651 CTATGTCTAC AAAGAGCACC CCTTTATTTT GAACCTTCAG GAAGACCAGA
701 TTGAAAATCT TAAACAGCAG CTGGGAATTT TAGTTCAAGG CCAAGAAGTC
751 ACCAGGCCCA TTATTGACTT TGAACATTGT AGTCTCCCTG AGGTCTTAAA
801 TCACAACCTG AAGAAATCAG GCTATGAGGT GCCAACTCCC ATTCAAATGC
851 AGATGATTCC TG'GGGACTT C'TGGGAAGAG ACATTCTGGC CAGTGCAGAT
901 ACTGGCTCAG GAAAAACAGC TGCTTTTCTT CTTCTGTGTA TCATGCGAGC
951 TTTATTCCGAG AGCAAACTC CATCTGCGCT CATTCTTACA CCAACCAGAG
1001 AGTTAGCCAT TCAGATAGAG AGACAAGCTA AAGAATTGAT GAGTGGCCTG
1051 CCACGCATGA AACTGTGCT TCTGTAGGG GGCTTACCCT TACCCCCACA
1101 GCTTTATCGT CTGCAACAAC ATGTTAAGGT TATCATAGCA ACCCTGGGC
1151 GACTTCTGGA TATAATAAAG CAGAGCTCTG TAGAACTCTG TGGTGTAAG
1201 ATTGTGGTAG TAGATGAAGC TGATACCATG TTAAAGATGG GTTTTCAACA
1251 ACAAGTGCTT GACATTTTGG AAAACATTCC TAATGATTGT CAGACCATT
1301 TGGTTTCAGC CACAATTCCA ACTAGCATAG AACAGCTAGC AAGCCAGCTT
1351 CTGCATAATC CTGTGAGAAT TATCACTGGA GAAAAGAAC TACCTTGTGC
1401 CAATGTACGT CAGATTATTT TGTGGGTAGA AGACCCAGCC AAAAAGAAAA
1451 AATTATTGGA AATTTTAAAT GATAAGAAAC TCTTTAAGCC TCCAGTGTTA
1501 GTATTGTGG ACTGCAAACT AGGAGCAGAT CTTTGTAGTG AAGCCGTTCA
1551 GAAAAACACA GGGCTGAAAA GCATATCTAT ACATTGCGAG AAGTCGCAAA
1601 TAGAAAGGAA AAACATATTG AAGGGATTAC TTGAAGGAGA CTATGAAGTT
1651 GTAGTGAGCA CAGGAGTCTT GGGACGAGGC CTAGACTTGA TCAGTGTCTAG
1701 GCTGGTTGTC AATTTTGATA TGCCTTCAAG TATGGATGAG TATGTCCATC
1751 AGGAAAATAC CTACAAGTCT ACTTGGAGGA ATCCCAGCA TTTTCAACAG
1801 GATGTCAGAA TGACCTTGGG CTATGTTGGC AAAGCACAAT CGGAAGAAGA
1851 CAACCAATTG AAGGTCAAAC TAGGCCTTAA AAAAAATTGT TCTTCTTAAA
1901 TGAAACTTTA TGTAAAGCCC AAGCTTCCTT TATGTAAAAA TAGGATACTC
1951 ACTAGGCTTT GGGGCTGACA ATGGTTTTTA AATCTTGCTA ATCTTCCCTG
2001 GAATGAAACC AGCATGACTC AAAGAGAAAA AGAGAGTCTA TAATATTTTC
2051 TAATCCCTGA GTTCTTTTCT TTATATATTA AAAAGGATTA TTAGGCTGGG
2101 TGTGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGGC CGAGGGGAGT
2151 GGATCACCTG AGTTCGAGAC CAGCCTAACC AACATGGAGA AACCTGTCT
2201 CTACTAAAAA TACAAAAATTA GCCAGGCGTG GTGGCGCATG CCTGTAATCC
2251 CAGCTACTCA GGAGGCTACA GCAGGAGAAT TGCTTGAAC TCGGGAGGCG
2301 AGCCAAGATC GCACCACTGC ACTCCAGCCT GGGCAACAAG AGTGAAGTCT
2351 TGTCTCAAAA TAATATTAAT GATAATAATA ATAATAATAA TAGGGATTAC
2401 TTGCATAAAT GTTCTTTTAA AATTATTGGC AGTATTGCTG AATGTATTTA
2451 GATTTTTCAC CCAAGTGACA ACAACTGAAT TCATAAAGAT TCATCAACAA
2501 GACCTGATAA AAAAAATGT AAGCATATTA TAGTGGATAC TTCCAAGACT
2551 CTTGGTCTAA CATGTATTAG AAAGCACAAG GAGCCAGGC ACAGGGGCTC
2601 CCGCCGGTAA TCCCAAGCT TTGGGAAGCC AAGGCAGGTG GATCGCTTGA
2651 GCTCAGGAGT TAGAGACCAG CCTGGGCAAC ATGGTGAAAT CCCGTCACCA
```

```

2701 CAAAAAATG CAAAAATTAA CTGGGCGTGG TGGCATGCAC CTGTAGTGGC-
2751 AGCTACTCTG GAGGCTGAGG TGAGGGGAAT CACCTGAGCC GGGGGAATCA
2801 CCTGAGCCCA GGGAGTTGA GGCTGCTGTG AGCCATGGTC ATGACACTGC
2851 CCTCCAGCCT GGACACAGA TTGAGACCCT GTCTCAAAAA AAAAAAAAAA
2901 AAAAA

```

BLAST Results

No BLAST result

Medline entries

Medline:

A putative mammalian RNA helicase with an arginine-serine-rich domain

Peptide information for frame 1

ORF from 157 bp to 1896 bp; peptide length: 580
 Category: strong similarity to known protein
 Prosite motifs: ATP_GTP_A (247-255)
 LEUCINE_ZIPPER (298-320)

```

1 MFVPRSLKIK RNANDDGKSC VAKIIPDPE DLQDKSRDV PVDVATEAA
51 TIDRHISESC PFPSPGGQLA EVHGVSPSEQ AKDSHPSEEP VKSFSKTQW
101 AEPGEPICV CGRYGEYICD KTDEDVCSLE CKAKHLLQVK EKEEKSKLSN
151 PQKADSEPE PLNASYVYKE HPFILNLQED QIENLKQQLG ILVQGEVTR
201 PIIDFEHCSL PEVLNHNHKK SGYEVPTPIQ MQMIPVGLLG RDILASADTG
251 SGKTAFFLLP VIMRALFESK TPSALILTPT RELAIQIERQ AKELMSGGLPR
301 MKTVLLVGG LPLPQLYRLQ QHVKVIIATP GRLLDIIKQS SVELCGVKIV
351 VVDEADTMLK MGFQQQVLDI LENIPNDCQT ILVSATIPTS IEQLASQLLH
401 NPVRIITGEK NLPCANVRQI ILWVEDPAKK KKLFEILNDK KLFKPPVLVF
451 VDCKLGADLL SEAVQKITGL KSISIHSEKS QIERKNILKG LLEGDYEVVV
501 STGVIGRGLD LISVRLVNF DMPSSMDEYV HQENTYKSTW RNPQHQQDV
551 RMTLGYVGKA QWEDNQLKV KLGLKKNCS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phfbr2_23b10, frame 1

PIR:A57514 RNA helicase HEL117 - rat, N = 2, Score = 615, P = 1.6e-60

TREMBL:AB018344_1 gene: "KIAA0801"; product: "KIAA0801 protein"; Homo sapiens mRNA for KIAA0801 protein, complete cds., N = 1, Score = 615, P = 2.8e-59

TREMBL:CEFO1F1_1 gene: "F01F1.7"; Caenorhabditis elegans cosmid F01F1., N = 2, Score = 365, P = 1.9e-58

TREMBL:AF083255_1 product: "RNA helicase-related protein"; Homo sapiens RNA helicase-related protein mRNA, complete cds., N = 2, Score = 556, P = 1.5e-57

PIR:S14048 RNA helicase dbp2 - fission yeast (Schizosaccharomyces pombe), N = 1, Score = 591, P = 1.6e-57

>PIR:A57514 RNA helicase HEL117 - rat
 Length = 1,032

HSPs:

Score = 615 (92.3 bits), Expect = 1.6e-60, Sum P(2) = 1.6e-60
 Identities = 140/394 (35%), Positives = 236/394 (59%)

```

Query: 144 EKSLSNPQKADSEPEPLNASYVYKEHPFILNLQEDQIENLKQQL-GILVQGEVTRPI 202
      ++ KL P P ++ Y E P + + +++ + ++ GI V+G+ +PI
Sbjct: 313 QQRKLLPEVDHGKIEYEPFRKNF-YVEVPELAKMSQEEVNVRLEMEGITVKGKCPKPI 371
Query: 203 IDFEHCSLPEVLNHNHKKSGYEVPTPIQMOMIPVGLLGRDILASADTGSGKTAFFLLPV- 261

```

Sbjct: 372 + C + + ++LKK GYE PTPIQ Q IP +.GRD++ A.TGSGKT AFLLP+
 KSWVQCGISMKILNSLKKHGYEKPPIQTQAIPAIMSGRDLIGIAKTGSGKTIAFLLPF 431

Query: 262 --IM--RALFESKTPSALILTPTRELAQIERQAKELMSGLPRMKTVLLVGGPLPFPOLY 317
 IM R+L E + P A+I+TPTRELA+QI ++ K+ L ++ V + GG + Q+

Sbjct: 432 RHIMDQRSLEEGERPIAVIMTPTRELAQITKECKKFSKTLG-LRVVCVYGGTGISEQIA 490

Query: 318 RLQQHVKVIIATPGRLLDIIKQSS---VELCGVKIVVVDEADTMLKMGFQQQVLDILENI 374
 L++ ++I+ TPGR++D++ +S L V VV+DEAD M MGF+ QV+ I++N+

Sbjct: 491 ELKRGAEIIVCTPGRMIDMLAANSGRVTNLRRVTYVVLDDEADRMFDMGFQVMRIVDNV 550

Query: 375 PNDCQTILVSATIPTSIEQLASQLLHNPVRIITGEKNLPCANVRQIILWVEDPAKKKKLF 434
 D QT++ SAT P ++E LA ++L P+ + G +++ C++V Q ++ +E+ K KL

Sbjct: 551 RPDRQTVMFSAITFPRAMEALARRILSKPIEVQVGRSVVCSDEVQVIVIEEEKKFLKLL 610

Query: 435 EILNDKKLFKPPVLVFDCKLGADLLSEAVQKITGLKSISIHSEKSQIERKNILKGLLEG 494
 E+L + V++FVD + AD L + + + + +S+H Q +R +I+ G

Sbjct: 611 ELLGHYQE-SGSVIIIFVDKQEHADGLLKDLMRAS-YPCMSLHGGIDQYDRDSIINDFKNG 668

Query: 495 DYEUVVSTGVLRGLDLISVRLVNVFMDPSSMDEYVHQ 532
 +++V+T V RGLD+ + LVVN+ P+ ++YVH+

Sbjct: 669 TCKLLVATSVAAARGLDVKHLILVNVNCPNHYEDYVHR 706

Score = 37 (5.6 bits), Expect = 1.6e-60, Sum P(2) = 1.6e-60
 Identities = 13/36 (36%), Positives = 17/36 (47%)

Query: 132 KAKHLLQVKEKEE---KSKLSNPQKADSEPEPLNA 164
 KA++ + KEK E SK K D E E +A

Sbjct: 113 KAENRSRSKEAEGGDSSKEKKKDKDDKEDEKEKDA 148

Pedant information for DKFZphfbr2_23b10, frame 1

Report for DKFZphfbr2_23b10.1

[LENGTH] 580
 [MW] 64572.24
 [pI] 6.13
 [HOMOL] TREMBL:CEFO1F1_1 gene: "F01F1.7"; Caenorhabditis elegans cosmid F01F1. 8e-61

[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YNL112w] 2e-53
 [FUNCAT] 04.01.04 rna processing [S. cerevisiae, YNL112w] 2e-53
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPL119c] 5e-53
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR204w] 2e-49
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YOR204w] 2e-49
 [FUNCAT] j mrna translation and ribosome biogenesis [H. influenzae, HI0231 RNA] 2e-46
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YLL008w] 3e-43
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YDL160c] 4e-39
 [FUNCAT] l genome replication, transcription, recombination and repair [H. influenzae, HI0892] 3e-35
 [FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YMR290c] 6e-34
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YOR046c] 3e-32
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YJL033w] 8e-30
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YDR194c] 5e-23
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL064c] 1e-16
 [FUNCAT] r general function prediction [M. jannaschii, MJ1401] 5e-11
 [FUNCAT] 11.10 cell death [S. cerevisiae, YMR190c] 1e-06
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YMR190c] 1e-06
 [BLOCKS] BL00115B Eukaryotic RNA polymerase II heptapeptide repeat proteins
 [BLOCKS] BL00039D DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039C DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039B DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039A DEAD-box subfamily ATP-dependent helicases proteins
 [PIRKW] nucleus 6e-53
 [PIRKW] RNA binding 9e-52
 [PIRKW] DEAD box 2e-43
 [PIRKW] transmembrane protein 1e-21
 [PIRKW] DNA binding 5e-48
 [PIRKW] ATP 4e-57
 [PIRKW] purine nucleotide binding 2e-43
 [PIRKW] P-loop 4e-57
 [PIRKW] hydrolase 6e-42
 [PIRKW] protein biosynthesis 2e-43
 [PIRKW] ATP binding 2e-50
 [SUPFAM] WW repeat homology 1e-49
 [SUPFAM] translation initiation factor eIF-4A 2e-43
 [SUPFAM] DEAD/H box helicase homology 4e-57
 [SUPFAM] recQ helicase homology 8e-06

```

[SUPFAM] unassigned DEAD/H-box-helicases 4e-57
[SUPFAM] ATP-dependent RNA helicase DBP1 2e-53
[SUPFAM] ATP-dependent RNA helicase DHH1 6e-40
[SUPFAM] tobacco ATP-dependent RNA helicase DB10 1e-49
[SUPFAM] Bloom's syndrome helicase 8e-06
[PROSITE] ATP_GTP_A 1
[PROSITE] LEUCINE_ZIPPER 1
[PROSITE] MYRISTYL 6
[PROSITE] CK2_PHOSPHO_SITE 8
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] PKC_PHOSPHO_SITE 7
[PROSITE] ASN_GLYCOSYLATION 1
[PFAM] Helicases conserved C-terminal domain
[PFAM] DEAD and DEAH box helicases
[KW] Alpha_Beta
[KW] LOW_COMPLEXITY 3.10 %

```

```

SEQ MFVPRSLKIKRNNDDGKSCVAKI IKDPEDLQLDKSRDVPVDAVATEAATIDRHISESC
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ PFPSPGGQLAEVHSVSPQGAQKSHPSSEEPVKSFSKTQRWAEPEGEPICVVCGRYGEYICD
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ KTDEDVCSLECKAKHLLQVKEKEEKS KLSNPQKADSEPEPLNASYVYKEHPFILNLQED
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ QIENLKKQLGILVQGVQEVTRPIIDFEHCSLPEVLNHNKSGYEVPTPIQMOMIPVGLLG
SEG .....
PRD hhhhhhhhhheeecccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ RDILASADTGSCKTAAFLLPVIMRALFESKTPSALILTPRELAIQIERQAKELMSGGLPR
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ MKTVLLVGGGLPLPPQLYRLQHVKVIIATPGRLLDIKQSSVELCGVKIVVDEADTMLK
SEG .....
PRD eeeeecccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ MGFAQQVLDILENIPNDCQITLVSATIPTSI EQLASQLLHNPVRIITGEKNLPCANVRQI
SEG .....
PRD cccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ ILWVEDPAKKKKLFEILNDKKLFKPPVLVFDCKLGADLLSEAVQKITGLKSIHSEKS
SEG .....
PRD eeccccchhhhhhhhhhhhhhhccccccccccccccccccccccccccccccccccccch

```

```

SEQ QIERKNILKGLLEGDYEVVSTGVLRGLDLISVRLVNFDMPPSSMDEYVHQENTYKSTW
SEG .....
PRD hhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccc

```

```

SEQ RNPQHFQQDVRMTLGYVGKAQWEEDNQLKVKLGLKKNCSS
SEG .....
PRD cccccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccc

```

Prosites for DKFZphfbr2_23b10.1

PS00001	163->167	ASN_GLYCOSYLATION	PDOC00001
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	97->100	PKC_PHOSPHO_SITE	PDOC00005
PS00005	251->254	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	513->516	PKC_PHOSPHO_SITE	PDOC00005
PS00005	535->538	PKC_PHOSPHO_SITE	PDOC00005
PS00005	539->542	PKC_PHOSPHO_SITE	PDOC00005
PS00006	122->126	CK2_PHOSPHO_SITE	PDOC00006
PS00006	156->160	CK2_PHOSPHO_SITE	PDOC00006
PS00006	209->213	CK2_PHOSPHO_SITE	PDOC00006
PS00006	221->225	CK2_PHOSPHO_SITE	PDOC00006
PS00006	340->344	CK2_PHOSPHO_SITE	PDOC00006
PS00006	389->393	CK2_PHOSPHO_SITE	PDOC00006
PS00006	480->484	CK2_PHOSPHO_SITE	PDOC00006
PS00006	524->528	CK2_PHOSPHO_SITE	PDOC00006
PS00007	489->497	TYR_PHOSPHO_SITE	PDOC00007
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	80->86	MYRISTYL	PDOC00008

PS00008	195->201	MYRISTYL	PDOC00008
PS00008	250->256	MYRISTYL	PDOC00008
PS00008	490->496	MYRISTYL	PDOC00008
PS00008	573->579	MYRISTYL	PDOC00008
PS00017	247->255	ATP_GTP_A	PDOC00017
PS00029	298->320	LEUCINE_ZIPPER	PDOC00029

Pfam for DKFZphfbr2_23b10.1

HMM_NAME	DEAD and DEAH box helicases		
HMM	*gLPWILRnIyeMGFEKPTPIQQaIPiILEGRDVMACAQTGSGKTAAF		
Query	209	SLPEVLNHNKKSGYEVPTPIQMOMIPVGLLRDILASADTSGSGKTAAF	257
HMM	1PMLQHIDwdPWPqpPQdPrALILAPTRELAMQIQEECRkFgkHMngIR		
Query	258	LLPVIMRALFES--KTPS---ALILTPTRELAIQIERQAKELMSGGLPRMK	302
HMM	ImcIYGGtnMRdQMRmLeRGpPHIVIAATPGRLIDHIERgtldLDRIeMLV		
Query	303	TVLLVGGLPLPPQLYRLQQHv-KVIIATPGRLDIIKQSSVELCGVKIVV	351
HMM	MDEADRLDMGFIDQIRrIMrqIPmpwNRQTMMSATMPdeIqELARrFM		
Query	352	VDEADTMLKMGFQQQVLDILENIP--NDCQTIIVSATIPTSIIEQLASQLL	399
HMM	RNPIRInIdMdElTtnEnIkQwYiyVerEMWKfdCLcrLie*		
Query	400	HNPVRIITGEKNLPCA-NVRQIILWVE-DPAKKKKLFEILN	438

HMM_NAME	Helicases conserved C-terminal domain		
HMM	*EileeWLknl.GIrvmYIHGdMpQeERdeIMddFnnGEynVLicTDVgg		
Query	458	DLLSEAVQKITGLKSISIHSEKSQIERKNILKGLLEGDYEVVSTGVLG	506
HMM	RGIDIPdVNHVINYDMPWNPEqYIQRIGRTgRIG*		
Query	507	RGLDLISVRLVNVNFDMPSSMDEYVH-QENTYKST	539

DKFZphfbr2_23521

group: signal transduction

DKFZphfbr2_23521.1 encodes a novel 193 amino acid protein which is nearly identical to bovine neurocalcin.

Neurocalcin is a Ca(2+)-binding protein with three putative Ca(2+)-binding domains (EF-hands). In cattle, 6 isoforms are differentially expressed in the central nervous system, retina and adrenal gland. Homology with recoverin indicates involvement in Ca²⁺ dependent activation of guanylate cyclase.

The new protein can find application in modulating/blocking the guanylate cyclase-pathway.

nearly identical to bovine neurocalcin

complete cds complete cDNA
EST hits

Sequenced by AGOWA

Locus: /map="574.6 cR from top of Chr8 linkage group"

Insert length: 3300 bp

Poly A stretch at pos. 3279, polyadenylation signal at pos. 3249

```
1 GGGGAGAATC TGGTGGATGC TGGACCTTGC TGCTGCTGCT ACTGCTGTTT
51 CCAGGGGGCTG CAGAGCATGG ACTGTTAAAT CTTGCACTTC TTCTGAGTGA
101 GCTGAATTCT TGCCGCCAGG ATGGGGAAAC AGAACAGCAA GCTGCGCCCG
151 GAGGTCATGC AGGACTTGCT GGAAAGCACA GACTTTACAG AGCATGAGAT
201 CCAGGAAATGG TATAAAGGCT TCTTGAGAGA CTGCCCCAGT GCACATTGTG
251 CAATGGAAGA GTTAAAGAAA ATATATGGGA ACTTTTCCCT TTATGGGGAT
301 GCTTCCAAAT TGCAGAGCA TGTCTTCCGC ACCTTCGATG CAAATGGAGA
351 TGGGACAATA GACTTTAGAG AATTCATCAT CGCCTTGAGT GTAACCTCGA
401 GGGGGAAGCT GGAGCAGAAG CTGAAATGGG CCTTCAGCAT GTACGACCTG
451 GACGGAAATG GCTATATCAG CAAGGCAGAG ATGCTAGTGA TCGTGCCAGGC
501 AATCTATAAG ATGGTTTCCT CTGTAATGAA AATGCCTGAA GATGAGTCAA
551 CCCCAGAGAA AAGAACAGAA AAGATCTTCC GCCAGATGGA CACCAATAGA
601 GACGGAAAAC TCTCCCTGGA AGAGTTCATC CGAGGAGCCA AAAGCGACCC
651 GTCCATTGTG CGCCTCCTGC AGTGCGACCC GAGCAGTGCC GGCCAGTTCT
701 GAGCCCTGCG CCCACCAATC GAATTGTAGA GCTGCTTG TGCCCTTTTG
751 ATTCTTCTTT TTAACAATTT TTTTTTTTTT TTGCCAAACA ATATCAATGG
801 TGATGCCGTC CCCTGTGCGG TCTGATGCGC CTTCTCCCGT GACGCCCTCA
851 GCCTCTTTTG TCGTGGATGC TTCGTGGGAA TGCCAGAGC CCCAGTGTGC
901 TTGTGGAGAG CATGGACAGA CTTCTGCTGT TTCATTGTTT GATGATTTTT
951 AATCGTTACT ATTATTTCTT TTTATTCTAA TGTCTCTGTT CTAAGACGTA
1001 AGACTCGGGG GTTGGGGCAA AAGAAGGGAA ACCCATCCAG TCCTGTGATT
1051 CTATTGCAAG CTTCAAGGGG CTTTTGTTTG AAAGACAAAA CTCCCCACCT
1101 GGGTCTGTTG TCACACGTGC CGTAGGGGTG ATGGATGGCA CCGGATGCTG
1151 GATTCGCCAA GAACAAGTTA CCCTCTGGGG TGAGGCTATT CCAGCGAGCT
1201 GGGACATTTT CCCATGGGGG CCCACTCCCC TCTCTCCCC AGCAGGCTGT
1251 AGTTTCTAAG CGTGAACAT TTCAAGATAA ATTAACAGAG GAGAGGAAAA
1301 AGATGGCTCA GCTATTTTTT CACAGGTTTA CACTAGTTGA GCTAATATGC
1351 GTGTCTTTGG AAATTAACA CAAATGGTAA CATATTCCAA AACCAGACCC
1401 ATCTTGTGTC CTATTGTGAT AAAATAAAAA GACGGCTGTA TATAACATAT
1451 TGGGTAATGC AGACCAAATT AAGTGTTTTG CTTCTTTTAA ATGAAATGCA
1501 TGTTTTAGTGA GCACTAATAC AATCTTATTC CAGAAGACTG TTTTGTAGTAG
1551 CTTATTGTGA AGTAAGACAA CTATAATGAA TGTCTGTCTT GTTTGGAAGT
1601 CATATCTGTC TTTGCACAAA TGTACCAATC GACAAGTATA TTTTATATAT
1651 TCCATAAAAA TACAAAGTAA CCCTGACTAG GGCCCAACTT TAATTTTGAA
1701 TGCATTTCCA GAGTGGCCAT GCCTAGAGGG CAGATGCAGA GCAGGTGGTA
1751 GTGGGACACG ACAATTGGAG CACAGGAATG TTAACATGTA TGACAGGGGA
1801 CCAGTAGGGT GGTTCCTCTC TCAGGCCCAG CAGCCCATTTG ACAGCATTAG
1851 ACTGCGGGCA TGGTGCTTTT CTGAGCAGAT CAATACTCTG CAGACTCGAA
1901 AAAACATCAC ATACATTCTT GGAACCTCCC AGTGGTTTAA TCTATGTGCA
1951 TGGTTAGGGA GCCAGGCCTG GAATATTTCAG TTTCCCTGCC CCTGTTAAAG
2001 AATCAGAGGT TGGGCAGTCA TCAAATTCAT CATAAAGACA TGGGCAAGTG
2051 TGTCTGTGGT TTCCAAGGCC CCCCTATGGA GAATCCAAAA GTATTTTCCA
2101 TTGCCCTGTG CTTTGAATGC AGACTTCTAT TTCCAGAAGT GACAGCACAA
2151 GTCTGAGTTG CTGTTTGGTC TGGTGACCTC AGACACACTA ATTTGAATTG
2201 AAAGCTAAGA GTAAAAATTT GCTGGTTACA GGCGAGTCAT ACTCTTGCAA
2251 GTAGTTAGCA AAGGGAGGCC CAAATTCTCA AGGTGTGTTA TGGGGAACCT
2301 GCCACTAAGA GAAGGCAGAG AGGTCCCTAG TGGGTATATT TGCTGCCAAG
2351 CCACTTGCCA AAGAAGAGGA ACCACAGAAA CAGAGACATC ATGACCAGGA
2401 GAAAAATGTG ACTAGACATG CTAACCTCCA GGTTTTATA TATGACTTGA
2451 GTCTGCTGTA TTGGCAGCA GAAATCCAAA TTTGTATGGT AGACCAAAAA
2501 GAACCAATC CATAGGGTGA AATTTTGAGA CCTAGACTCT GTAAAAATAA
```

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2551 TCCTAGTCTT CCTCCAGGGG TCAGTTCCTC ACAGTGGTTC TGTACCAAAA
2601 CTTGCCAAAT TCCTCCATGG CCAAGTGTTA AAATCTGTGT TTGGAATAA
2651 GCGAATTAAC CTAAGACACA GAAGGCAGAC TGGGTGAGGA GACCTAGCAT
2701 GCCCTATTGG CAGTGCTCAG GAGCTGCATC CCACTTTTCC CTGCTCTGAA
2751 TCGAAGTCCT AGTTCCTTCC TTTGATTCTC CTTTGGTAGG TCGAATCAGT
2801 TAATGTTTTG AGAAACCTGC CTGGGCTCTG CCCTTAGTCA TGACATCTCG
2851 CTGAGCCAGA CCCACTCTGT TCCTTGGAAC CTAGAGCTGG AGTGAGGAGT
2901 AGAGGTCTCC GGCTATTCCA GAAAGAAAAG TGAGCCACAT GCAGGCTGAT
2951 GAATGCCGAC ACTTCCAGAA TGTATAGAAA TAGTCCCTGT CCTGGCCTGC
3001 CACTGACCCT GTCTGTATT TCTCGGAGGT TGTTTTCTC CTTCTCCTTC
3051 CCAGGAAGGT CTTTGTATGT CGAATCCAGT GCACTCAAGT TTGGCCAAGG
3101 GACTCCACAG CACCCAGAGG ACTGCATGCC TCAAGGTTTA TGTCACCTCT
3151 CTGCTGGGCT GTTCATTGTC ATTGCTGTGT TCAGGGACCT TTGGAAATAA
3201 AACCTGTTCT GTCCCAAATA AAACCAGCCT GTGATGTTCA AGGGACTGGA
3251 ATAAAGTGGC TTACGACCTG AAGGATTCTA AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

Entry HS431350 from database EMBL:
human STS WI-15914.
Score = 1308, P = 3.1e-53, identities = 276/285

Entry HSG19929 from database EMBL:
human STS A002C26.
Score = 926, P = 1.5e-35, identities = 186/187

Entry AF052142 from database EMBL:
Homo sapiens clone 24665 mRNA sequence.
Score = 7378, P = 0.0e+00, identities = 1482/1487
3' UTR

Medline entries

93247712:
Neurocalcin family: a novel calcium-binding protein abundant in bovine central nervous system.

94045365:
Distinct regional localization of neurocalcin, a Ca(2+)-binding protein, in the bovine adrenal gland.

96407688:
Crystallization and preliminary X-ray crystallographic studies of recombinant bovine neurocalcin delta.

96066284:
Distribution pattern of three neural calcium-binding proteins (NCS-1, VILIP and recoverin) in chicken, bovine and rat retina.

Peptide information for frame 1

ORF from 121 bp to 699 bp; peptide length: 193
Category: strong similarity to known protein
Prosite motifs: EF_HAND (73-86)
EF_HAND (109-122)
EF_HAND (157-170)

```

1 MGKQNSKLRP EVMQDLLEST DFTEHEIQEW YKGFLRDCPS GHLSMEEFKK
51 IYGNFFPYGD ASKFAEHVFR TFDANGDGTI DFREFIALLS VTSRGKLEQK
101 LKWAFSMYDL DNGYISKAE MLVIVQAIYK MVSSVMKMPE DESTPEKRTE
151 KIFRQMDTNR DGKLSLEEFI RGAKS DPSIV RLLQCDPSSA GQF

```

BLASTP hits

Entry JH0616 from database PIR:
neurocalcin (clone pCalN) - bovine

Score = 1001, P = 5.2e-101, identities = 192/193, positives = 192/193

Entry GGU91630_1 from database TREMBL:

product: "neurocalcin"; Gallus gallus neurocalcin mRNA, complete cds.

Score = 998, P = 1.1e-100, identities = 191/193, positives = 192/193

Entry NECD_BOVIN from database SWISSPROT:

NEUROCALCIN DELTA.

Score = 996, P = 1.8e-100, identities = 191/192, positives = 191/192

Entry S47565 from database PIR:

BDR-1 protein - human

Score = 934, P = 6.6e-94, identities = 174/193, positives = 187/193

Entry I50676 from database PIR:

gene Rem-1 protein - chicken >TREMBL:GGREM1_1 gene: "Rem-1"; G.gallus

rem-1 mRNA

Score = 933, P = 8.4e-94, identities = 174/193, positives = 186/193

Alert BLASTP hits for DKFZphfbr2_23b21, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_23b21, frame 1

Report for DKFZphfbr2_23b21.1

```
[LENGTH]      193
[MW]           22215.30
[pI]           5.35
[HOMOL]       PIR:JH0616 neurocalcin (clone pCalN) - bovine 1e-109
[FUNCAT]      98 classification not yet clear-cut [S. cerevisiae, YDR373w] 3e-54
[FUNCAT]      30.03 organization of cytoplasm [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]      03.07 pheromone response, mating-type determination, sex-specific proteins
[S. cerevisiae, YKL190w] 2e-18
[FUNCAT]      03.01 cell growth [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]      13.04 homeostasis of other ions [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]      04.05.01.04 transcriptional control [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]      30.04 organization of cytoskeleton - [S. cerevisiae, YBR109c] 0.001
[FUNCAT]      08.19 cellular import [S. cerevisiae, YBR109c] 0.001
[FUNCAT]      03.22 cell cycle control and mitosis [S. cerevisiae, YBR109c] 0.001
[FUNCAT]      03.04 budding, cell polarity and filament formation [S. cerevisiae, YBR109c]
0.001
[FUNCAT]      10.02.99 other morphogenetic activities [S. cerevisiae, YBR109c] 0.001
[FUNCAT]      30.05 organization of centrosome [S. cerevisiae, YBR109c] 0.001
[BLOCKS]      BL00018
[SCOP]        dlrec_ 1.34.1.5.18 Recoverin [bovine (Bos taurus) 8e-55
[SCOP]        dljsa_ 1.34.1.5.17 Recoverin [human (Homo sapiens) 5e-58
[SCOP]        dlrcob_ 1.34.1.5.16 Calcineurin regulatory subunit (B-chain 1e-06
[SCOP]        d2mysc_ 1.34.1.5.15 Myosin Regulatory Chain [chicken (Gallu 2e-29
[SCOP]        dlscmc_ 1.34.1.5.14 Myosin Regulatory Chain [bay scallo 5e-33
[SCOP]        d2mysb_ 1.34.1.5.13 Myosin Essential Chain [chicken (Gallu 4e-26
[SCOP]        dlscmb_ 1.34.1.5.12 Myosin Essential Chain [bay scallo 6e-27
[SCOP]        dlclm_ 1.34.1.5.11 Calmodulin [Paramecium tetraurelia 1e-15
[SCOP]        d4cln_ 1.34.1.5.10 Calmodulin [Drosophila melanogaster 2e-16
[SCOP]        dlcfcc_ 1.34.1.5.9 Calmodulin [African frog (Xenopus laevis) 2e-16
[SCOP]        dlahr_ 1.34.1.5.8 Calmodulin [chicken gallus gallus 4e-16
[SCOP]        d3cln_ 1.34.1.5.7 Calmodulin [rat (Rattus rattus) 2e-16
[SCOP]        dltrcb_ 1.34.1.5.6 Calmodulin [bovine (Bos taurus) 8e-08
[SCOP]        dlcll_ 1.34.1.5.5 Calmodulin [human (Homo sapiens) 2e-16
[SCOP]        dlrtpl_ 1.34.1.4.5 Parvalbumin [rat (Rattus rattus) 8e-06
[SCOP]        d5tnc_ 1.34.1.5.2 Troponin C [turkey (Meleagris gallopavo) 3e-13
[SCOP]        dlpvaa_ 1.34.1.4.3 Parvalbumin [pike (Esox lucius) 6e-06
[SCOP]        dltnp_ 1.34.1.5.1 Troponin C [chicken (Gallus gallus) 9e-11
[EC]          2.7.1.107 Diacylglycerol kinase 2e-08
[PIRKW]       blocked amino end 1e-100
[PIRKW]       phosphotransferase 2e-08
[PIRKW]       duplication 4e-17
[PIRKW]       tandem repeat 7e-06
[PIRKW]       heterodimer 4e-17
[PIRKW]       heart 6e-09
[PIRKW]       zinc 2e-08
[PIRKW]       serine/threonine-specific protein kinase 1e-06
[PIRKW]       muscle contraction 1e-08
[PIRKW]       acetylated amino end 4e-09
[PIRKW]       ATP 2e-08
[PIRKW]       skeletal muscle 6e-09
```


[PIRKW] signal transduction 1e-91
 [PIRKW] protein kinase 2e-08
 [PIRKW] calcium binding 1e-100
 [PIRKW] alternative splicing 2e-13
 [PIRKW] methylated amino acid 1e-09
 [PIRKW] thin filaments 1e-08
 [PIRKW] lipoprotein 1e-101
 [PIRKW] cardiac muscle 6e-09
 [PIRKW] muscle 6e-09
 [PIRKW] myristylation 1e-100
 [PIRKW] EF hand 1e-101
 [PIRKW] retina 2e-51
 [SUPFAM] calcium-dependent protein kinase 2e-08
 [SUPFAM] unassigned calmodulin-related proteins 8e-41
 [SUPFAM] spec-related protein LpS1 7e-06
 [SUPFAM] calmodulin repeat homology 1e-101
 [SUPFAM] human diacylglycerol kinase 2e-08
 [SUPFAM] protein kinase C zinc-binding repeat homology 2e-08
 [SUPFAM] protein kinase homology 2e-08
 [SUPFAM] calmodulin 1e-101
 [PROSITE] EF_HAND_3
 [PROSITE] CK2_PHOSPHO_SITE 7
 [PROSITE] PKC_PHOSPHO_SITE 3
 [PFAM] EF_hand
 [KW] All_Alpha
 [KW] 3D

SEQ MGKQNSKLRPEVMQDLESTDFTEHEIQEWYKGLRDCPSGHLSMEEFKKIYGNFFPYGD
 1rec-HHHHHHHHHTTTCCCHHHHHHHHHHHHTTTTEEEHHHHHHHHHHHTTTTC

 SEQ ASKFAEHVFTFDANGDGTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLGNGYISKAE
 1rec- HHHHHHHHHHHH-----CEEHHHHHHHHHHHCCCGGGHHHHHHHHHTTTTCCCEEHHH

 SEQ MLVIVQAIYKMVSSVMKPEDESTPEKRTEKIFROMDTNRDGKLSLEEFIRGAKS DPSIV
 1rec- HHHHHHHHHHCCTTGGGCTTTTCHHHHHHHHHHHHCCTTTTECHHHHHHHHHHCHHHH

 SEQ RLICCDPSSAGQF
 1rec- HHHCCCH.....

Prosites for DKFZphfbr2_23b21.1

PS00005	92->95	PKC_PHOSPHO_SITE	PDOC00005
PS00005	149->152	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00006	23->27	CK2_PHOSPHO_SITE	PDOC00006
PS00006	44->48	CK2_PHOSPHO_SITE	PDOC00006
PS00006	106->110	CK2_PHOSPHO_SITE	PDOC00006
PS00006	117->121	CK2_PHOSPHO_SITE	PDOC00006
PS00006	143->147	CK2_PHOSPHO_SITE	PDOC00006
PS00006	158->162	CK2_PHOSPHO_SITE	PDOC00006
PS00006	165->169	CK2_PHOSPHO_SITE	PDOC00006
PS00018	73->86	EF_HAND	PDOC00018
PS00018	109->122	EF_HAND	PDOC00018
PS00018	157->170	EF_HAND	PDOC00018

Pfam for DKFZphfbr2_23b21.1

HMM_NAME EF hand
 HMM *MFrmMDkDGDGyIDFEEFmeMMkem*
 +FR +D +GDG+IDF EF+ +++
 Query 68 VFRTFDANGDGTIDFREFIIALSVT 92

 30.75 100 128 1 29 dkfzphfbr2_23b21.1 nearly identical to bovine neurocalcin
 Alignment to HMM consensus:
 Query *EIQEMFrmMDkDGDGyIDFEEFmeMMkem*
 +++F+M+D DG+GYI++ E++++++
 dkfzphfbr2 100 KLKWAFSMYDLGNGYISKAEMLVIVQAI 128

 Query 176 1 29 dkfzphfbr2_23b21.1 nearly identical to bovine neurocalcin
 Alignment to HMM consensus:
 HMM *EIQEMFrmMDkDGDGyIDFEEFmeMMkem*
 +++FR MD+++DG+++ EEF++ K!
 Query 148 RTEKIFRQMDTNRDGKLSLEEFIRGAKSD 176

DKFZphfbr2_23f2

group: brain derived

DKFZphfbr2_23f2 encodes a novel 182 amino acid protein with weak similarity to *S. pombe* Vps29p.

No informative BLAST results; no predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to Vps29p

complete cDNA, complete cds, EST hits

S. cerevisiae and *S. pombe* Vps29p are involved in vacuolar protein sorting

part of the cDNA is encoded by HSAC2350, splice pattern 4 exons

Sequenced by AGOWA

Locus: /map="12q24"

Insert length: 1016 bp

Poly A stretch at pos. 996, polyadenylation signal at pos. 974

```

1 GAATGGGGAG GAGCCAGAGG AAGAGGGCGG CGACGGTGGT GGTGACTGAG
51 CGGAGCCCCG TGACAGGATG TTGGTGTGG TATTAGGAGA TCTGCACATC
101 CCACACCGGT GCAACAGTTT GCCAGCTAAA TTCAAAAAAC TCCTGGTGCC
151 AGGAAAAATT CAGCACATTC TCTGCACAGG AAACCTTTGC ACCAAAGAGA
201 GTTATGACTA CCTCAAGACT CTGGCTGGTG ATGTTTCATAT TGTGAGAGGA
251 GACTTCGATG AGAATCTGAA TTATCCAGAA CAGAAAGTTG TGAATGTTGG
301 ACAGTTCAAA ATTGGTCTGA TCCATGGACA TCAAGTTATT CCATGGGGAG
351 ATATGGCCAG CTTAGCCCTG TTGCAGAGGC AATTTGATGT GGACATTCTT
401 ATCTCGGGAC ACACACACAA ATCTGAAGCA TTTGAGCATG AAAATAAATT
451 CTACATTAAT CCAGTTCTG CCACTGGGGC ATATAATGCC TTGGAAACAA
501 ACATTATTCC ATCATTGTG TTGATGGATA TCCAGGCTTC TACAGTGGTC
551 ACCTATGTGT ATCAGCTAAT TGGAGATGAT GTGAAAGTAG AACGAATCGA
601 ATACAAAAAA CCTTAAAGCC AGGCCTGTCT TGATGATTTT TGGTTTTTTT
651 TCATTGTCCT GTTGAAATCA AGTAATTAAG CATTTAAGAG CCACAAAAAT
701 GTATCACTTT TATAATATT TGCAGTAAAA TATAATACCA TCTTCTCTGT
751 TAATACATAA TTGCTCCAAG CTTCTGTAA ACTATAAGAA TATATTAGT
801 TTACAGTATA TGGATTCTAT GAAAAATGT CCACAACACA GTAATTGGTC
851 ACTTGTTAAG AAAAATTTAT CCTTGTAAGT ATCTTCAAAG TTGATATTG
901 GAACTTTATT CCAAAAGTAG TGCATGTGGA GAAAGAATCT AGACTTTCTT
951 GTATACATTT TTCTCTTCTC CAGTAATAAA CAATTACCTT TCATTGAAAA
1001 AAAAAAAAAA AAAAAA

```

BLAST Results

Entry HSAC2350 from database EMBLNEW:

Homo sapiens 12q24 PAC P424M6 Length = 167,217

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 68 bp to 613 bp; peptide length: 182

Category: similarity to known protein

Prosite motifs: RGD (60-63)

```

1 MLVLVLGLDH IPHRCNSLPA KFKLLVPGK IQHILCTGNL CTKESYDYLK
51 TLAGDVHIVR GDFDENLNP EQKVTVGQF KIGLIHGHQV IPWGDMSLA
101 LLQRQFDVDI LISGHTHKSE AFEHENKFYI NPGSATGAYN ALETNIIPSF

```

BLASTP hits

Entry AB011824_1 from database TREMBL:
 "Vps29"; Schizosaccharomyces pombe mRNA for Vps29,
 partial cds. Schizosaccharomyces pombe (fission yeast)
 Length = 176
 Score = 189 (66.5 bits), Expect = 2.7e-27, $\text{Sun P}(2) = 2.7e-27$
 Identities = 33/72 (45%), Positives = 50/72 (69%)

No Alert BLASTP hits found

Pedant information for DKFZphfbr2 23f2, frame 2

Report for DKFZphfbr2 23f2.2

```

[LENGTH]      182
[MW]           20445.84
[pI]           6.29
[HOMOL]        TREMBL:CE2K1128_6 gene: "ZK1128.8"; Caenorhabditis elegans cosmid ZK1128 2e-51

[FUNCAT]       06.04 protein targeting, sorting and translocation [S. cerevisiae, YHR012w]
le-27
[FUNCAT]       08.13 vacuolar transport [S. cerevisiae, YHR012w] le-27
[FUNCAT]       08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YHR012w]
le-27
[FUNCAT]       30.08 organization of golgi [S. cerevisiae, YHR012w] le-27
[FUNCAT]       09.25 vacuolar and lysosomal biogenesis [S. cerevisiae, YHR012w] le-27
[FUNCAT]       r general function prediction [M. jannaschii, MJ0623] le-16
[BLOCKS]       BL01269D
[BLOCKS]       BL01269A
[PROSITE]      RGD 1
[PROSITE]      MYRISTYL 4
[PROSITE]      PKC_PHOSPHO_SITE 1
[KW]           Alpha Beta

```

```

SEQ      MLVLVLGDLHIPHRCNSLPKAFKKLLVPGKIQHILCTGNLCTKESYDYLKTLAGDVHIVR
PRD      ccccccccccccccccccchhhhhhhhhhhccceeeeeeccccchhhhhhhhhhhccceeee

SEQ      GDFDENLNYPEQKVVTVGQFKIGLIHGHQVIPWGDMSALALLQRQFVDVILISGHTHKSE
PRD      cccccccccccceeeeeeccccceeeccccccccchhhhhhhhhhhccceeeeeecccccc

SEQ      AFEHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTVYVYQLIGDDVKVERIEYK
PRD      cccccccccccccccccccccccccccccccccceeeeeeccccceeeeeeccccceeeeeeec

SEQ      KP
PRD      CC

```

Prosites for DKFZphfbr2 23f2.2

PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00008	38->44	MYRISTYL	PDOC00008
PS00008	83->89	MYRISTYL	PDOC00008
PS00008	133->139	MYRISTYL	PDOC00008
PS00008	137->143	MYRISTYL	PDOC00008
PS00016	60->63	RGD	PDOC00016

(No Pfam data available for DKF2phfbr2 23f2.2)

DKF2phfbr2_23124

group: intracellular transport and trafficking

DKF2phfbr2_23124.2 encodes a novel 348 amino acid protein with similarity to human glycoprotein gp36b and canine VIP36 glycoprotein.

The vesicular protein VIP36 (36 kDa vesicular integral membrane protein) shows homology to leguminous plant lectins. The protein is localized to the Golgi apparatus, endosomal and vesicular structures and the plasma membrane. VIP36 binds to sugar residues of glycosphingolipids and/or glycosylphosphatidyl-inositol anchors and might provide a link between the extracellular/luminal face of glycolipid rafts and the cytoplasmic protein segregation machinery. Gp36 is located within the endoplasmatic reticulum. For the novel protein, a lectin character is predicted. Due to the intracellular localisation of the homolog proteins, it should be involved in intracellular transport and trafficking.

The new protein can find application in modulating/blocking intracellular transport and trafficking.

strong similarity to human GP36b glycoprotein

complete cDNA, complete cds, EST hits
potential start at 3p 29 matches kozak consensus ANNatgG
similarity to lectins,

Sequenced by AGOWA

Locus: /map="2"

Insert length: 2416 bp

Poly A stretch at pos. 2394, no polyadenylation signal found

```

1  GGGGGATGAA GGGTCGTTGG TGGGAAAGAT GGCGGCGACT CTGGGACCCC
51  TTGGGTCGTG GCAGCAGTGG CGGCGATGTT TGTCGGCTCG GGATGGGTCC
101 AGGATGTTAC TCCTTCTTCT TTTGTTGGGG TCTGGGCAGG GGCCACAGCA
151 AGTCGGGGCG GGTCAAACGT TCGAGTACTT GAAACGGGAG CACTCGCTGT
201 CGAAGCCCTA CCAGGGTGTG GGCACAGGCA GTTCCTCACT GTGGAATCTG
251 ATGGGCAATG CCATGGTGAT GACCCAGTAT ATCCGCCTTA CCCAGATAT
301 GCAAAGTAAA CAGGGTGCCCT TGTGGAACCG GGTGCCATGT TTCCTGAGAG
351 ACTGGGAGTT GCAGGTGCAC TTCAAAATCC ATGGACAAGG AAAGAAGAAT
401 CTGCATGGGG ATGGCTTGGC AATCTGGTAC ACAAGGATC GGATGCAGCC
451 AGGGCCTGTG TTTGGAACA TGGACAAATT TGTGGGGCTG GGAGTATTTG
501 TAGACACCTA CCCCATTGAG GAGAAGCAGC AAGAGCGGGT ATTCCCCTAC
551 ATCTCAGCCA TTGGTGAACAA CGGCTCCCTC AGCTATGATC ATGAGCGGGA
601 TGGGCGGCCT ACAGAGCTGG GAGGCTGCAC AGCCATTGTC CGCAATCTTC
651 ATTACGACAC CTCCTGGTG ATTCTGCTACG TCAAGAGGCA TTTGACGATA
701 ATGATGGATA TTGATGGCAA GCATGAGTGG AGGGACTGCA TTGAAGTGCC
751 CGGAGTCCGC TTGCCCGCG GCTACTACTT CGGCACCTCC TCCATCACTG
801 GGGATCTCTC AGATAATCAT GATGTCAATT CTTGAAGTT GTTTGAAGT
851 ACAGTGGAGA GAACCCAGAG AGAGGAAAAG CTCCATCGAG ATGTGTTCTT
901 GCCCTCAGTG GACAATATGA AGCTGCCTGA GATGACAGCT CCCTGCGCCG
951 CCCTGAGTGG CCTGGCCCTC TTCCTCATCG TCTTTTCTC CCTGTGTTT
1001 TCTGTATTTG CCATAGTCAT TGGTATCATA CTCTACAACA AATGGCAGGA
1051 ACAGAGCCGA AAGCGCTTCT ACTGAGCCCT CCGTCTGCCA CCCTTTTGT
1101 GACTGTCAAC CATGAGGTAT GGAAGGAGCG GGCCTGGGCC TGAGCATGCA
1151 GCCTGGAGAG TGTTCTTGTC TCTAGCAGCT GGTGGGGGAC TATATTCTGT
1201 CACTGGAGTT TTGAATGCAG GGACCCCGCA TTCCCATGGT TGTGCATGGG
1251 GACATCTAAC TCTGCTCTGG GAAGCCACCC ACCCCAGGGC AATGCTGCTG
1301 TGATGTGCCT TTCCCTGCAG TCCTTCCATG TGGGAGCAGA GGTGTGAAGA
1351 GAATTTACGT GGTGTGATG CCAAAATCAC GGAACAGAAT TTCATAGCCC
1401 AGGCTGCCGT GTTGTGTTGAC TCAGAAGGCC CTCTACTTTC AGTTTGAAT
1451 CCACAAAGAA TTAAGAACTG GTAACACCAC AGGCTTTCTG ACCATCCATT
1501 CGTTGGGTTT TGCATTGAC CCAACCCCTC GCCTACCTGA GGAGCTTTCT
1551 TTGGAACACA GGATGGAAAC TTCTTCCCTG CCTTACCTTC CTTTCACTCC
1601 ATTCATTGTC CTCTGTGTG GCAACCTGAG CTGGGAAAGG CATTGGATG
1651 CCTCTCTGTT GGGGCTGGG GCTGCAGAAC ACACCTGCGT TTCGCTGGCC
1701 TTCATTAGGT GGCCCTAGGG AGATGGCTTT CTGCTTTGGA TCACTGTTCC
1751 CTAGCATGGG TCTTGGGTCT ATTGGCATGT CCATGGCCTT CCAATCAAG
1801 TCTCTTCAGG CCCTCAGTGA AGTTTGGCTA AAGGTTGGTG TAAAAATCAA
1851 GAGAAGCCTG GAAGACACCA TGGATGCCAT GGATTAGCTG TGCAACTGAC
1901 CAGCTCCAGG TTTGATCAAA CCAAAAGCAA CATTGTGTCAT GTGGTCTGAC
1951 CATGTGGAGA TGTTTCTGGA CTGTCTAGAG CCTGCTTAGC TGCATGTTTT
2001 GTAGTTACGA TTTTGGGAAT CCCTCTTTGA GTGCTGAAAG TGTAAGGAAG
2051 CTTTCTTCTT ACACCTTGGG CTTGGATATT GCCCAGAGAA GAAATTTGGC
2101 TTTTTTTTCT TAATGGACAA GGGACAGTTG CTGTTCTCAT GTTCCAAGTC
2151 TGAGAGCAAC AGACCCCTCAT CATCTGTGCC TGGAAGAGTT CACTGTCATT
2201 GAGCAGCACA GCCTGAGTGC TGGCCCTGTG CAACCCCTAT TCCACTGCCT

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2251 TATTTGACAA GGGGTTACAT GCTGCTCACC TTACTGCCCT GGGATTAAAT
 2301 CAGTTACAGG CCAGAGTCTC CTTGGAGGGC CTGGAACCTCT GAGTCCTCCT
 2351 ATGAACCTCT GTAGCCTAAA TGAAATTCTT AAAATCACCG ATGGAACCAA
 2401 AAAAAAAAAA AAAAAA

BLAST Results

Entry HS622145 from database EMBL:

human STS WI-6746.

Score = 1079, P = 5.1e-43, identities = 219/223

Entry G42541 from database EMBLNEW:

SHGC-58649 Human Homo sapiens STS genomic, sequence tagged site.

Score = 1091, P = 1.7e-43, identities = 219/220

Medline entries

94265253:

A putative novel class of animal lectins in the secretory pathway homologous to leguminous lectins.

94208543:

VIP36, a novel component of glycolipid rafts and exocytic carrier vesicles in epithelial cells.

Peptide information for frame 2

ORF from 29 bp to 1072 bp; peptide length: 348
 Category: strong similarity to known protein

1 MAATLGPLGS WQQWRRCLSA RDGSRMLLLL LLLGSGQGPO QVGAGQTFEY
 51 LKREHSLSKP YQGVGTGSSS LWNLMGNAMV MTQYIRLTPD MQSKQCALWN
 101 RVPCFLRDWE LQVHFKEHQ GKKNLHGDGL AIWYTKDRMQ PGPVFGNMDK
 151 FVGLGVFVDT YPNEEKQQR VFPYISAMVN NGSLSYDHER DGRPTLGGC
 201 TAIVRNLYHD TFLVIRYVKR HLTIMMDIDG KHEWRDCIEV PGRVLRPGYY
 251 FGTSSITGDL SDNHDVISLK LFELTVERTP EEEKLHRDVF LPSVDNMKLP
 301 EMTAPLPPLS GLALFLIVFF SLVFSVFAIV IGIILYNKWQ EQSRKRKY

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_23124, frame 2

PIR:G01447 GP36b glycoprotein - human, N = 1, Score = 1001, P = 5.9e-101

SWISSPROT:VP36_CANFA VESICULAR INTEGRAL-MEMBRANE PROTEIN VIP36 PRECURSOR (VIP36)., N = 1, Score = 990, P = 8.6e-100

TREMBL:CET04G9_2 gene: "T04G9.3"; Caenorhabditis elegans cosmid T04G9., N = 1, Score = 614, P = 6e-60

PIR:S42626 ER-golgi intermediate compartment protein - human, N = 2, Score = 397, P = 1e-42

>PIR:G01447 GP36b glycoprotein - human
 Length = 356

HSPs:

Score = 1001 (150.2 bits), Expect = 5.9e-101, P = 5.9e-101
 Identities = 197/356 (55%), Positives = 256/356 (71%)

Query: 1 MAATLGPLGSWQQWRRCLSA RDG-----SRMLLLLLLLGSGQGPOQVGAGQTFEYLK 52
 MAA G + W RRCL R G + L LLLLLGS + G + E+LK
 Sbjct: 1 MAAE-GWIWRWGWRRC LG-RPGLLGPGPGPTTFLFLLLLLGSVTA--DITDGNS-EHLK 55

Query: 53 REHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQKQALWNRVPCFLRDWELQ 112
 REHSL KPYQGVG+ S LW+ G+ M+ +QY+RLTPD +SK+G++WN PCFL+DWE+
 Sbjct: 56 REHSLIKPYQGVGSSSMPLWDFQGSTMLTSQYVRLTPDERSKEGSIWNHQPFCFLKDWEHM 115

Query: 113 VHFKIHGQGGKKNLHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDITYPNEEKQOQERV 172
 VHFK+HG GKKNLHGDG+A+WYT+DR+ PGPVFG+ D F GL +F+DTYPN+E ERVF
 Sbjct: 116 VHFKVHGTGKKNLHGDGIALWYTRDLVPGPVFGSKDNFHLAIFLDITYPNDETT-ERVF 174

Query: 173 PYISAMVNNGSLSYDHERDGRPTLGGCTAIVRNHLYDTFLVIRYVKRHLTIMMDIDGKH 232
 PYIS MVNNGSLSYDH +DGR TEL GCTA RN +DTFL +RY + LT+M D++ K+
 Sbjct: 175 PYISVMVNNGSLSYDHSKDGRTLAGCTADFRNRDHDFTLAVRYSRGRITVMTDLEDKN 234

Query: 233 EWRDCIEVPGVRLPRGYFGTSSITGDLSNDHVISLKLFEFTVERTPEEEKLHRDVF 292
 EW++CI++ GVRLP GYFYG S+ TGDLSNDH+IS+KLF+L VE TP+EE + P
 Sbjct: 235 EWKNCIDITGVRLPTGYFYGASAGTGDLSNDHDIISMKLFQLMVEHTPDEESIDWTKIEP 294

Query: 293 SVDNMKLPENTAPLP-----PLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK 345
 SV+ +K P+ P PL+G +FL++ +L+ V V+G +++ K QE++ K
 Sbjct: 295 SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLCALLGIVVCAVVGAVVFQKRQERN-K 353

Query: 346 RFY 348
 RFY
 Sbjct: 354 RFY 356

Pedant information for DKFZphfbr2_23124, frame 2

Report for DKFZphfbr2_23124.2

[LENGTH] 348
 [MW] 39711.10
 [pI] 8.55
 [HOMOL] PIR:G01447 GP36b glycoprotein - human le-101
 [PIRKW] lectin 2e-37
 [PIRKW] transmembrane protein 2e-37
 [PIRKW] endoplasmic reticulum 2e-37
 [PIRKW] Golgi apparatus 2e-37
 [PROSITE] AMIDATION 1
 [PROSITE] MYRISTYL 5
 [PROSITE] CK2_PHOSPHO_SITE 2
 [PROSITE] GLYCOSAMINOGLYCAN 1
 [PROSITE] PKC_PHOSPHO_SITE 3
 [PROSITE] ASN_GLYCOSYLATION 1
 [KW] Alpha_Beta
 [KW] SIGNAL PEPTIDE 39
 [KW] LOW_COMPLEXITY 7.76 %

SEQ MAATLGLPLGSWQWRRCLSDRGSRMLLLLLLLGSGQGPQVAGQTFEYLKREHSLSKP
 SEGXXXXXXXXX.....
 PRD ccc

SEQ YQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQKQALWNRVPCFLRDWELQVHFKIHGQ
 SEG
 PRD ccccccccccecc

SEQ GKKNLHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDITYPNEEKQOQERVFPYISAMVN
 SEG
 PRD ccccccccccecc

SEQ NGSLSYDHERDGRPTLGGCTAIVRNHLYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEV
 SEG
 PRD ccc

SEQ PGVRLPRGYFGTSSITGDLSNDHVISLKLFEFTVERTPEEEKLHRDVFPSVDNMKLP
 SEG
 PRD ccc

SEQ EMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
 SEGXXXXXXXXXXXXXXXXXXXXXXXXX.....
 PRD ccc

Prosites for DKFZphfbr2_23124.2

PS00001	181->185	ASN_GLYCOSYLATION	PDOC00001
PS00002	35->39	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	19->22	PKC_PHOSPHO_SITE	PDOC00005

PS00005	268->271	PKC_PHOSPHO_SITE	PDOC00005
PS00005	343->346	PKC_PHOSPHO_SITE	PDOC00005
PS00006	19->23	CK2_PHOSPHO_SITE	PDOC00006
PS00006	279->283	CK2_PHOSPHO_SITE	PDOC00006
PS00008	43->49	MYRISTYL	PDOC00008
PS00008	63->69	MYRISTYL	PDOC00008
PS00008	65->71	MYRISTYL	PDOC00008
PS00008	96->102	MYRISTYL	PDOC00008
PS00008	198->204	MYRISTYL	PDOC00008
PS00009	120->124	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_23124.2)

DKF2phfbr2_23n16

group: signal transduction

DKF2phfbr2_23n16.1 encodes a novel 292 amino acid protein with weak similarity to putative phosphatidylinositol-4-phosphate 5-kinase of *Arabidopsis thaliana*.

The novel proteins contains a WW domain which has been originally described as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes. Examples of proteins containing the WW domain are Dystrophin, Utrophin, vertebrate YAP protein (binds the SH3 domain of the Yes oncoprotein), murine NEDD-4 (embryonic development and differentiation of the central nervous system), IQGAP (human GTPase activating protein acting on ras). Therefore the new protein should be involved in intracellular signal transduction.

The new protein can find application in modulating/blocking intracellular signal transduction pathways.

similarity to putative phosphatidylinositol-4-phosphate 5-kinase

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 2936 bp

Poly A stretch at pos. 2916, polyadenylation signal at pos. 2873

```

1  GGGGGCGCTC  CCGAGAAAGA  GTGAGGGCGC  GACGCGCACC  AACGGTGGAG
51  GGATGTTTCA  GCAGCCCCTG  AGAAGGAAGA  GGAGGAAGCT  GAGGGCCCGC
101  TGAGGGCGCA  GGACCTGAGG  GAGTCCTACA  TCCAGCTCGT  CCAGGGTGTG
151  CAGGAGTGGC  AGGATGGTTG  CATGTACCAG  GGGGAGTTTG  GGTGGAACAT
201  GAAGCTTGGA  TATGGCAAAT  TCTCTGGGCC  CACAGGCGAG  TCATACCATG
251  GGCAGTTTTA  CCGGGACCAC  TGCCATGGCC  TGGGTACCTA  CATGTGGCCA
301  GATGGCTCCA  GTTTCACGGG  CACATTTTAC  CTCAGCCACC  GAGAAGGCTA
351  CGGCACCATG  TACATGAAGA  CACGGCTTTT  CCAGACTCAC  TGCCACAACG
401  ACATTGTCAA  CTTTCTCCTG  GACTGTGGGG  CCGACGTGAA  CAAGTGCTCA
451  GATGAGGGTC  TCACGGCACT  CAGCATGTGT  TTCTCTCTCC  ACTACCCCGC
501  CCAGTCCTTC  AAGCCCAATG  TTGCTGAACG  GACCATACCT  GAGCCCCAGG
551  AACCTCCAAA  ATTCCAGTT  GTTCCAATCC  TTTTCATCAT  ATTTATGGAC
601  ACAAACCTGG  AGTCTCTGTA  CTATGAGGTG  AACGTGCCTT  CCCAGGGTAG
651  CTATGAGCTG  AGGCCACCGC  CAGCACCAC  GCTCTTGCCA  CGCGTCTCAG
701  GCAGCCACGA  GGGCGGCCAC  TTCCAGGACA  CCGGGCAGTG  TGGGGGGTCC
751  ATAGACCACA  GGAGCAGCTC  TCTGAAGGGG  GACTCCCCGT  TGGTGAAGGG
801  CAGCCTTGGC  CATGTGGAAG  GCGGGCTTGA  GGACGTGTTG  GGAGACACAG
851  ACCGGGGCAG  TCTGTGCAGT  GCTGAGACGA  AATTGAGTGC  CAACTTGTGT
901  GTGTGCGACT  TCTCCATCGA  GCTCTGCGAG  GCCATGCTGG  AGAGAAGCGC
951  CCAGTCCCAC  AGCTTGCTGA  AGATGGCCTC  GCCCTCACCG  TGCACCAGCA
1001  GCTTCGACAA  AGGACCATG  CGGAGGATGG  CGCTGTCCAT  GATCGAGTAG
1051  GTCTGGCAC  CAGCTGGTGG  GGGTGGAGGG  CCACCATCAG  GGCTGAATCC
1101  TATGCTCAGC  AGACCCACGT  CTC'TTCCCTG  TGCCAGTGGG  AGGCGTTGTG
1151  TCTGGAGATG  TGTGTCTGAA  TGTGTGAGCA  TCCCTGTGTC  GGTGGCTCCA
1201  TGCCATGGCC  AGCCCTGTGG  GGGTGCCACG  GTGACGGGCT  GTTTTCAGTG
1251  CCACCCAGC  CCTGTGGGGG  TGCCACGGTG  ACGGGCTGTT  TTCAGTACCA
1301  CGCCAGCCCT  GCTTTGGCCT  TTGCCACTGG  CCTGAAGTGT  CTCTGTGGGA
1351  GCCTCAGCAG  GGGCCACTGT  CAGGGGTCTT  ATCCTAGCCA  TAGTGCACGT
1401  GATGCACACC  TGCTTGGGCA  GCTCTCACAC  CCCTGCTGTC  CACCCTGTCT
1451  ATACCACTGT  GTCTCAAAAT  GTGGTCTATG  CACCCCGGGG  GGTCCAAGAC
1501  CCTTTCAGGG  AGTCTGTGGG  GTCAAAATGA  TTCTCTTGAT  AACCCTGAGA
1551  CTCTGTTAGC  CTTCTCCTTG  TGTGTATGTT  GGTGGATGGT  ATGAAGACAG
1601  GGCGGTGACG  ACCACAGCC  CCCAGCGTGC  AGGGCAGCAG  TGCCCGCCCT
1651  GCTTGGGGGC  ATGTTATTCC  TTCACCACGG  TGTGCACTTG  CGGGGATGCC
1701  TGTCTCACTG  AAGAAATGCT  TTGACTAAGC  AGAAAAGCAA  TGACAAATTG
1751  CATTAAATCT  TGTCTCTTGC  GTACACACCC  CTCGAATATT  CTGGGTGCGA
1801  AAACATGGGA  AGGACACTGA  TGTGTGTCTG  CCACAGACCA  AGGCACACCG
1851  CTTCCCGCA  AGAAGCGCTT  CCCCAGGGC  CAGAGTAGCA  ACAGAATGCG
1901  GCATCTTCCC  AACCTCCTGC  CCCATTTTGT  ATTGGAAGAA  TGACCACTGG
1951  TATGTGGCTG  TTCATTCTCC  TGAACACAGC  CTGCCACTTT  AAGGAAAACA
2001  TATGACACTA  TTTGTTGCTG  GCGAAATTTA  CATTTTCAAG  TGAATAGCAG
2051  AATTCTGGAC  ACTTGCCACC  ACCACCAAAA  CCTTCATAGC  TTCCCTTAAC
2101  TTTGAGACAT  GGTGTTCAG  AGGTTTTTCA  CGTGAGATGG  CGTTAGCAGC
2151  GCAGTTTTGT  GATACTGCCT  GAAGACATGC  CGACAGTGCC  CAGATCTCTT

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2201 CTATTGGTGA GCCAGCTTTT CCCACACGGC CAAGTTCTGA TGTGAAACCA
2251 TTGCCAGGTG GGTGAAGATC CATTGACAGT GAGAGGTGGG CCCGTGGGCT
2301 TCAGTGCAGC CAGGCGCAGA AGGCTGGTTC ATGAGTGTCC AGCTCCGCCA
2351 GGTAGCTAGC TCACCACCCC CAGCCTGGGT TCATGTAGTT CAAATAGGAA
2401 GACCACGATG ATCAGAAAGG CTGCTCAAAT ACTCCTTCGT CCAGCCGCGT
2451 ACCTGGGGGA GGCTGAATCT CCACTCACTT CCACCAAGGC TGTGCAGAGC
2501 AGATAGGGGA ATCCAGCAAA GGTGGAAAAC AGTGCCATCC TTCTCCCCAA
2551 CTGGTTTTGT TTTGTAAAT AACTTTTTGT GACAGTGTTA CTTATTAGTA
2601 ACATGCAGTG GGTGTGTAT GGTAAACAAG TTGGTGAGCA TTATTGAGAG
2651 GTGAAGCCAG CTGAGCTTCT GGGTTGGGTG GGGACTTGA GAACCTTTGT
2701 GTCTAGCTAA AGGATTGTAA ATGCACCAAT CAATGCTCAG TGTCTAGCTA
2751 AAGGATTGTA AATGCACCAA TCAGCACTCT GTAAATTTGA CCAATCAGCG
2801 TTCTGTAAAA TGGACCAATC AGTGGTCTGT AAAATGGACC AGTCAGCAGG
2851 ATGTGGGCGG GGCCAAAAA GGAATAAAA GCTGGCCACC GCCAGGCTCC
2901 CCACCAGCCT GCAGCGAAAA AAAAAAAAAA AAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 172 bp to 1047 bp; peptide length: 292
 Category: similarity to unknown protein
 Prosite motifs: WW_DOMAIN_1 (19-24)

```

1 MYQGEFGLNM KLGYGKFSWP TGESYHGQFY RDHCHGLGTY MWPDGSSFTG
51 TFYLSHREGY GTMYMKTRLF QTHCHNDIVN LLLDCGADV N KCSDEGLTAL
101 SMCFLHLYPA QSFKNVAER TIPEPQEPK FPVVPILSSS FMDTNLESly
151 YEVNVPSQGS YELRPPAPL LLPRVSGSHE GSHFQDTGQC GGSIDHRSSS
201 LKGDSPLVKG SLGHVESGLE DVLGDTDRGS LCSAETKFES NLVCVDFSIE
251 LSQAMLERSA QSHSLKMAS PSPCTSSFDK GTMRRMALSM IE

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_23n16, frame 1

TREMBL:AB005902_1 product: "AtPIP5K1"; Arabidopsis thaliana mRNA for
 AtPIP5K1, complete cds., N = 2, Score = 138, P = 1.1e-06

TREMBL:AF019380_1 product: "putative phosphatidylinositol-4-phosphate
 5-kinase"; Arabidopsis thaliana putative
 phosphatidylinositol-4-phosphate 5-kinase mRNA, complete cds., N = 2,
 Score = 133, P = 1.4e-06

PIR:T02098 probable phosphatidylinositol-4-phosphate 5-kinase -
 Arabidopsis thaliana, N = 2, Score = 135, P = 6.7e-06

>TREMBL:AB005902_1 product: "AtPIP5K1"; Arabidopsis thaliana mRNA for
 AtPIP5K1, complete cds.
 Length = 683

HSPs:

Score = 138 (20.7 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
 Identities = 23/61 (37%), Positives = 35/61 (57%)

```

Query:      1 MYQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGY 60
            MY+G++      G GKFSWP+G +Y G+F      G GT+      DG ++ GT+      + G+
Sbjct:     34 MYEGDWKRGRKASGKGKFSWPSGATYEGFEKSGRMEGFGTFTGADGDTYRGTWVADRKHGH 93

Query:      61 G 61
            G
Sbjct:     94 G 94

```

Score = 112 (16.8 bits), Expect = 9.7e-04, Sum P(2) = 9.7e-04
Identities = 19/51 (37%), Positives = 27/51 (52%)

Query: 12 LGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYLSHREGYGT 62
+G GK+ W G Y G + R G G + WP G+++ G F EG+GT
Sbjct: 22 IGSGKYLWKDGCMEYEGDWKRGKASGKGKFSWPSGATYEGEFKSGRMEGFGT 72

Score = 97 (14.6 bits), Expect = 4.4e-02, Sum P(2) = 4.3e-02
Identities = 19/60 (31%), Positives = 32/60 (53%)

Query: 2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYLSHREGY 61
Y+GEF G+G F+ G++Y G+ D HG G + +G + GT+ + ++G G
Sbjct: 58 YEGEFKSGRMEGFGTFTGADGDTYRGTWVADRKHGQKRYANGDFYEGTWRRNLQDGR 117

Score = 93 (14.0 bits), Expect = 1.2e-01, Sum P(2) = 1.1e-01
Identities = 18/62 (29%), Positives = 34/62 (54%)

Query: 2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYLSHREGY 61
Y+G + + K G+G+ + G+ Y G + R+ G G Y+W +G+ +TG + + G G
Sbjct: 81 YRGTWVADRKHGQKRYANGDFYEGTWRRNLQDGRGRYVWRNGNQYTGEWRIGVISGKG 140

Query: 62 TM 63
+
Sbjct: 141 LL 142

Score = 91 (13.7 bits), Expect = 2.0e-01, Sum P(2) = 1.8e-01
Identities = 18/51 (35%), Positives = 24/51 (47%)

Query: 2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYL 52
Y GE+ + + G G WP G Y G + G G + W DGSS G +
Sbjct: 127 YTGEWRIGVISGKGLLVWPNNGRYEGLWENGIPKNGVFTWSDGSSSCVGAW 177

Score = 90 (13.5 bits), Expect = 2.6e-01, Sum P(2) = 2.3e-01
Identities = 17/60 (28%), Positives = 31/60 (51%)

Query: 2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYLSHREGY 61
Y+G + N++ G G++ W G Y G++ G G +WP+G+ + G + +G G
Sbjct: 104 YECTWRRNLQDGRGRYVWRNGNQYTGEWRIGVISGKGLLVWPNNGRYEGLWENGIPKNG 163

Score = 45 (6.8 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
Identities = 14/62 (22%), Positives = 26/62 (41%)

Query: 215 VESGLEDLVLDTRGSLCSAETKFESNLCVCD--SIELSQAMLERSAQSHSLKMASPS 272
V+SG + G+ +C E+ E+ CD ++E S +R + + +
Sbjct: 205 VDSCAGSLGGEKVFPRICIWESDGEAGDITCDIIDNVEASMIYRDRISVDRDGRFQFKKN 264

Query: 273 PC 274
PC
Sbjct: 265 PC 266

Pedant information for DKFZphfbr2_23n16, frame 1

Report for DKFZphfbr2_23n16.1

(LENGTH) 292
(MW) 32214.44
(pI) 5.51
(HOMOL) TREMBL:AB005902_1 product: "AtPIP5K1"; Arabidopsis thaliana mRNA for AtPIP5K1,
complete cds. 7e-08
(BLOCKS) BL01137A Hypothetical YBL055c/yjjv family proteins
(PROSITE) WW_DOMAIN_1 1
(PROSITE) MYRISTYL 5
(PROSITE) CK2_PHOSPHO_SITE 7
(PROSITE) PKC_PHOSPHO_SITE 5
(KW) Alpha_Beta
(KW) LOW_COMPLEXITY 4.11 %

SEQ MYQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYLSHREGY
SEG
PRD cc
SEQ GTMYMKTRLRFQTHCHNDIVNLLDCGADVKNKCSDEGLTALSMCFLHYPASFKPNVAER
SEG
PRD cc
SEQ TIEPEQPEPPKFPVVPILSSSFMDTNLESLEYEVNVPSQGSYELRPPAPLLLPRVSGSHE

```

SEG .....XXXXXXXXXX.....
PRD eccccccccceeeeeccccccccceeeeecccccccccccccccccccccc

SEQ GGHFQDTGQCGGSIDHRSSSLKGDSPLVKGS LGHVESGLEVDLGDTRGSLCSAETKFES
SEG .....
PRD cccccccccccccccccccccceccccccccccccccccccccceeeeecccc

SEQ NLCVCDFSIELSQA MLERSAQSHSLKMASPSPCTSSFDKGTMRMALSMIE
SEG .....
PRD cccccchhhhhhhhhhhhhhhhhhhhhccccccccccccccccchhhhhhhccc

```

Prosites for DKFZphfbr2_23n16.1

PS00005	55->58	PKC_PHOSPHO_SITE	PDOC00005
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	200->203	PKC_PHOSPHO_SITE	PDOC00005
PS00005	226->229	PKC_PHOSPHO_SITE	PDOC00005
PS00005	282->285	PKC_PHOSPHO_SITE	PDOC00005
PS00006	55->59	CK2_PHOSPHO_SITE	PDOC00006
PS00006	121->125	CK2_PHOSPHO_SITE	PDOC00006
PS00006	140->144	CK2_PHOSPHO_SITE	PDOC00006
PS00006	144->148	CK2_PHOSPHO_SITE	PDOC00006
PS00006	217->221	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00006	276->280	CK2_PHOSPHO_SITE	PDOC00006
PS00008	45->51	MYRISTYL	PDOC00008
PS00008	86->92	MYRISTYL	PDOC00008
PS00008	177->183	MYRISTYL	PDOC00008
PS00008	188->194	MYRISTYL	PDOC00008
PS00008	229->235	MYRISTYL	PDOC00008
PS01159	19->44	WW_DOMAIN_1	PDOC50020

(No Pfam data available for DKFZphfbr2_23n16.1)

DKFZphfbr2_23o24

group: brain derived

DKFZphfbr2_23o24 encodes a novel 139 amino acid protein with similarity to CAAX-box proteins.

The CAAX box is a prenyl group binding site found in a number of eukaryotic proteins, such as which is found in Ras- and ras-like proteins such as Rho, Rab, Rac, Ral, and Rap, as well as in nuclear lamins A and B, some G protein alpha and gamma subunits and some dnaJ-like proteins. These proteins are posttranslationally modified at this site by the attachment of either a farnesyl or a geranyl-geranyl group to a cysteine residue.

No informative BLAST results; no predictive prosite, pfam or SCOP motif

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to lectins

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 3564 bp

Poly A stretch at pos. 3541, no polyadenylation signal found

```
1 GAATGGCTCC GCAGATGGCC GGCACGTGAGA GCCAGCAAGA AGCGGAGGAG
51 ATGGGCTTTC AGCAGGGGGT TGGGGGGGGA GCTTTAACT GAGCCCTGTA
101 AACATGGCAG AACTGCTCAG TGGGAGACTC TCAGCACAGA CGGTCATGGG
151 GAAGTGAGTG CAGTTCATTT GTAATCTTGT TGTCCAGTTC TGGGTTTTTT
201 TTGTTTGTTC CGTAACTTTA AAGGTATGCA CTTTATATAG ATTTATTTAT
251 TTGCTGGGAC CGTTACTCAG AGTTCCTAGA AATGTACACA GCTTTTTTAC
301 CAGGGTTACT CCTCAGAATC ACTTGCTACT TCTTTAAATG AATGAATGAA
351 TGTGCCAGGC CCTATGCCTG GAGGTTGGGA GCTTCATCTA CATCACATTC
401 TAACAGGTGA CCACTGGGGT AAGCACTGTG TGAATGCAAA GCCAGGGTGT
451 GTTTCCATCA ACACCCAGAT GACCGTGCCT ATGTGCCCTT GTTGTCTCTC
501 CTCCAGGCTC CCCTCTCAC CCCACCCCTT TCTGCAGCTC CTCTATCTAA
551 CATCTCGCCT GGTGAGGTCA CGGCTTAGCC TGTGCGCCAG TGGCCCCACC
601 ACCATCCTTC CCCCTGTGCA GATTGGAGGA GGCCAGGTCT CTCCCCCTAG
651 CTCCTATGTC CCCTTCACCC CCCATGGCAC AGATGAGACA TTCACAGACT
701 TTGCAGATGA TGGAAAGAGAA GACTCCAGGT TGCCAGGTGT GTCCACTCTC
751 AGGAACCCCC AGCCCAAGCC TCACTGCTCG TGTTCCTCAG CAACCCAGC
801 ACGGGGGATA CGCCGGTGCT GTTTCCTGCT TCAGATACAA CCAGTTACCA
851 GAAACGACCT CACCCCTCCA ACCACTTTC AAGGTGCCAG GACAGAGAAG
901 CCCTTCACTG GCCCAACCCG GGCAGTTGAC AGAGGGATGC CCTCCTTGGA
951 GGGGAGCCTC ACCTCTACCC ACAGGGCCGC GGCCTTGCTC TGGATTCTCA
1001 CCGGGGCAGT CACGTCAGGA TGGAGAGGTC CCATGTCAGC CAGTCTTTG
1051 GTGGGGGTCA TGTAAGTCTG AATGACCTGC CGATGGTCCA GGCTGAGCCA
1101 GGGGAGCTGA CCTGGGGTGC CTTTTTGGTG CTTACTCTGA CTTGAGTTGG
1151 ATTCATGCCA CAGACCCACC TTCTTGAGCA ACAACACATA TAGCCACCAA
1201 CACAAGAGCC AGGCACACAC TGAGCAGAGA AAGTCCCTGT CGCCTCACCA
1251 CCCAAAAACT CCAGCTTTGC AGAGACCAAG GTTCTTCTCT ACCTTTGCAG
1301 AAGCCTCTGT GACCAAAACC GGAGCTTGCC CTCTGAGGC CTCTAGCATT
1351 TCTCCAGGTG TTTTTCAGAG GACTTGGTTT AAATTTGTTT ACCCCAAATG
1401 TGGTCTTTCC CGGATCATGA AAGGATCTGC CGCAAAGGTG AATCTGAGTC
1451 TCCTCAGAGT CATATGAGAC TGAAACTGCT TATAACATTT CCGTGACCTA
1501 ATAAGTCTTC CAAAATGTA GGGTATTAAG AGTTTAGTGA CATTAAAAAG
1551 TTAGTTCGAA AATATCGTGA TTCAGGTATA TTTAGACATT TGATTCATGC
1601 CAAATTGCCA CTGTTAACAG AAAACACACC CCAAGCACAT TAATGCCTAG
1651 ATATTTCAAA CCCTTTCTG CCCACACATT CTTAAAAATA ATATACTGAG
1701 AAATCTATAT ACAGGTTTTT TTTTAATTAG CTTGGAAAAG AGCAGTTGTA
1751 TTCTGTTTGA ACAGCTGCTA ATGTCAATTC CTGTGGGAAG AAAGACCAAA
1801 GAACATGGAG TTACACCAAG AATTTTAAAA CAAAGACGCT GTCCCTTCC
1851 TGAGCACCGT GCAGCCAAGA CTGAGAGATC AGTCTGAGAC CTGTGATTAA
1901 GGAGTGTTTT CTACATAGCG TATAATTATG GAGCCACACA AGTGGGCCAT
1951 TACTCTGTTG AGTGCTTCAT GTTTGAGGTA TTTTCGTGTT CCAACTTACA
2001 TTAAGTCTT TATAAACAG GAAAAATCCA CGAGCAGGTA TTGACACTAT
2051 CCATATTAGA TCATCACAAA ATTATATATA TAGCAGAGTC ATAAACAATG
2101 AGAAACGGTC TTCCCACT TGCTTTAAAT GGCCATGACC TAGTGTTAG
2151 GGAAAGCAGT AAAATCAGCG AGGAGCTCGT GGGAAAAATG AGACGGGCCC
2201 TGAGGGGGTG ACTCATGGGC CAAGCAGGGC CACACAGGTA CCAGGCCGCC
2251 ACAGCTCTCT CTGCTCTCTA CTCTCTGGAG ACTGGAATTC CTTTACTGCC
2301 TCCTTTCTGA CATTTCCTAG ACATCAGACT TTGCTACTTA GTACACAAAC
2351 GGGGTTCCTT TTTAAATTTG TTAATCTTAG TTAGCATTTG CAGAAGCTGT
2401 GAAAAATTAC AGAGAGATGA TGTGTTGGGT AAGAGATGGT TTAAGATGCC
```

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2451 AGCTTGCTGT TTTTCATTAA GTGTCTTGAA AATGAGTAAG TGGCGTTCCT
2501 GGAGGGGAAC AATCATATAA TTCCGCAGGG TGGGTCTAAA CTTGTTTTCT
2551 GATAGTGTTT AGCAGCTCAT GGCTCTGAGG GCACCTGATA ACACAGCAGC
2601 CAGGCGCTGA TGAGAAGTGT GTGCCAGACA GACCCGAGTG TGGCTTGGCT
2651 CTTGCCATTAT GTTCCTTTCT CTGTTCAGAG AAGCGTGAGA TGAGATTTTG
2701 TGATTATATT GCACTCCTTG GGCTGACTTT CCCATGCACA GAATGTTTTA
2751 CACATCCTGA TAGCTGAGCT GAAAATGCAA AGAGAAGGGA AAATGCCCTA
2801 AATTGTTCTG GCTAATTTAG AAGCAGCAGG CCTTGGAAGT CTTTGTCCTG
2851 TGTCCCTGAA CAAATCTTAT GGGAGCTCTG GTACCTATGC CAGAAAATGC
2901 ACATAGGCAC AACACTTTTA CATAACGTT CACACACCCC ACCCTTATGG
2951 AGAACTTTTT TCTAAATAAG AGAAAGAAAA ATTTTAAGAC TTACAAGTTA
3001 TGTTTTAGGTA TTTTACATGG TTCAGAAAAC AAGACATGAA GCGGTATAAA
3051 CTGAGAAGTC TTGTTCCAC AACCCACGT GCCAGGTACA CATAACCATT
3101 TTTATTCACC TCTAGCTTGT GCTTCCAATG TTTGTTAGGC ATATGTAAAT
3151 AAGTGAATAG ATAAGCATTT CTCCCTCCTT TTGCTGACAT GAGTGGTGGC
3201 ATGTTTTGCG CCTGGCTTTT ATCCCTTGAC CCCATTCCAG TACCTAGAGA
3251 CCTGCTTCAT TTTTTTAGAT GTGTAATACT TCATGTGTGC GTGTGCCTTA
3301 GTGATTAACCT CGTGCCTGT GCAGGGACAT CGGGCTGGGA TCAGTTTGTT
3351 CACTGATATA TACAGCGCTG CGGGAGATAC CCTCACATGT GTATCATTG
3401 GTCCATGTGC AGGTGTGTCT GGAAGATAGA ATTCTAGGCG TAGAATTGAT
3451 AGGTAAAATG TATTTATAGG GAAAAAATCA ATATAAACT TTGCGTGTA
3501 TGATATTGTC GCTTTTTT TTTTAATTT TTTACCCAAA TAGTAAAAAA
3551 AAAAAAAAAA AAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 656 bp to 1072 bp; peptide length: 139
 Category: similarity to known protein

```

1 MSPSPMAQM RHSQSLQME EKTPGCQVCP LSGTPSPSLT ARVPSQPQHG
51 GYAGAVSLLR YNQLPETTSP LQPLSKVPGQ RSPSLAHPGQ LTEGCPPWRG
101 ASPLPTGPRP CPGFSPGQSR QDGEVPCQPV LWWGSCSLK

```

BLASTP hits

Entry CEEGAP7_1 from database TREMBL:
 gene: "EGAP7.1"; Caenorhabditis elegans cosmid EGAP7.
 Score = 123, P = 2.3e-07, identities = 35/103, positives = 44/103

Entry MMBPC35_1 from database TREMBL:
 Mouse carbohydrate binding protein 35 mRNA, 3' end.
 Score = 113, P = 2.2e-06, identities = 40/103, positives = 44/103

Entry A28651 from database PIR:
 galactose-specific lectin - mouse >TREMBL:MMMAC2A_1 Mouse mRNA for
 Mac-2 antigen
 Score = 113, P = 2.2e-06, identities = 40/103, positives = 44/103

Alert BLASTP hits for DKFZphfbr2_23o24, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_23o24, frame 2

Report for DKFZphfbr2_23o24.2

```

[LENGTH]      139
[MW]           14748.91
[pI]           8.90
[PROSITE]     PRENYLATION 1

```

```

SEQ      QDGEVPCQPVLWWGSCSLK
PRD      CCCCCCCCCCCCCCCCCCCC

```

Prosites for DKFZphfbr2_23o24.2

PS00005	40->43	PKC_PHOSPHO_SITE	PDOC00005
PS00006	119->123	CK2_PHOSPHO_SITE	PDOC00006
PS00008	50->56	MYRISTYL	PDOC00008
PS00013	126->137	PROKAR_LIPOPROTEIN	PDOC00013
PS00294	136->140	PRENYLATION	PDOC00266

(No Pfam data available for DKFZphfbr2_23o24.2)

DKF2phfbr2_23o5

group: brain derived

DKF2phfbr2_23o5 encodes a novel 360 amino acid protein with no known similarity

No informative BLAST results; no predictive prosite, pfam or SCOP motif

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

potential start at Bp 24 matches Kozak consensus ANNatgG

Sequenced by AGOWA

Locus: /map="7q21-q22"

Insert length: 1736 bp

Poly A stretch at pos. 1714, polyadenylation signal at pos. 1680

```
1 GGGGGAGGAT CAAAGTAGGC AAGATGGCGT CGAGCGGCGG GGAGCCAGGG
51 AGTTTATTTG ATCACCACGT CCAGAGGGCG GTATGCGACA CACGGGCCAA
101 ATATCGAGAG GGACGACGGC CTCGTGCTGT GAAGGTATAT ACAATCAATT
151 TGGAATCTCA GTACTTATTA ATACAAGGAG TTCCTGCTGT GGGAGTCATG
201 AAGGAATTAG TTGAGCGATT CGCTTTATAT GGTGCAATTG AACAGTACAA
251 TGCTCTAGAT GAATACCCAG CAGAAGACTT TACTGAAGTT TATCTTATTA
301 AATTTATGAA CTTACAAAGT GCAAGGACAG CCAAGAGAAA AATGGATGAA
351 CAGAGTTTCT TCGGTGGATT GCTTCATGTG TGCTATGCTC CAGAATTGTA
401 AACAGTTGAA GAAACTAGAA AAAAATAACA AATGCGGAAG GCATATGTAG
451 TAAAAACTAC TGAATAATAA GACCATACG TGACAAAGAA GAAATTGGTT
501 ACAGAGCATA AAGACACAGA GGATTTTAGA CAAGACTTCC ACTCAGAGAT
551 GTCTGGATTT TGTAAAGCTG CTTTGAACAC TTCTGCAGGG AACTCAAATC
601 CTTATCTTCC GTATTCTCTG GAATTGCCTT TATGTTATTT CTCCTCAAAA
651 TGTATGTGTT CATCCGGGGG ACCTGTAGAC AGAGCACCAG ACTCCTCTAA
701 GGATGGTAGA AACCATCATA AAACAATGGG GCATTATAAC CACAATGACT
751 CTTTGGCGAA AACACAGATA AACTCTTTGA AAAAATCAGT GGCCTGCCCT
801 GGTGCACAAA AGCCTATTAC GTCTTCAGAG GCAGTTGACA GATTTATGCC
851 TAGGACAACA CAACTGCAGG AGCGCAAAAG AAGAAGAGAA GATGATCGTA
901 AACTTGGAAC TTTTCTTCAA ACAAACCCAA CTGGTAATGA GATTATGATT
951 GGACCTCTGT TACCAGACAT CTCTAAAGTG GATATGCACG ATGACTCATT
1001 GAATACAACG GCGAATTAA TCCGGCATAA ACTTAAAGAG GTATTTTCATC
1051 TGTGCCAAAG CCTCCAGAGG ACAAGCCAGA AGATGTACAT ACAAGTCATC
1101 CATTAAACA AAGAAGAAGA ATATAGAGTG CCAGCAGCAA CTTAGTATTT
1151 TCTAAAAAGA ACATTTATTA TTTATTTTGA GCCTGTCTAT TTAATTCCTC
1201 AAGAGATTTT ACTGCTGGTA TTTTGTGATG CACTCCTCTT TGTAATTTC
1251 TTCAAGCCAT TTGTCTAAAG TCATTCTTTT GTTTTGTGGG AGATGGAGTC
1301 TTGCTCTGTT GCCCAGGCTG GAATGCAGTG GCGTGATCTC GGCTCACTGC
1351 AACCTCCACC TCCCGGTTT AAGCGATTCT CCGCTCAG CTTCTGAGT
1401 ATCTGGGATT ACAGGCGTGC ACCACCATGC CTGGCTAAGT TTTGTGTTT
1451 TTTTAGTAGA GATGGGTTT CACCATATTG GTCAGGCTGG TCTCGAATC
1501 CTGACCTGTG GATACACCTG CCTCAGCCTC CCAAAGGAT GAGCCACCGC
1551 GCCTGGCCCA TTTCTTCTT TTTTGACCCA TACTTAATGT TGCAGAAACT
1601 ATTCTTGTC TAACATTATC TCTCATGTAC AGTAATTATA TGTAATTATA
1651 TTGAAGCAAA TATGGAACCT TTACAATAGA AATAAAGATA GGCAGCCAGC
1701 GTCTGTTTCC AATTATAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry AC005156 from database EMBL:
Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.
Score = 2897, P = 2.4e-154, identities = 583/586
2 exons covering Bp 465-1723

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 24 bp to 1103 bp; peptide length: 360
Category: similarity to unknown protein

```

1 MASSGGEPGS LFDHHVQRAV CDTRAKYREG RRPRAVKVYT INLESQYLLI
51 QGVPAVGVMK ELVERFALYG AIEQYNALDE YPAEDFTEVY LIKFMNLQSA
101 RTAKRKMDEQ SFFGGLLHVC YAPEFETVEE TRKKLQMRKA YVVKTTENKD
151 HYVTKKKLVT EHKDTEDEFQ DFHSEMSGFC KAALNTSAGN SNPYLPYSCE
201 LPLCYFSSKC MCSSGGPVDR APDSSKDGGRN HHKTMGHYNH NDSLRTQIN
251 SLKNSVACPG AQKAITSEA VDRFMPRTTQ LQERKRRRED DRKLGTFLOT
301 NPTGNEIMIG PLLPDISKVD MHDDSLNTTA NLIRHKLKEV FHLQSLQRT
351 SQKMYIQVIH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phfbr2_23o5, frame 3

TREMBL:AC005824_10 gene: "F15K20.11"; Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence., N = 2, Score = 114, P = 3.6e-11

>TREMBL:AC005824_10 gene: "F15K20.11"; Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.
Length = 227

HSPs:

Score = 114 (17.1 bits), Expect = 3.6e-11, Sum P(2) = 3.6e-11
Identities = 21/41 (51%), Positives = 29/41 (70%)

Query: 103 AKRKMDEQSFFGGLLHVVCYAPEFETVEESTRKKLQMRKAYVV 143
AKRK+DE SF G L + YAPE+E V +T+ KL+ R+ V+
Sbjct: 51 AKRKLEDESSFLGNRLQISYAPEYENVNDTKDKLESRRKEVL 91

Score = 107 (16.1 bits), Expect = 2.6e-10, Sum P(2) = 2.6e-10
Identities = 50/191 (26%), Positives = 83/191 (43%)

Query: 103 AKRKMDEQSFFGGLLHVVCYAPEFETVEESTRKKLQMRKAYVVKTENKDHVYVTKKKLVTEH 162
AKRK+DE SF G L + YAPE+E V +T+ KL+ R+ V+ + T + VT+
Sbjct: 51 AKRKLEDESSFLGNRLQISYAPEYENVNDTKDKLESRRKEVLARLNPQKEKSTSQ--VTKL 108

Query: 163 KDTEDFRQDFHSEMSGFCFAALNTSAGNSNPYLPYSCELPYFSSKCMSSGGPVDRAP 222
+ D S + + GN+ P S + YF+S M + V
Sbjct: 109 AGPALTOTDNVSSQRREMEYQFHR--GNA-PVTRVSSDOE--YFASSSMNQTVKTV---- 159

Query: 223 DSSKDGGRNHHKTMGHYNHNDLSLRKTQINSLKNSVACPGAQKAITSSSEAVDRFMPRTTQLQ 282
K + + + +H + ++ N + P +Q S R P ++Q+Q
Sbjct: 160 -REKLNKTRREENISLSHCKQIEESG-NQKRLQ---PSSQTQPEESGNQKRLQP-SSQIQ 213

Query: 283 -ERKRRREDDRK 293
+ KR R D+R+
Sbjct: 214 PDLKRTRVDNRR 225

Score = 102 (15.3 bits), Expect = 3.6e-11, Sum P(2) = 3.6e-11
Identities = 22/55 (40%), Positives = 38/55 (69%)

Query: 26 KYREGRRPRAVKVYTINLESQYLLIQGVPAVGVMKELVERFALYGAEQY--NALDE 80
+Y++ P AV+VYT+ ES+Y++++ VPA+G +L+ F YG +E++ LDE
Sbjct: 3 RYKD-ETP-AVRVYTVCDSESRMIVRNPALGCGDDLMLRLFMTYGEVEEFAKRLDE 57

Pedant information for DKF2phfbr2_23o5, frame 3

Report for DKF2phfbr2_23o5.3

```

[LENGTH]      360
[MW]           41105.85
[pI]           8.89
[HOMOL]        TREMBL:AC005824_10 gene: "F15K20.11"; Arabidopsis thaliana chromosome II BAC
F15K20 genomic sequence, complete sequence. 5e-12
[PROSITE]      AMIDATION      1
[PROSITE]      MYRISTYL       2
[PROSITE]      CK2_PHOSPHO_SITE 7

```


SEQ	MASSGGEPGSLFDHHVQRAVCDTRAKYREGRRPRAVKVYTINLESQYLLIQGVPAVGVMK
SEG
PRD	ccccccccceeeceeeehhhhhhhhccccceeeeeeccccceeeeeeccccchhhh
SEQ	ELVERFALYGAIEQYNALDEYPAEDFTEVYLIKFMNLQSARTAKRMDEQSFFGGLLHVC
SEG
PRD	hhhhhhhhhhhhhhhhhhhhccccceeeeeeeghhhhhhhhhhhhhhhhhhhhccccceeee
SEQ	YAPFETVEETRKKLQMRKAYVVKTTENKDHYVTKKKLVTEHKDTEDFRQDFHSEMSGFC
SEG
PRD	eccchhhhhhhhhhhhhhhhhheeeccccceeeeeeccccchhhhhhhhhccccce
SEQ	KAALNTSAGNSNPYLPYSCELPLCYFSSKCMCSSGGPVDRAPDSSKODGRNHKTMGHYNH
SEG
PRD	eeeeccccccccccccccccceeecccccccccccccccccccccccccccccccccc
SEQ	NDSLRTQINSLKNSVACPGAQKAITSSAVDREMPRTTQLQERKRRREDRKLGTFLQT
SEGxxxxxxxxxxxxxxxx.....
PRD	ccccceeeccccccccccccceeeecceeeccccchhhhhhhhhhhccccceeeeee
SEQ	NPTGNEIMIGPLLPDISKVDMDHDSLNTTANLIRHKLKEVFLHCQSLQRTSQKMYIQVIH
SEG
PRD	ccccceeeccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccc

PS000001	185->189	ASN_GLYCOSYLATION	PDOC000001
PS000001	241->245	ASN_GLYCOSYLATION	PDOC000001
PS000001	327->331	ASN_GLYCOSYLATION	PDOC000001
PS000005	99->102	PKC_PHOSPHO_SITE	PDOC000005
PS000005	102->105	PKC_PHOSPHO_SITE	PDOC000005
PS000005	131->134	PKC_PHOSPHO_SITE	PDOC000005
PS000005	154->157	PKC_PHOSPHO_SITE	PDOC000005
PS000005	207->210	PKC_PHOSPHO_SITE	PDOC000005
PS000005	224->227	PKC_PHOSPHO_SITE	PDOC000005
PS000005	243->246	PKC_PHOSPHO_SITE	PDOC000005
PS000005	251->254	PKC_PHOSPHO_SITE	PDOC000005
PS000005	351->354	PKC_PHOSPHO_SITE	PDOC000005
PS000006	4->8	CK2_PHOSPHO_SITE	PDOC000006
PS000006	10->14	CK2_PHOSPHO_SITE	PDOC000006
PS000006	127->131	CK2_PHOSPHO_SITE	PDOC000006
PS000006	224->228	CK2_PHOSPHO_SITE	PDOC000006
PS000006	266->270	CK2_PHOSPHO_SITE	PDOC000006
PS000006	303->307	CK2_PHOSPHO_SITE	PDOC000006
PS000006	317->321	CK2_PHOSPHO_SITE	PDOC000006
PS000008	5->11	MYRISTYL	PDOC000008
PS000008	260->266	MYRISTYL	PDOC000008
PS000009	29->33	AMIDATION	PDOC000009

194

DKFZphfbr2_2a2

group: brain derived

DKFZphfbr2_2a2.3 encodes a novel 167 amino acid protein with weak similarity to human 52K autoantigen Ro/SS-A

The novel protein contains a C3HC4 Zinc finger "RING finger" motive. This domain is probably involved in mediating protein-protein interactions. Proteins containing a RING-finger are: mammalian V(D)J recombination activating protein (RAG1), mouse rpt-1, human rfp, human 52 Kd Ro/SS-A protein and others.

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to 52K autoantigen Ro/SS-A - human

complete cDNA, complete cds, few EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 1376 bp

Poly A stretch at pos. 1355, polyadenylation⁷ signal at pos. 1340

```
1 GGGGACTCCA AATTAGAAAG GGGACGTCTA GTGGGTGCCC CGGGAGGGGT
51 GGGGGGAGCG GTCCTGGAAA TAATCTGTCC TCTGTCGCCG GGAACGGCG
101 AGGTAGTTCC TTCGCGGTGG AGAGACCTGG AATGGCCAAA TATCAAGGTG
151 AAGTTCAAAG TTTGAAACTG GATGATGATT CAGTTATAGA AGGAGTAAGC
201 GACCAAGTAC TTGTGGCAGT TGTGGTCAGT TTCGCTTTGA TTGCTACCTT
251 GGTATATGCA CTTTTCAGAA ATGTACATCA AAACATTAC CAGAAAAACC
301 AGGAGCTAGT AAGGGTACTT CGAGAACAGC TTCAAACAGA ACAGGATGCA
351 CCTGCTGCCA CTCGACAGCA GTTCTACACT GACATGTACT GTCCCATCTG
401 CCTGCACCAA GCCTCCTTCC CGGTGGAGAC CAACTGTGGA CATCTTTTTT
451 GTGGTGCCTG CATTATTGCT TACTGGCGAT ATGGTTCATG GCTTGGGGCA
501 ATCAGTTGTC CAATCTGTAG ACAAACGGTA ACCTTACTCC TAACAGTATT
551 TGGTGAAGAT GATCAGTCTC AGGATGTTCT GAGATTGCAT CAGGATATTA
601 ATGATTATAA CCGGAGATTC TCAGGGCAAC CCTGATCTAT TATGGAGAGA
651 ATTATGGATC TACCCACTTT ACTGAGGCAT GCATTCAGGG AAATGTTTTT
701 AGTCGGGGGC CTTTCTGGA TGTTCGCAT CAGGATAATA CTTTGTTTAA
751 TGGGAGCTTT TTTCTATCTT ATATCACCTC TAGATTTTGT ACCTGAAGCC
801 TTGTTTGGA TTCTAGGCTT TCTAGATGAT TTCTTTGTCA TCTTTTATT
851 GCTTATCTAC ATCTCTATTA TGTATCGAGA AGTGATAACC CAAAGGCTAA
901 CTAGATGAAA AAGGAAACAA AACTGAGTTT ACTAGGATAT CTGAGCTAAT
951 GTAGAACATC AAACAGAAGG ACCCATGGCA GTATAAGCA ATGAAGCAAT
1001 GGAGTATTAT CTCACAAATA TAAAACCACT ATAAGACAAA CATTTGATTA
1051 TCATTTGACA AATACCTAGG TATAACTGGA ATTTTCATGT TTGAAGTTCT
1101 AATATTAAAG TTAGAATTAT AATGATCTAC AGTTGTATCT TGATTCTATG
1151 TTGTCTGAAA AAAATATGGA ATTATATAAA AAGGGATGCT TTTATATATT
1201 TTTCTTTTCC CCAGAATTAC TTAGATTAAT TAGATGTATA GTAAAAATATT
1251 GTTAAATGTC AGTTTATCCA TCTATCCTT CTCAGCAGGT ACCTATATGA
1301 TAATATATAG CTGTGAAACT CATCTAAATA TTTTGTTC AATAAAATAT
1351 TATATACTAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 132 bp to 632 bp; peptide length: 167
Category: similarity to known protein
Classification: unset

Prosites motifs: ZINC_FINGER_C3HC4 (102-112)

1 MAKYQGEVQS LKLDSDSVIE GVSDQVLVAV VVSFALIATL VYALFRNVHQ
51 NIHPENQELV RVLREQLQTE QDAPAATROQ FYTDMYCPIC LHQASFPVET
101 NCGHLFCGAC IAYWRYGSW LGAISCPICR QTVTLLLTVF GEDDQSQDVL
151 RLHQDINDYN RRFSGQP

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2a2, frame 3

TREMBL:CEY38F1A_8 gene: "Y38F1A.2"; Caenorhabditis elegans cosmid
Y38F1A, N = 1, Score = 194, P = 2e-15

PIR:T05222 hypothetical protein F17I5.130 - Arabidopsis thaliana, N =
1, Score = 159, P = 1.4e-10

TREMBLNEW:AB025011_1 gene: "TRIF"; product: "Trif-d"; Mus musculus
mRNA for Trif-d, complete cds., N = 1, Score = 108, P = 2.6e-06

PIR:A37241 52K autoantigen Ro/SS-A - human, N = 1, Score = 115, P =
5e-05

>TREMBL:CEY38F1A_8 gene: "Y38F1A.2"; Caenorhabditis elegans cosmid Y38F1A
Length = 283

HSPs:

Score = 194 (29.1 bits), Expect = 2.0e-15, P = 2.0e-15
Identities = 52/149 (34%), Positives = 78/149 (52%)

Query: 16 DSVIEGVSDQVLVAVVVSFALIATLVYALFRNVHQNIHPENQELVRLREQLQTEQDAPA 75
D +E ++ Q+ +A+ V F ++ + A Q E R Q+ T++
Sbjct: 41 DPDVE-LATQITMAIAVIF-IVKAIFDAWQSRRRQRAASRMENAE--RNQIITQRRISE 96
Query: 76 ATRQQFYTDMYCPICLHQASFPVETNCGHLFCGACIIAYWRYGSWLGA-ISCPICRQTVT 134
A Q + CPICL ASFPV T+CGH+FC CII YW+ + C +CR T
Sbjct: 97 ALHQSSHE---CPICLANASFPVLTDGHIHCCECIIQYWQQSKAIVTPCDCAMCRSTFY 153
Query: 135 LLLTV---FGEDDQSQDVLRLHQ-DINDYNRRFS 164
+LL V G +++ D ++ + I+DYNRRFS
Sbjct: 154 MLLPVHWPTMGTSSEETDDHIQENNIRIDYNNRRFS 188

Pedant information for DKFZphfbr2_2a2, frame 3

Report for DKFZphfbr2_2a2.3

[LENGTH] 167
[MW] 18941.65
[pI] 4.91
[HOMOL] TREMBL:CEY38F1A_8 gene: "Y38F1A.2"; Caenorhabditis elegans cosmid Y38F1A 1e-13
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YDR265w] 1e-04
[FUNCAT] 30.19 peroxisomal organization [S. cerevisiae, YDR265w] 1e-04
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR323c] 2e-04
[BLOCKS] BL00518 Zinc finger, C3HC4 type, proteins
[PROSITE] ZINC_FINGER_C3HC4 1
[PFAM] Zinc finger, C3HC4 type (RING finger)
[KW] Irregular
[KW] 3D
[KW] LOW_COMPLEXITY 6.59 %

SEQ MAKYQGEVQSLKLDSDSVIEGVSDQVLVAVVVSFALIATLVYALFRNVHQNIHPENQELV
SEGxxxxxxxxxxxxx.....
1rmd-
SEQ RVLREQLQTEQDAPAATROQFYTDMYCPICLHQASFPVETNCGHLFCGACIIAYWRYGSW
SEG
1rmd-HHHHHHBTTTTTEETTTEETTTTEEEHHHHH--HHHHH
SEQ LGAISCPICRQTVTLLLTVFGEEDDQSQDVLRLHQDINDYNRRFSGQP

SEG
 lrmd- HCCB-TTTT.....

Prosite for DKFZphfbr2_2a2.3

PS00518 102->112 ZINC_FINGER_C3HC4 PDOC00449

Pfam for DKFZphfbr2_2a2.3

HMM_NAME Zinc finger, C3HC4 type (RING finger)
 HMM *CPICFcTFQlDyPWPfdePmMlPCgHsFCypCIrrW.....CP
 CPIC L+ P++++CGH+FC +CI+ + CP
 Query 87 CPIC-----LHQ---ASFPPVETNCGHLFCGACIIAYWRYGSWLGAISCP 127
 HMM mC*
 +C
 Query 128 IC 129

DKFZphfbr2_2b17

group: transmembrane protein

DKFZphfbr2_2b17 encodes a novel 285 amino acid protein with similarity to D. melanogaster 30K protein.

The protein contains 3 transmembrane regions.
No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to Drosophila hypothetical 30K protein

complete cDNA, complete cds, EST hits
TRANSMEMBRANE 3

Sequenced by Qiagen

Locus: unknown

Insert length: 1426 bp

Poly A stretch at pos. 1345, polyadenylation signal at pos. 1330

```
1 GGGGGTATTT CCAAGGACTC CAAAGCGAGG CCGGGGACTG AAGGTGTGGG
51 TGTCGAGCCC TCTGGCAGAG GGTAAACCTG GGTCAAATGC ACGGATTCTC
101 ACCTCGTACA GTTACGCTCT CCCGCGGCAC GTCCGCGAGG ACTTGAAGTC
151 CTGAGCGGCTC AAGTTTGTCC GTAGGTCGAG AGAAGGCCAT GGAGGTGCCG
201 CCACCGGCAC CGCGGAGCTT TCTCTGTAGA GCATTGTGCC TATTTCCTCCG
251 AGTCTTTGCT GCCGAAGCTG TGAAGTCCGA TTCGGAAGTC CTTGAGGAGC
301 GTCAGAAGCG GCTTCCCTAC GTCCAGAGC CCTATTACCC GGAATCTGGA
351 TGGGACCGCC TCCGGGAGCT GTTGGGCAA GATGAACAGC AGAGAATTTC
401 AAAGGACCTT GCTAATATCT GTAAGACGGC GGCTACAGCA GGCATCATTC
451 GCTGGGTGTA TGGGGGAATA CCAGCTTTTA TTCATGCTAA ACAACAATAC
501 ATTGAGCAGA GCCAGGCAGA AATTTATCAT AACCGGTTTG ATGCTGTGCA
551 ATCTGCACAT CGTGCTGCCA CACGAGGCTT CATTCGTTAT GGCTGGCGCT
601 GGGGTGGGAG AACTGCAGTG TTTGTGACTA TATTCAACAC AGTGAACACT
651 AGTCTGAATG TATACCGAAA TAAAGATGCC TTAAGCCATT TTGTAATTGC
701 AGGAGCTGTC ACGGGAAGTC TTTTATAGGAT AAACGTAGGC CTGCGTGGCC
751 TGGTGGCTGG TGGCATAATT GGAGCCTTGC TGGGCACTCC TGTAGGAGGC
801 CTGCTGATGG CATTTTCAGAA GTACTCTGGT GAGACTGTTC AGGAAAGAAA
851 ACAGAAGGAT CGAAAGGCAC TCCATGAGCT AAAACTGGAA GAGTGGAAAG
901 GCAGACTACA AGTTACTGAG CACCTCCCTG AGAAAATTGA AAGTAGTTTA
951 CAGGAAGATG AACCTGAGAA TGATGCTAAG AAAATTGAAG CACTGCTAAA
1001 CCTTCCTAGA AACCTTCAG TAATAGATAA ACAAGACAAG GACTGAAAGT
1051 GCTCTGAACT TGAACTCAC TGGAGAGCTG AAGGGAGCTG CCATGTCCGA
1101 TGAATGCCAA CAGACAGGCC ACTCTTTGGT CAGCCTGCTG ACAAATTTAA
1151 GTGCTGGTAC CTGTGGTGGC AGTGGCTTGC TCTTGTCTTT TTCTTTTCTT
1201 TTTAACTAAG AATGGGGCTG TTGTACTCTC ACTTTACTTA TCCTTAAATT
1251 TAAATACATA CTTATGTTTG TATTAATCTA TCAATATATG CATACATGAA
1301 TATATCCACC CACCTAGATT TTAAGCAGTA AATAAACAT TTCGCAAAAG
1351 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HSG19630 from database EMBL:
human STS A001T27.
Score = 961, P = 1.2e-36, identities = 193/194

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 189 bp to 1043 bp; peptide length: 285
Category: similarity to unknown protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2 2b17. frame 3

```
>PIR:JQ1024 hypothetical 30K protein (DmRPL40 5' region) - fruit fly
(Drosophila melanogaster)
Length = 261
```

HSPs:

Score = 312 (46.8 bits), Expect = 6.1e-28, P = 6.1e-28
Identities = 68/231 (29%), Positives = 125/231 (54%)

```

Query:      30 ADSEVLEERQKRLPYVPEPPYPYPSGWDRLRELFGKDEQQRISKDLANICKTAATAGIIGW 89
            AD V +E + ++ E+G +RL+++F DE I +L ++ + +IG
Sbjct:      23 ADEIVDQKENTYKAFASKPPEETGLERLRKQMFTIDEFGSIFSELNSVYQAGFLGFLIGA 82

Query:      90 VYGGIPAFIHAQQQYIEQSQAIEIYHNRFDAVQSAHRAATRGFIYGRWRGWRTAVFVTIF 149
            + YGG+ A ++E +QA ++ F DA + T F + G++GWR +F T +
Sbjct:      83 IYGGVTQSRVAYMNFEMENNQATAFKSHFDAKKKLQDQFTVNFAKGGGFKWGRVGLFTTSY 142

Query:      150 NTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAF 209
            + T ++VYR K ++ ++ AG++TGS+++++CLRG+ AGGIIG LG G +
Sbjct:      143 FGIITCMSVYRGKSSIYEYLAAGSITGSLYKVSGLRGMAAGGIIGGFLGGVAGVTSLLL 202

Query:      210 QKYSGETVQERKQKDRKALHELKLEEWKGRQLQVTEHLPEKIESSLQEDEPE 260
            K SG +++E ++ ++K RL E++ + + +++ PE
Sbjct:      203 MKASGTSMEE-----VRYWQYKWLRLDRDENTIOAFKLTEDENPE 242

```

Pedant information for DKFZphfbr2 2b17, frame 3

Report for DKFZphfbr2 2b17.3

```

[LENGTH]          285
[MW]               32177.88
[pI]               8.65
[HOMOL]            PIR:JQ1024 hypothetical 30K protein (DmRP140 5' region) - fruit fly (Drosophila
melanogaster) 7e-20
[PROSITE]          MYRISTYL          7
[PROSITE]          CK2_PHOSPHO_SITE      5
[PROSITE]          ASN_GLYCOSYLATION     1
[KW]               SIGNAL_PEPTIDE 25
[KW]               TRANSMEMBRANE 3
[KW]               LOW COMPLEXITY      5.96 %

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SEQ      MEVPPAPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRE
SEG
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM      .....

SEQ      LFGKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAQQYIEQSQAIEIYHNRFDV
SEG
PRD      hhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM      .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ      QSAHRAATRGFIRYGRWRGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSFLR
SEG
PRD      hhhhhhhhhhhccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM      .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ      INVGLRGLVAGGIIGALLGTPVGGLLMAFQKYSGETVOERKQKDRKALHELKLEEWKGR

```

SEG ..xx
PRD ecc
MEM MMM

SEQ QVTEHLPEKIESSLQEDEPENDAKKIEALLNLPRNPSVIDKQDKD
SEG
PRD ccc
MEM

Prosites for DKFZphfbr2_2b17.3

PS00001	153->157	ASN_GLYCOSYLATION	PDOC00001
PS00006	53->57	CK2_PHOSPHO_SITE	PDOC00006
PS00006	108->112	CK2_PHOSPHO_SITE	PDOC00006
PS00006	216->220	CK2_PHOSPHO_SITE	PDOC00006
PS00006	253->257	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00008	92->98	MYRISTYL	PDOC00008
PS00008	172->178	MYRISTYL	PDOC00008
PS00008	187->193	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008
PS00008	195->201	MYRISTYL	PDOC00008
PS00008	199->205	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_2b17.3)

DKFZphfbr2_2b5

group: cell structure and motility

DKFZphfbr2_2b5 encodes a novel 957 amino acid protein with strong similarity to collagens.

The novel protein contains the typical (xxG)_n repeat of collagen proteins and a Pfam von Willebrand factor type A domain. Therefore, the protein seems to be a new collagen alpha chain.

The new protein can find application in modulation of connective tissue, bone and cartilage development and maintenance.

similarity to collagen proteins

shows typical (xxG)_n repeat of collagen proteins
[PFAM] von Willebrand factor type A domain

Sequenced by Qiagen

Locus: /map="6"

Insert length: 4160 bp

Poly A stretch at pos. 4141, polyadenylation signal at pos. 4119

```
1 GGGGGCCCCG TGCAGGGAGA ACGGACTCCG GCGGAGGGC AGCCAATCCG
51 TTTCAGCGCA GGTCTTGCTC GGGTTGGGCT TGCCACTGCC TGGAAACATAC
101 CTGTCCCCCT GCGCAACAC TCAGCTGGCT GCGACCGCAA CCCCAGCCT
151 GGACACTGCG CCAGGAATCC TAAACCAA ATATTAGAAC GAAACAGAA
201 ACATGGCTCA CTATATTACA TTTCTCTGCA TGGTTTGGT GCTGCTTCTT
251 CAGAACTCTG TGTAGCTGA AGATGGGGAA GTAAGATCAA GTTGCTGTAC
301 TGTCCGACA GATTTAGTT TCATCTTAGA TGGCTCTTAT AGTGTGGCC
351 CAGAAAACCT TGAATAGTG AAAAAGTGGC TTGTCAATAT CAAAAAAAC
401 TTGACATAG GCCCAAGTT TATCAAGTT GGAAGCTTC AATATAGTGA
451 CTACCCTGTG CTGGAGATTC CTCTCGGAAG CTATGATTCA GGAGAACATT
501 TGACGGCACC AGTGGAAATCC ATACTCTACT TAGGAGGAAA CACAAAGACA
551 GCGAAGGCCA TCCAGTTTGC GCTCGATTAC CTTTTTGACA AGTCTCAGC
601 ATTTCTGACT AAGATAGCAG TGGTACTTAC GGATGGCAAG TCCCAAGATG
651 ACGTCAAGGA TGCAGCTCAA GCAGCAAGAG ATAGTAAGAT AACATTATT
701 GCTATTGGTG TTGGTTTACA AACAGAAAGAT GCCGAACCTA GAGCTATTGC
751 CAACAAGCCT TCGTCTACTT ATGTGTTTGA TGTGGAAGAC TATATTGCAA
801 TATCCAAATC AAGGGAAGTG ATGAAGCAGA AACTTTGTGA AGAATCTGTC
851 TGTCCAACAC GAATTCCTAGT GGCAGCTCGT GATGAAAGGG GATTTGATAT
901 TCTTTTGGGT TTAGATGTAA ATAAAAAGGT TAAGAAAAGA ATACAGCTTT
951 CACCAAAAAA GATAAAAGGA TATGAAGTAA CATCAAAAGT TGATTTATCA
1001 GAACCTACAA GCAATGTTTT CCCAGAAGGT CTCTCTCCAT CATATGTATT
1051 TGTGTCTACT CAAAGATTGA AAGTCAAGAA AATTGCGGAT TTATGGAGAA
1101 TATTAACACT TGATGGAAGG CCACAATAG CAGTTACCTT AAATGGTGTG
1151 GACAAAATCT TATTATTAC AACAAACAGC GTAATTAATG GCTCACAAAT
1201 GGTTACCTTT GCTAACCTTC AAGTTAAGAC GTTGTTTGAT GAAGGCTGGC
1251 ACCAAATTCG TCTCTTAGTA ACAGAACAAAG ATGTGACTTT GTATATTGAT
1301 GACCAACAAA TGTAAAACAA GCCCTTACAT CCAGTTTATG GGATCTTGAT
1351 CAATGGGCAA ACCCAAAATG GAAAATATTC TGGAAAAGAA GAAACTGTTC
1401 AGTTTGATGT CCAAAAAGTTG CGAATCTACT GTGACCCAGA ACAGAACAAAC
1451 CGGGAGACAG CATGTGAGAT TCCTGGATTT AATGGAGAGT GCCTTAATGG
1501 TCCAGTGATG GTAGGTTCAA CTCCAGCTCC CTGTATTGTG CCTCCGGGAA
1551 AACCAAGGACT TCAAGGCCCC AAAGGTGACC CTGGACTGCC TGGGAACCTT
1601 GGCTACCCTG GACAACCTGG TCAAGATGGT AAGCCTGGAT ATCAGGGAAT
1651 TGCAGGGACA CCAGGTGTTT CAGGATCTCC AGGAATACAA GGAGCTCGAG
1701 GACTACCAGG TTACAAAGGA GAACCAGGGC GAGATGGTGA CAAGGGTGAT
1751 CGTGGACTTC CTGGTTTTC TGGGCTTCAT GGCATGCCAG GATCAAAGGG
1801 TGAAATGGGT GCCAAAGGAG ACAAAGGATC ACCTGGATTT TATGGCAAAA
1851 AGGGTGCAAA AGGTGAAAAG GGAATGCTG GCTTCCCTGG CCTCCCTGGA
1901 CCTGCTGGAG AACCAGGAAG ACATGGAAGG GATGGATTAA TGGGTAGTCC
1951 CGGTTTCAAG GGAGAAGCAG GATCCCTGG TGCTCCGGGG CAGGATGGAA
2001 CACGGGGAGA GCCTGGAATC CCAGGATTTC CTGGAACCG AGGATTAAATG
2051 GGCCAAAAGG GAGAAATTGG GCCTCCAGGA CAGCAAGGAA AAAAAGGAGC
2101 CCCAGGGATG CCTGTTTAA TGGGAAGCAA TGGCTACCA GGCCAGCCTG
2151 GAACACCGGG ATCTAAGGGA AGCAAAGGTG AACCTGGAAT TCAAGGGATG
2201 CCTGGGGCTT CAGGGCTCAA GGGAGAACCA GGAGCAACGG GTTCCCCAGG
2251 AGAACCAGGA TACATGGGTT TACCCGGGAT TCAAGGAAAA AAGGGGGACA
2301 AAGGAAATCA AGGTGAAAAA GGTATTCAGG GTCAAAAGGG AGAAAAATGGA
2351 AGACAGGGAA TTCCAGGGCA ACAGGGAATT CAAGGCCATC ATGGTGCAAA
2401 AGGAGAGAGA GTTGAAAAGG GAGAACCTGG TGTCCGAGGT GCCATTGGAT
2451 CAAAAGGAGA ATCTGGGGTG GATGGCTTGA TGGGGCCCGC AGGTCTTAAG
2501 GGGCAACCTG GGGATCCAGG TCCTCAGGGA CCCCAGGTT TGGATGGGAA
2551 GCGCGGAAGA GAGTTTTCAG ACAAATTTAT TCGACAAGTT TGCACAGATG
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2601 TAATAAGAGC CCAGCTACCA GTCTTACTTC AGAGTGAAG AATTAGAAAT
2651 TGTGATCATT GCCTGTCCCA ACATGGCTCC CCGGGTATTC CTGGGCCACC
2701 TGGTCCGATA GGCCAGAGG GTCCCAGAGG ATTACCTGGT TTGCCAGGAA
2751 GAGATGGTGT TCCTGGATTA GTGGGTGTCC CTGGACCTCC AGGTGTCAGA
2801 GGATTAAAAG GCCTACCAGG AAGAAATGGG GAAAAAGGGA GCCAAGGGTT
2851 TGGGTATCCT GGAGAACAAAG GTCCTCCTGG TCCCCCAGGT CCAGAGGGCC
2901 CTCCTGGAAT AAGCAAAGAA GGTCTCCAG GAGACCCAGG TCTCCCTGGC
2951 AAAGATGGAG ACCATGGAAC ACCTGGAATC CAAGGGCAAC CAGGCCCCCC
3001 AGGCATCTGC GACCCATCAC TATGTTTTAG TGTAAATTGCC AGAAGAGATC
3051 CGTTCAGAAA AGGACCAAAC TATTAGTGTC TGATGCCTCA TTCAGCAGCC
3101 TAGGCATGGT GCTTTTTCTG TGGTCTTTTG CATCTCAGGA AGATAACCAA
3151 CAGTATCCCT TGAAAAGAAA CTTAAGTACC TCGGTGTTTT TATTTTTTTT
3201 TTCTTTTGGG AAAAAATATA AAAGATCACA TATACTGATT TTAAGGCTC
3251 CTCAGTCATT TGGAGCCCTT GGATTAGCAG CATTAAATTAA ATCTCAAGGG
3301 TTTCTTGTAAG AGTCCATTTA TGTAATCAA AGTGAATAT AAAAATCCAC
3351 CATTGCCTGT TAGCCAGTCA GTTTTAGTCA CTGTGAAATA TTTACATTTC
3401 AGCCTCCATG CAGTAGAGAT TTGAGTTTAA TTTTATGTCC ATGTGACTTT
3451 CATGTTTCCT ATCTCATAGC TCATGCTACT ACATAAGCCA AAACATGTAT
3501 CTCATCATTG GAGTAAGAT CAGGGCTGAT ATTCACCTGG GATAGACAGT
3551 ATTGGTGAAC TACTCATTTA CTACAGTGTC TCAGCCTTGA TAAAGGGCAG
3601 TGGATTGCCT GTTGTTCGGT GTTGTGAATA GCACCTCTGA ATAAGATTAG
3651 AGTGTTCCTT AATTCATTTC AAACCTCTAA ATTAGATTAA TGGTGGTGCT
3701 AAGAAAGAGT ATTAATTACT TTGGGAATGG TCAAATTAA CATTAAAAAC
3751 ATTTTAGACA AAAAGTTTCA TTGTACATTC AAAGAAAATG TAAGTTTGGA
3801 AGTACTAAAA GACTATTTTA TACTTGTGTA TTAATCGGAA TGTTTGTGT
3851 ATGCTTCAT TTTCCATTTC ACTTATATGT GCATGTCCAT ATATGTTAAT
3901 TTTTATTGTA GCAAAGCTAA TGGAAATAAA GCTAATGCTC TAGTTGAAAG
3951 AAAAGGAAAA CTCCTGAAAT CCTGAAATGT CTTGTTATTT TTAGCTGACT
4001 GTAAATATT ATGAACAGTC TTTGTGTATT GTGCTTAATG CTTTGTGTAAG
4051 AAACAGAATT TGAATATTT CATCCTTGTC ATGCTCAAAA TTTTGTTACA
4101 TGCTTGTTAT TCAGAGTATA ATAAAGTTT GTACAGGCCT GAAAAAATAA
4151 AAAAAAATAA

```

BLAST Results

Entry HS682J15 from database EMBLNEW:
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 682J15
 Score = 6240, P = 0.0e+00, identities = 1256/1263
 13 exons matching Bp 2015-4118

Entry HS708F5 from database EMBLNEW:
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 708F5
 Score = 2775, P = 1.0e-221, identities = 739/912
 10 exons matching Bp 5-1745

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 203 bp to 3073 bp; peptide length: 957
 Category: similarity to known protein

```

1 MAHYITFLCM VLVLLQNSV LAEDGEVRSS CRTAPDLVF ILDGYSVGP
51 ENFEIVKKWL VNITKNFDIG PKFIQGVVQ YSDYPVLEIP LGSYDSGEHL
101 TAAVESILYL-GGNTKTGKAI-QFALDYLFDK SSRFLTIAV-VLTDGKSQDD
151 VKDAAQAARD SKITLFAIGV GSETEDAE LR AIANKPSSTY VFYVEDYIAI
201 SKIREVMKQK LCEESVCPTR IPVAARDERG FDILLGLDVN KVKKKRIQLS
251 PKKIKGYEVT SKVDLSELT NVPFEGLPSS YVVFSTQRFK VKKIWDLWRI
301 LTIDGRPQIA VTLNGVDKIL LETTTSVING SQVVTANPQ VKTLFDEGWH
351 QIRLLVTEQD VTLYIDDQOI ENKPLHPVLG ILINGQTQIG KYSGKEETVQ
401 FDVQKLRIY DPEQNNRETA CEIPGFNGEC LNGPSDVGST PAPCICPPGK
451 PGLQGPKGDP GLPKNPGYPG QPGQDCKPGY QGIAGTPGVP GSPGIQARG
501 LPGYKGEPR DGDKGDRGLP GFPGHLGMPG SKGEMGAKGD KGSFGFYGKK
551 GAKGEKNAG FPGLPGPAGE PGRHGKDGLM GSPGFKGEAG SPGAPGQDGT
601 RGEPIGPGF GNRGLMCQKG EIGPPGOQK KGAPGMPGLM GSNGPSGPG
651 TPGSKGSKGE PGIQGMFGAS GLKGEPEGAT SPGEPPGYMGL PGIQGKKGDK
701 GNQGEKIQG QKGENGROI PGQOQIQGH GAKGERGEKG FPGVRGAIGS
751 KGESGVDLGM GPAGPKGQPG DPGPQGPPL DKGKPGREFSE QFIRQVCTDV
801 IRAOLPVLLQ SGRIRNCDHC LSQHGSPGIP GPPGPIGPEG PRGLPGLPGR

```

851 DGVPLVGVLP GRPGVRLKLG LPGRNGEKGS QGFGYPGEQG PPGPPGPEGP
 901 PGISKEGPPG DPGLPGKGDG HGKPGIQGP GPPGICDPSL CFSVIARRDP
 951 FRKGPNY

BLASTP hits

Entry HSCOL7A1X_1 from database TREMBL:
 gene: "COL7A1"; product: "collagen type VII"; Homo sapiens (clones:
 CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic
 region and (COL7A1) gene, complete cds.
 Score = 949, P = 3.4e-122, identities = 237/553, positives = 281/553

Entry CA17_HUMAN from database SWISSPROT:
 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC
 COLLAGEN). >TREMBL:HSCOL7A1_1 gene: "COL7A1"; product: "alpha-1 type
 VII collagen"; Human alpha-1 type VII collagen (COL7A1) mRNA, complete
 cds.
 Score = 949, P = 3.6e-122, identities = 237/553, positives = 281/553

Alert BLASTP hits for DKFZphfbr2_2b5, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2b5, frame 2

Report for DKFZphfbr2_2b5.2

[LENGTH]	957
[MW]	99413.38
[pI]	8.49
[HOMOL]	PIR:A40020 collagen alpha 1(XII) chain precursor - chicken 9e-90
[BLOCKS]	BL011198 Copper-fist domain proteins
[BLOCKS]	BL003138
[BLOCKS]	BL01113A Clq domain proteins
[BLOCKS]	BL00420A Speract receptor repeat proteins domain proteins
[SCOP]	dlzoob_ 3.45.1.1.1 Integrin CD11a/CD18 (LFA-1) [Human (Hom 2e-58
[SCOP]	dlido_ 3.45.1.1.2 Integrin CR3 (CD11b/CD18), alpha subunit [Huma 8e-62
[EC]	3.1.1.7 Acetylcholinesterase 7e-24
[PIRKW]	blocked amino end 1e-43
[PIRKW]	duplication 7e-46
[PIRKW]	cornea 1e-35
[PIRKW]	lung 2e-40
[PIRKW]	leukocyte 1e-42
[PIRKW]	skin 1e-40
[PIRKW]	transmembrane protein 1e-37
[PIRKW]	cartilage 3e-59
[PIRKW]	hydroxylysine 4e-62
[PIRKW]	connective tissue 3e-43
[PIRKW]	triple helix 5e-82
[PIRKW]	homotrimer 2e-37
[PIRKW]	bone 6e-40
[PIRKW]	Alport syndrome 1e-42
[PIRKW]	laminin binding 2e-40
[PIRKW]	liver 2e-40
[PIRKW]	glycoprotein 5e-82
[PIRKW]	carboxylic ester hydrolase 7e-24
[PIRKW]	disulfide bond 7e-46
[PIRKW]	cell binding 7e-46
[PIRKW]	heterotrimer 4e-62
[PIRKW]	calcium binding 8e-28
[PIRKW]	alternative splicing 5e-82
[PIRKW]	coiled coil 5e-82
[PIRKW]	basement membrane 7e-46
[PIRKW]	trimer 5e-82
[PIRKW]	pyroglutamic acid 3e-43
[PIRKW]	hydroxyproline 4e-62
[PIRKW]	extracellular matrix 5e-82
[PIRKW]	chondroitin sulfate proteoglycan 6e-41
[PIRKW]	sulfoprotein 7e-39
[PIRKW]	kidney 1e-42
[PIRKW]	angiogenesis inhibitor 6e-36
[PIRKW]	Ehlers-Danlos syndrome 2e-40
[SUPFAM]	fibronectin type III repeat homology 5e-82
[SUPFAM]	scavenger receptor cysteine-rich domain homology 1e-37
[SUPFAM]	C-type lectin homology 6e-30
[SUPFAM]	collagen alpha 2(I) chain 5e-40
[SUPFAM]	collagen alpha 1(I) chain 6e-44

[SUPFAM] fibrillar collagen carboxyl-terminal homology 6e-44
 [SUPFAM] animal Kunitz-type proteinase inhibitor homology 2e-38
 [SUPFAM] fibronectin type II repeat homology 6e-21
 [SUPFAM] complement C1q carboxyl-terminal homology 1e-38
 [SUPFAM] collagen alpha 3(VI) chain 2e-31
 [SUPFAM] collagen alpha 1(IV) chain 7e-46
 [SUPFAM] collagen alpha 1(VI) chain 2e-37
 [SUPFAM] von Willebrand factor type C repeat homology 6e-44
 [SUPFAM] unassigned collagens 4e-62
 [SUPFAM] von Willebrand factor type A repeat homology 5e-82
 [SUPFAM] collagen alpha 1(XIV) chain 5e-82
 [SUPFAM] pulmonary surfactant protein D 6e-30
 [SUPFAM] collagen alpha 1(V) chain 7e-39
 [SUPFAM] collagen alpha 1(VIII) chain 1e-38
 [SUPFAM] EGF homology 1e-35
 [PROSITE] AMIDATION 3
 [PROSITE] MYRISTYL 14
 [PROSITE] CK2_PHOSPHO_SITE 13
 [PROSITE] PKC_PHOSPHO_SITE 8
 [PROSITE] ASN_GLYCOSYLATION 2
 [PFAM] von Willebrand factor type A domain
 [KW] Irregular
 [KW] 3D
 [KW] SIGNAL_PEPTIDE 23
 [KW] LOW_COMPLEXITY 24.24 %

SEQ MAHYITFLCMVLVLLQLNSVLAEDGEVRSSCRTAPTDLVFLDGSYSVGPENFEIVKKWL
 SEG
 latzBCCCEEEEEEECCCCCHHHHHHHHHHH

SEQ VNITKNFDIGPKFIQVGWVQYSDYPVLEIPLGSYDSGEHLTAAVESILYLGGNTKTGKAI
 SEG
 latzB HHHHHHCCBTTTTEEEEEETTTTEEEEETTTTTHHHHHHHHHHCCCCCCCCCHHHHH

SEQ QFALDYLFDKSSRFLTKIAVVLTDGKSQDDVKDAAQAARDSKITLFAIGVGSETEDAELR
 SEG
 latzB HHHHHHHHCCTTTTTEEEEEEECCCTTTTHHHHHHHHHHHHCEEEEEEECCCCCHHHHH

SEQ AIANKPSSTYVFYVEDYIAISKIREVMKQKLCEESVCPTRIPVAARDERGFIDILLGLDVN
 SEG
 latzB HHHGGGGGGGCECHHHHHHHHHCHHHHHHHH.....

SEQ KKVKKRIQLSPKKIKGYEVTSKVDLSELTSNVFPEGLPPSYVFWSTQRFKVKKIWDLWRI
 SEG
 latzB

SEQ LTIDGRPQIAVTLNGVDKILLFTTTSVINGSQVVTFANPQVKTLFDEGWHQIRLLVTEQD
 SEG
 latzB

SEQ VTLYIDDQQIENKPLHPVLGILINGQTQIGKYSKKEETVQFDVQKLRIYCDPEQNNRETA
 SEG
 latzB

SEQ CEIPGFNGECLNGPSDVGSTPAPCICPPGKPGLOGPKGDPLPGNPGYPGQPGQDGKPGY
 SEG
 latzB

SEQ QGIAGTPGVPGSPGIQGARGLPYKGEPRDGDGDRGLPGFPGLHGMPSGKGMGAAGD
 SEG xx.....
 latzB

SEQ KGSPGFYKKGAKGEKGNAGFPGLPGPAGEPRHGKDGLMGSPGFKEAGSPGAPGQDGT
 SEG
 latzB

SEQ RGEPIPGFPGNRGLMGQKEIGPPGQGGKKGAPGMPGLMGSNGSPGQPGTPGSKGSKGE
 SEG
 latzB

SEQ PGIQGMPGASGLKGEPGATGSPGEPGYMGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGI
 SEG
 latzB

SEQ PGQGGIQGHHGAKGERGEKGEVGRGAIGSKGESVDGLMPAGPKQPGDPGPGPPGL
 SEG
 latzB

SEQ DGKPGREFSEQFIRQVCTDVIRAQLPVLQLSGRIRNCDHCLSQHSGSPGIPGPPGPIGPEG
 SEG

```

latzB .....
SEQ   PRGLPGLPGRDGVPLVGVPGRPVRLKGLPGRNGEXSGFGYPGEQGPPEGPPGEGP
SEG   xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
latzB .....
SEQ   PGISKEGPPGDPGLPGKGDGDKGKPGIQGPQPGPGICDPSLCFSVIARRDPFRKGPNY
SEG   xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
latzB .....

```

Prosites for DKFZphfbr2_2b5.2

PS00001	62->66	ASN_GLYCOSYLATION	PDOC00001
PS00001	329->333	ASN_GLYCOSYLATION	PDOC00001
PS00005	30->33	PKC_PHOSPHO_SITE	PDOC00005
PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00005	131->134	PKC_PHOSPHO_SITE	PDOC00005
PS00005	250->253	PKC_PHOSPHO_SITE	PDOC00005
PS00005	260->263	PKC_PHOSPHO_SITE	PDOC00005
PS00005	286->289	PKC_PHOSPHO_SITE	PDOC00005
PS00005	393->396	PKC_PHOSPHO_SITE	PDOC00005
PS00005	811->814	PKC_PHOSPHO_SITE	PDOC00005
PS00006	147->151	CK2_PHOSPHO_SITE	PDOC00006
PS00006	172->176	CK2_PHOSPHO_SITE	PDOC00006
PS00006	261->265	CK2_PHOSPHO_SITE	PDOC00006
PS00006	343->347	CK2_PHOSPHO_SITE	PDOC00006
PS00006	357->361	CK2_PHOSPHO_SITE	PDOC00006
PS00006	393->397	CK2_PHOSPHO_SITE	PDOC00006
PS00006	419->423	CK2_PHOSPHO_SITE	PDOC00006
PS00006	531->535	CK2_PHOSPHO_SITE	PDOC00006
PS00006	600->604	CK2_PHOSPHO_SITE	PDOC00006
PS00006	657->661	CK2_PHOSPHO_SITE	PDOC00006
PS00006	681->685	CK2_PHOSPHO_SITE	PDOC00006
PS00006	750->754	CK2_PHOSPHO_SITE	PDOC00006
PS00006	754->758	CK2_PHOSPHO_SITE	PDOC00006
PS00008	92->98	MYRISTYL	PDOC00008
PS00008	112->118	MYRISTYL	PDOC00008
PS00008	236->242	MYRISTYL	PDOC00008
PS00008	276->282	MYRISTYL	PDOC00008
PS00008	380->386	MYRISTYL	PDOC00008
PS00008	494->500	MYRISTYL	PDOC00008
PS00008	527->533	MYRISTYL	PDOC00008
PS00008	596->602	MYRISTYL	PDOC00008
PS00008	638->644	MYRISTYL	PDOC00008
PS00008	650->656	MYRISTYL	PDOC00008
PS00008	653->659	MYRISTYL	PDOC00008
PS00008	665->671	MYRISTYL	PDOC00008
PS00008	743->749	MYRISTYL	PDOC00008
PS00008	746->752	MYRISTYL	PDOC00008
PS00009	547->551	AMIDATION	PDOC00009
PS00009	628->632	AMIDATION	PDOC00009
PS00009	694->698	AMIDATION	PDOC00009

Pfam for DKFZphfbr2_2b5.2

HMM_NAME	von Willebrand factor type A domain	
HMM	*DIVFLIDGSdSIGpqnFNrMKDFIerMMERMDigPDwIRVGVVQYSdNP	
Query	37	DLVFILDGSSVSGPENFEIVKKWLVNITKNFDIGPKFIQVGVVQYSDYP 85
HMM	RqEmrFmFNDYQNKeEILQaIqqMMYWMgggTNTGeAIQYVvrNMFwee	
Query	86	VLE--IPLGSYDSGEHLTAAVESIL-YLGGNTKTGKAIQFALDYLFDKSS 132
HMM	GmRWenvPQVMIIITDGRSQQDDIRDpIneMrrmaGIqvFaIGIGNhDNnn	
Query	133	RF---LTKIAVVLTDGKSQQDDVKDAAQAARD-SKITLFAIGVGSETE-- 175
HMM	WeELReIASePdEdHVFyVdDFeeLdnMqeql*	
Query	176	DAELRAIANKPSSTYVFYVEDYIAISKIREVM 207

DKFZphfbr2_2c1

group: brain derived

DKFZphfbr2_2c1 encodes a novel 697 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 3973 bp

Poly A stretch at pos. 3914, polyadenylation signal at pos. 3900

```
1 GGGGGGATTT CGGCGGCGGA AACATGGCGG TCGCGGCGCG GCCGGTAACG
51 GAGAAAGTTT ACGCCGACAC TGGCCTGTAT TAGCGCGTAT GGCCTCGGGC
101 CCTCGTTCCT CAAGGCGTGC CGCCTCCCTG TTCTCAGTCG CAGGCTGAAG
151 CCTTGTCTGC TCTCCTCCTT TTTGGTTTGG TTTTGAACT GACTCCGAGG
201 GTTGGGAGAG CGCGTTGGTG GCGACGGCCG AGTCAGATCA CTATAAACAA
251 AATTTCCACA AGAGAAAATG TTGAAATAGG AGTTGCGGAT ACATTGGATA
301 TACTGGATGA AATACAAAGC GTTAATTTT GTAACGTGAG GGAAAAGCCC
351 ACATTGCTGG TTACATGTGT AAATCACTGC GTTATTGCTT TAGTCATTGT
401 CTCTATTTAG CAATGACAAG ACTGGAAGAA GTAAATAGAG AAGTGAACAT
451 GCATTCTTCA GTGCGGTATC TTGGCTATTT AGCCAGAATC AATTTATTGG
501 TTGCTATATG CTTAGGTCTA TACGTAAGAT GGGAAAAAAC AGCAAATTCC
551 TTAATTTTGG TAATTTTAT TCTTGGTCTT TTTGTTCTTG GAATCGCCAG
601 CATACTCTAT TACTATTTT CAATGGAAGC AGCAAGTTA AGTCTCTCCA
651 ATCTTTGGTT TGGATTCCTG CTTGGCCTCC TATGTTTCT TGATAATTCA
701 TCCTTTAAAG ATGATGTAAA AGAAGAATCA ACCAAATATT TGCTTCTAAC
751 ATCCATAGTG TTAAGGATAT TGTGCTCTCT GGTGGAGAGA ATTTCTGGCT
801 ATGTCCGTC ACGGCCCACT TACTAACCA CAGTTGAATT TCTGGAGCTT
851 GTTGGATTGG CCATTGCCAG CACAACATAG TTGGTGGAGA AGTCTCTGAG
901 TGTCAATTTG CTTGTTGTAG CTCTGGCTAT GCTGATTATT GATCTGAGAA
951 TGAAATCTTT CTTAGCTATT CCAAACCTAG TTATTTTTCG AGTTTTGTGA
1001 TTTTTTTCCT CATTTGAAAC TCCCAAAAAT CCGATTGCTT TTGCGTGTTC
1051 TTTTATTGTC CTGATAACTG ATCCTTTCTT TGACATTAT TTTAGTGGAC
1101 TTTCAGTAAC TGAAAGATGG AAACCCCTTT TGTACCGTGG AAGAATTTGC
1151 AGAAGACTTT CAGTCGTTTT TGCTGGAATG ATTGAGCTTA CATTTTTTAT
1201 TCTTTCCGCA TTCAAACCTA GAGACACTCA CCTCTGGTAT TTTGTAATAC
1251 CTGGCTTTTC CATTTTTGGG ATTTTCAGGA TGATTTGTCA TATTATTTT
1301 CTTTAACTC TTTGGGGATT CCATACCAA TTAATGACT GCCATAAAGT
1351 ATATTTTACT CACAGGACAG ATTACAATAG CCTTGATAGA ATCATGGCAT
1401 CCAAAGGGAT GCGCCATTTT TGCTTGATTT CAGAGCAGTT GGTGTTCTTT
1451 AGTCTTCTTG CAACAGCGAT TTTGGGAGCA GTTTCCTGGC AGCCAACAAA
1501 TGGAAATTTT TTAGCATGT TCCTAATCGT TTTGCCATTG GAATCCATGG
1551 CTCATGGGCT CTTCCATGAA TTGGGTAAC GTTTAGGAGG AACATCTGTT
1601 GGATATGCTA TTGTGATTCC CACCAACTTC TGCAGTCCTG ATGGTCAGCC
1651 AACACTGCTT CCCCAGAAC ATGTACAGGA GTTAAATTG AGGTCTACTG
1701 GCATGCTCAA TGCTATCCAA AGATTTTTCG CATATCATAT GATTGAGACC
1751 TATGGATGTG ACTATTCCAC AAGTGGACTG TCATTTGATA CTCTGCATTC
1801 CAAACTAAAA GCTTTCCTCG AACTTCGGAC AGTGGATGGA CCCAGACATG
1851 ATACGTATAT TTTGTATTAC AGTGGGCACA CCCATGGTAC AGGAGAGTGG
1901 GCTCTAGCAG GTGGAGATAC ACTACGCCTT GACACACTTA TAGAATGGTG
1951 GAGAGAAAAG AATGGTTCCT TTTGTTCCCG GCTTATTATC GTATTAGACA
2001 GCGAAAATTC AACCCCTTGG GTGAAAGAAG TGAGGAAAAT TAATGACCAG
2051 TATATTGAGC TGCAAGGAGC AGAGTTGATA AAAACAGTAG ATATTGAAGA
2101 AGCTGACCCG CCACAGCTAG GTGACTTTAC AAAAGACTGG GTAGAATATA
2151 ACTGCAACTC CTGTAATAAC ATCTGCTGGA CTGAAAAGGG ACCGACAGTG
2201 AAAGCAGTAT ATGGTGTGTC AAAACGGTGG AGTGACTACA CTCTGCATTT
2251 GCCAACGGGA AGCGATGTGG CCAAGCACTG GATGTTACAC TTTCTCTGTA
2301 TTACATATCC CCTAGTGAT TTGGCAAAAT GGTATGCGG TCTGAACCTT
2351 TTTTGGATCT GCAAAACCTT TTTTAGGTGC TTGAAAAGAT TAAAAATGAG
2401 TTGGTTTCTT CTTACTGTGC TGGACACAGG ACAAGGCTTC AAACCTGTCA
2451 AATCTTAATT TGACCCCAA AGCGGGATAT TAATAAGCAC TCATACTACC
2501 AATTATCACT AACTTGCCAT TTTTGTATG CTGTATTTT ATTTGTGGAA
2551 AATACCTTGC TACTTCTGTA GCTGCTCTCA CTTTGTCTTT TCTTAAGTAA
2601 TTATGGGTATA TATAAGGCGT TGGGAAAAAA CATTTTATAA TGAAAGTATG
2651 TAGGGAGTCA AATGCTTACT GTAAATGCAT AAGAGACGTT AAAAATAACA
2701 CTGCACTTTC AGGAATGTTT GCTTATGGTC CTGATTAGAA AGAAACAGTT
```

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2751 GTCTATGCTC TGCAATGGTC AATGATGAAT TACTAATGCC TTATTTTCTA
2801 GGCATATAAT AATAGTTTAG AGAATGTAGA CCAGATAAAT TTGTTTACTG
2851 TTTTAAGAAA ACTACCAGTT TACTTACAGA AGATTCTTTT TTCCAAACAG
2901 TAGGTTTCAT CCAAGACCAT TTGAAGAACT GCAAACCTCTT TCTCTTAGAA
2951 AAGAAAGAGG GCAGCCTAAA ATAAACGCAA AATTTGCTTA TACTCCATCA
3001 CATTACAGATG TCTTGGTTGT GACTTATTAC CAGTGTGGCA GAGAACCCAA
3051 GTTACATTTT AGATCAAAAT ATTCTTTATG TAGGTATTGT TAAAAGGCTA
3101 GAGCCTACAA GTTGCTCTTC CATGCGTTGG TCAGGGGGCC CTGAAAACAC
3151 TGGTAATATT AAGAGTCTTT CTCAGGGTAA CTTAATGTTT TCTTAATGAA
3201 CAGTGTTCCT AGCTACAAAT TCTTCCAATA AATTGCTCTC CTTTTTGAAA
3251 AGTACTCTCA TAGAAGAAAT TTAGCAATTT CTCGTTGACT GACTCAGTCT
3301 ATTTTAAATA TTCAGAAAAG ATTTTGATCC CCATTGAGTT AATGCTCTGC
3351 CTTGAAAATT ATTTTCTGA TCCTTGTTAG TGATAACATT TTTTCTCTAC
3401 TGAAGGTCAG AGGATAGGAA ACAAGTATTT CTCTTCTGGT ATACATGTAA
3451 TGTATTCTGT AAAAAAGTAT TCATATTGGC AATTTTAGTT AGGCATAATA
3501 TTGTGGTTGT AATTTTAAA ACTTAGTGT TTGTCTGATT AAAGCAGGCA
3551 CTGATCAGGG TATCTCCTAA GAGGTAATTC ACTTCTTATT CCTTCCCAAT
3601 AATTATTACA TTCTAAATTT TCATCTATGA GAAATAACAA ACAAGAAGGG
3651 AATAGAATTA AATTGGGTA TAATCTAATC TTCATTGTTT AAATGGTTTG
3701 CCTTCTCACC ATTGAAGCCA TTTTTTATA GCCTCAGAAA GAGGAAATAA
3751 TGCCTCCACC ATTTTCTACC TGGTGACTTG AAAATTGAAC TTTTAAGTTA
3801 GGAAGAAGTT AGAGTCAGGG AACTTGTATA CCACTATCTA TGCAGCATTG
3851 TTATAGTCTG ATTATTTCTG TGTTTTGAAT ATGATTTTCC TAATGCTCTA
3901 AATAAAATTT TGTAAAAAAT CAAAAAATAA AAAAAAATAA CTTATCGATA
3951 CCGTCGACCT CGATGATGTC GAC

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 365 bp to 2455 bp; peptide length: 697
 Category: putative protein
 Classification: unset

```

1 MCKSLRYCFS HCLYLAMTRL EEVNREVMNH SSVRYLGYLA RINLLVAICL
51 GLYVVRWEKTA NSLILVIFIL GLFVLGIASI LYYYFSMEAA SLSSLNLWFG
101 FLLGLLCFLD NSSFKNDVKE ESTKYLLLTS IVLRILCSLV ERISGYVRHR
151 PTLTITVEFL ELVGFAIAST TMLVEKSLSV ILLVVALAML IIDLRMKSFL
201 AIPNLVIFAV LFFFSSLETP KNPIAFACFF ICLITDFFLD IYFSGLSVTE
251 RWKPFLYRGR ICRRLSVVFA GMIELTFFIL SAFKLROTHL WYFVIPGFSI
301 FGIFRMICHI IFLTLWGFH TKLNDCHKVY FTHRTDYNLS DRIMASKGMR
351 HFCLISEQLV FFSLLATAIL GAVSWQPTNG IFLSMFLIVL PLESMAGHLF
401 HELGNCLGGT SVGYAIVIPT NFCSPDGQPT LLPPEHVQEL NLRSTGMLNA
451 IQRFAYHMI ETYGCYSTS GLSFDLHLSK LKAFLELRTV DGPRHDTYIL
501 YYSGHTHGTG EWALAGGDTL RLDTLIEWWR EKNGSFCSRL IIVLDSNST
551 PWVKEVRKIN DQYIAVQGA E LIKTVOIEEA DPPQLGDFTK DWVEYNCNSC
601 NNICWTEKGR TVKAVYGVSK RWSDYTLHLP TGSDVAKHWM LHFPRITYPL
651 VHLANWLCLG NLFWICKTCF RCLRLKMSW FLPTVLDTGQ GFKLKVS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phfbr2_2c1, frame 2

PIR:A71148 hypothetical protein PH0395 - *Pyrococcus horikoshii*, N = 1,
 Score = 96, P = 0.12

>PIR:A71148 hypothetical protein PH0395 - *Pyrococcus horikoshii*
 Length = 288

HSPs:

Score = 96 (14.4 bits), Expect = 1.3e-01, P = 1.2e-01
 Identities = 59/234 (25%), Positives = 116/234 (49%)

Pedant information for DKFZphfbr2_2c1, frame 2

Report for DKF2phfbr2 2c1.2

```
[LENGTH]      697
[MW]           79741.46
[pI]           8.41
[KW]           TRANSMEMBRANE 11
[KW]           LOW COMPLEXITY 9.76 %
```

[illegible]

```
SEG .....
PRD eeeeeccccccchhhhhhccceeeccceeeeeeeccccccccccccceeeccccc
MEM .....

SEQ NNICWTEKGRTVKAVYGVSKRWSDYTLHLPTGSDVAKHWMLHFPRITYPLVHLANWLCGL
SEG .....
PRD ceeeeccccceeeeeeeccccceeeccccchhhhhhccccccchhhhhhhhcc
MEM .....

SEQ NLFWICKTCFRCLKRLKMSWFLPTVLDTGQGFKLVS
SEG .....
PRD eeeeehhhhhhhhhhhhccceeecccccccccc
MEM .....
```

(No Prosite data available for DKFZphfbr2_2c1.2)

(No Pfam data available for DKFZphfbr2_2c1.2)

DKF2phfbr2_2c17

group: signal transduction

DKF2phfbr2_2c17.3 encodes a novel 446 amino acid protein with similarity to yeast YMR131c and mammalian retinoblastoma-binding protein RbAp46

The protein contains 1 WD-40 repeat, which is typical for the beta-transducin subunit of G-proteins. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

The new protein can find application in modulating/blocking G-protein-dependent pathways.

similarity to YMR131c and retinoblastoma-binding protein RbAp46

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 2248 bp

Poly A stretch at pos. 2230, polyadenylation signal at pos. 2200

```
1 TGGGGAAGAT GCGGCGCGCG AAGGGTCGCG GTCGCACGTG TGAACCGGG
51 GAACCCATGG AAGCCGAGTC CGGCGACACA AGTTCGAGG GCCCGGCCCA
101 GGTCTACCTG CCCGCCCGGG GCGCGCCGCT ACGCGAAGGG GAGGAGCTGG
151 TCATGGACGA GGAGGCCAT GTGCTCTACC ACCGAGCGCA GACTGGCGCC
201 CCCTGTCTCA GCTTTGACAT AGTCCGGGAT CACCTGGGAG ACAACCGGAC
251 AGAGCTTCCT CTTACACTTT ACTTGCTGCT TGGGACCCAG GCTGAGAGCG
301 CCCAGAGCAA CAGACTGATG ATGCTTCGGA TGCACAATCT GCATGGGACA
351 AAGCCCCCAC CCTCAGAGGG CAGTGATGAA GAAGAAGAGG AGGAAGATGA
401 AGAGGATGAA GAAGAGCGGA AACCTCAGCT GGAGCTGGCC ATGGTGCCCC
451 ACTATGGTGG CATCAACCGA GTTCGGGTGT CATGGCTGGG TGAAGAGCCT
501 GTGGCTGGGG TGTGGTCAGA GAAGGCCAG GTGGAGGTGT TTGCGCTGCG
551 GCGGCTTCTG CAGGTGGTGG AGGAGCCCCA GGCCCTGGCA GCCTTCCTCC
601 GGGATGAGCA GGCCCAAATG AAGCCCATCT TCTCCTTCGC TGGACACATG
651 GCGGAGGGCT TTGCCCTTGA CTGGTCCCCC CGGGTGACCG GTCGCCCTGT
701 GACCGGTGAC TGTCAAAAGA ACATCCACCT CTGGACACCT ACGGACGGCG
751 GGTCTCTGCA CGTGGACACG CGGCCATTCT TGGGCCACAC AGGCTCTGTG
801 GAGGACCTGC AGTGGTCACC GACTGAGAAC ACGGTGTTTG CCTCTGTCTC
851 AGCTGACGCC TCCATCCGCA TCTGGGACAT CCGGGCAGCC CCCAGCAAGG
901 CTTGATGCTC CACACAGTCA ACCGCCATG ATGGGGACGT CAATGTCTAT
951 AGCTGGAGCC GCGGGGAGCC CTTCTGTGTC AGTGGCGGGG ATGATGGGGC
1001 CCTCAAGATC TGGGACCTTC GGCAGTTCAA GTCTGGTTCC CCAGTGGCCA
1051 CCTTCAAGCA GCACGTGGCC CCCGTGACCT CCGTCGAGTG GCACCCCCAG
1101 GACAGCGGGG TCTTTGAGC CTGGGGTGCA GACCACCAGA TCACACAGTG
1151 GGACCTGGCA GTGGAGCGGG ACCCTGAGGC GGGCGACGTG GAGGCCGACC
1201 CCGGACTGGC CGACCTCCCG CAGCAGCTGC TGTTCGTGCA CCAGGGCGAG
1251 ACCGAGCTGA AGGAGCTGCA CTGGCACCCG CAGTGCCAGG GGCTCCTGGT
1301 CAGCAGCGCG CTGTCAGGCT TCACCATCTT CCGCACCATC AGCGTCTGAG
1351 GCGTCCCACT GGCTCTGATC TTGCTTCCTG CTTGGAACAT GAAGTCAAT
1401 TGGGCTCCCC TGGAGGGGT TCATTAGGT CTGTTGACTG AGACTGGCCG
1451 GCCTGTGGGC TGGCGTATG GATTCTGTTT GACGTATTGT TCTCTAGAAG
1501 GCCTGGCTCT GATCCAGTGA CCCCTCTCAC CAAAGAACTC GGTTAACCA
1551 GGGCTCTGTA AGACCACTCC CACCCAGAGA CTGTGTGGC CTGGTGTGGC
1601 CTGTGTGTCT GATTCCTTCC TGTCAGCTGT GACCCATTG ACCTGTGTCC
1651 CCAGAACCCA CTTTTTGTG TGTTCGTTG AGACCGAGTC TTGGTCTCTC
1701 GCCCAGGCTG GAGTGCAGTA GCACGATCTT GGCTCACTGC AACCTCCGCC
1751 TCCTGGGTTA AAGTGATTCT CTCAGCTCAG TCTCCAGGT AGCTGGGAT
1801 ACAGGCATGT GCCACCACAC CCGTTAATT TTTGTATTT TAGTAGAGAC
1851 GGGGTTTCAC CATGTTGGCC AGGCTGGTCT CAAATCTTG ATCTCAAGTG
1901 ATCTGTCCGC CCCGGCCTCC CAGAGTGCTG GGTGGGAT ACAGGCGTGA
1951 GCCACCGCGT CCGGCTCAGG ACCCAGTTT GGCTGCTGGT TCCAGCAGG
2001 GGACTCGGGG GATATACAGT GGCTGCACCA AATTGGAGGT GTGGGTTTCT
2051 CCAACACAAT TTGCTTCTGC CCGTTGTCTT CCTGCCAGT GGGTTTGGCC
2101 AGGATTTCTC CGTGTGGGGG CTACATGCGA CCCTCTCCCC TCCTCCCTGA
2151 CTTTAGAGGC TGGTGCTGTG TCGGGAGGAA GGTGAGGGCT CCTGAGCAGC
2201 AATAAAGGAC CAGGAAGAGG CTGAGGTGG AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 9 bp to 1346 bp; peptide length: 446
 Category: similarity to known protein
 Classification: unset
 Prosite motifs: WD_REPEATS (323-338)

```

1 MAARKGRRRT CETGEPMEAE SGDTSSSEGA QVYLPGRGPP LREGELVMD
51 EEAYVLYHRA QTGAPCLSFD IVRDHLGDNR TELPLTLYLC AGTQAESAQS
101 NRLMLLRMHN LHGTPPPSE GSDEEEEEED EDEEERKPO LELAMVPHYG
151 GINRVRVSWL GEEPVAGVWS EKGQVEVFAL RRLQVVEEP QALAAFLRDE
201 QAQMKPISF AGHMGEGFAL DWSPRVTGRL LTGDCQKNIH LWTPTDGGSW
251 HVDQRPFGVH TRSVEDLQWS PTENTVFASC SADASIRIWD IRAAPSKACM
301 LTTVAHDGD VNVISWSRRE PFLLSGGDDG ALKIWDLRQF KSGSPVATFK
351 QHVAPVTSVE WHPQDSGVFA ASGADHQITQ WDLAVERDPE AGDVEADPGL
401 ADLPQQLLF HQGETELKEL HWHPCPCPLL VSTALSGFTI FRTISV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2c17, frame 3

TREMBL:AC005917_14 gene: "F3P11.14"; product: "putative WD-40 repeat protein"; Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence., N = 1, Score = 910, P = 2.7e-91

PIR:S53061 hypothetical protein YMR131c - yeast (Saccharomyces cerevisiae), N = 1, Score = 691, P = 4.3e-68

PIR:I49367 retinoblastoma-binding protein mRbAp46 - mouse, N = 1, Score = 338, P = 1.1e-30

PIR:I39181 retinoblastoma-binding protein RbAp46 - human, N = 1, Score = 338, P = 1.1e-30

>TREMBL:AC005917_14 gene: "F3P11.14"; product: "putative WD-40 repeat protein"; Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence.
 Length = 469

HSPs:

Score = 910 (136.5 bits), Expect = 2.7e-91, P = 2.7e-91
 Identities = 195/442 (44%), Positives = 259/442 (58%)

```

Query:   18 EAESGDTSSSEGAQVYLPGRGPPPLREGEELVMDDEEAYVLYHRAQTGAPCLSFDIVRDHLG 77
          EA S + S P +V+ PG L +GEEL D AY H G PCLSFDI+ D LG
Sbjct:   18 EASSSEIPSI-PTRVWQPGVDT-LEDGEELQCDPSAYNSLHGFEHVGWPCLSFDILGDKLG 75

Query:   78 DNRTPLTLYLCAGTQAESAQSNRLMLLRMHNLHGTP---PPSEGSDEEEEEDEED- 133
          NRTE P TLY+ AGTQAE A N + + ++ N+ G + P + G+ E+E+E+DE+D
Sbjct:   76 LNRTFPHTLYMVAGTQAEKAHNSIGLFKITNVSGKRRDVPKTFNGGEDEDEDEDDDS 135

Query:   134 -----EEERKPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKQVEVFALRRLLQ 185
          E + P.+++ V H+G +NR+R + W++ G V+V+ + L
Sbjct:   136 DSDDDDGDDEASKTPNIQVRRVAHHGCVNIRAMPQNSH-ICVSWADSGHVQVWDMSSHLN 194

Query:   186 VVEEPQALAAFLRDEQAQMKPISFAGHMGEGFALDWSPRVTGRLLTGDCQKNIHLWTPT 245
          + E + P+ +F+GH EG+A+DWSP GRLL+GDC+ IHLW P
Sbjct:   195 ALAESETEGKDGTSPLVNLQAPLVNFSGHKDEGYAIDWSPATAGRLLSGDCKSMIHLWEPA 254

Query:   246 DGGSWHVDQRPFGVHTRSVEDLQWSPPTENTVFASCSDADASIRIWDIRAAPSKACMLTTVT 305
          G SW VD PF GHT SVEDLQWSP E VFASCS D S+ +WDIR S A +
Sbjct:   255 SG-SWAVDIPFAGHTASVEDLQWSPAENVFASCSVDGSAVAVWDIRLGKSPAL---SFK 310

Query:   306 AHDGDNVNVISWSRREPFL-LL-SGGDDGALKIWDLRQFKSGSPV-ATFKQHVAPVTSVEWHP 363
          AH+ DNVNVISW+R +L SG DDG I DLR K G V A F+ H P+TS+EW
Sbjct:   311 AHNADVNVISWNRLASCMASGSDDGTFISIRDLRLIKGGDAVVAHFYHKHPITSIEWSA 370

```

Query: 364 QDSGVFAASGADHQITQWDLAVERDPE-----AGDVEADPGLADLPQQLLFVHQGETEL 417
 ++ A + D+Q+T WDL++E+D E A E DLP QLLFVHQG+ +L
 Sbjct: 371 HEASTLAVTSGDNQLTIWDLSELEKDEEEAEFNAQTKELVNTPDQLPQLLFVHQGQKDL 430

Query: 418 KELHWHPPQCPGLLVSTALSGFTIFRTISV 446
 KELHWH Q PG+++STA GF I ++
 Sbjct: 431 KELHWHNQIPGMIISTAGDGFNILMPYNI 459

Pedant information for DKFZphfbr2_2c17, frame 3

Report for DKFZphfbr2_2c17.3

[LENGTH] 446
 [MW] 49447.38
 [pI] 4.82
 [HOMOL] TREMBL:AC005917_14 gene: "F3P11.14"; product: "putative WD-40 repeat protein";
 Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence. 1e-90
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YMR131c] 4e-65
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YEL056w] 4e-15
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YEL056w] 4e-15
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YEL056w] 4e-15
 [FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YBR195c] 2e-13
 [FUNCAT] 10.04.09 regulation of g-protein activity [S. cerevisiae, YBR195c] 2e-13
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YBR195c] 2e-13
 [FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YBR195c] 2e-13
 [FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YBR195c] 2e-13
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YPR178w] 1e-11
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPR178w] 1e-11
 [FUNCAT] 06.13 proteolysis [S. cerevisiae, YGL003c] 4e-09
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YGL003c] 4e-09
 [FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YDL145c] 5e-09
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL145c] 5e-09
 [FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YBR198c] 6e-09
 TAF90 - TFIID subunit] 6e-09
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YMR116c] 5e-08
 [FUNCAT] 02.16 fermentation [S. cerevisiae, YMR116c] 5e-08
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YLR429w] 3e-07
 [FUNCAT] 30.19 peroxisomal organization [S. cerevisiae, YDR142c] 3e-06
 [FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YDR142c] 3e-06
 [FUNCAT] 08.10 peroxisomal transport [S. cerevisiae, YDR142c] 3e-06
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YLR129w] 4e-06
 [FUNCAT] 08.01 nuclear transport [S. cerevisiae, YER107c] 4e-06
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YKL021c] 4e-06
 [FUNCAT] 04.07 rna transport [S. cerevisiae, YER107c] 4e-06
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YCR057c] 2e-05
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YCR057c] 2e-05
 [FUNCAT] 01.01.04 regulation of amino-acid metabolism [S. cerevisiae, YIL046w] 2e-05
 [FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YIL046w] 2e-05
 [FUNCAT] 04.01.04 rrna processing [S. cerevisiae, YLL011w] 3e-05
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YOR212w] 5e-05
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YOR212w] 5e-05
 [FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YOR212w] 5e-05
 [BLOCKS] BL00678
 [SCOP] d2trcb_2.51.3.1.1 Transducin (heterotrimeric G protein), gamma 5e-29
 [PIRKW] plasma 6e-07
 [PIRKW] duplication 4e-12
 [PIRKW] hormone 6e-07
 [PIRKW] transmembrane protein 1e-07
 [PIRKW] stomach 6e-07
 [PIRKW] actin binding 1e-07
 [PIRKW] leucine zipper 1e-07
 [PIRKW] signal transduction 2e-06
 [PIRKW] heterotrimer 2e-06
 [PIRKW] peripheral membrane protein 6e-07
 [PIRKW] GTP binding 2e-06
 [SUPFAM] WD repeat homology 1e-63
 [SUPFAM] yeast coatomer complex alpha chain 1e-07
 [SUPFAM] GTP-binding regulatory protein beta chain 4e-07
 [SUPFAM] PRL1 protein 8e-09

[SUPFAM] MS11 protein 4e-12
 [SUPFAM] coatamer complex beta' chain 1e-09
 [PROSITE] WD_REPEATS 1
 [PFAM] WD domain, G-beta repeats
 [KW] All_Beta
 [KW] 3D
 [KW] LOW_COMPLEXITY 3.14 %

```

SEQ      MAARKGRRRTCETGEPMEAESGDTSSSEGPAQVYLPGRGPPLREGEELVMDEEAYVLYHRA
SEG      .....
lgotB    .....

SEQ      QTGAPCLSFDIVRDHLGDNRTPLTLTYLCAGTQAESAQSNRLMMLRMHNLHGTKPPSPSE
SEG      .....
lgotB    .....

SEQ      GSDEEEEEDEEDEEERKPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKQVEVFAL
SEG      ..xxxxxxxxxxxxxx
lgotB    .....

SEQ      RRLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEFGALDWSPRVTGRLLTGDCQKNIH
SEG      .....
lgotB    .....EEEECCCCEEEEETTT-TCEEEEEETTTTEE

SEQ      LWTPTDGGSWHVDQRPFVGHTRSVEDLQWSPTENTVFASCSADASIRIWDIRAAPSKACM
SEG      .....
lgotB    EEETTTT----CEEEEECCCCEEEEETTTTCE-EETTTTTEEEEEETTT--TEEEE

SEQ      LTTVTAHDGDVNVISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVPVTSVE
SEG      .....
lgotB    EECBTTBTCEEEEEETTTTTEEEEEETTTTEEEEE.....

SEQ      WHPQDSGVFAASGADHQITQWDLAVERDPEAGDVEADPGLADLPQQLLFVHQGETELKEL
SEG      .....
lgotB    .....

SEQ      HWHPOCPGLLVSTALSGFTIFRTISV
SEG      .....
lgotB    .....

```

Prosites for DKFzphfbr2_2c17.3

PS00678 323->338 WD_REPEATS PDOC00574

Pfam for DKFzphfbr2_2c17.3

HMM_NAME WD domain, G-beta repeats

HMM *MrGHnnWVWCVaFSPDGGrWFIvSGSWDgTCRLWD*
 ++GH+ V ++ +SP + +++S S D ++R+WD

Query 257 FVGHTRSVEDLQWSPTENTVFASCSADASIRIWD 290

24.88 304 336 1 34 dkfzphfbr2_2c17.3 similarity to YMR131c and retinoblastoma-binding protein RbAp46

Alignment to HMM consensus:

Query *MrGHnnWVWCVaFSPDGGrWFIvSGSWDgTCRLWD*
 + H+++V+ +++S + ++SG++DG +++WD

dkfzphfbr2 304 VTAHDGDVNVISWSRREPFLLSGGDDGALKIWD 336

DKFZphfbr2_2c18

group: brain associated

DKFZphfbr2_2c18 encodes a novel 302 amino acid protein with weak similarity to cyclin-dependent kinase p130-PITSLRE.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to cyclin-dependent kinase p130-PITSLRE

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 2835 bp

Poly A stretch at pos. 2817, polyadenylation signal at pos. 2796

```
1 TGGGGCGGAC GCGGAGGGAG TCCAGAGCCT TGAGCCCGGT GCTCCTCCCT
51 CGGCGAGCGG TGGCTCTGCG GCCGCTGGAG TAAACACTGC CTTTGTTCCT
101 TAGCGCCTCG TCTTTCGTCTG CCGCGTGCCC TCACGCCGCC GGGCTCTGGC
151 CGGCCCCGCC TCGGTCCTTG AACCCCATTT CGGCTCGTGC CGTGCGGATG
201 CAGCTGCCGG GCCTGGGTTT GGGCATTGAG CGGGAGGAGG AGGAGGAGCG
251 GCGGCGCCTG GCGGCGCATGC GATGGGGAAC TGCTGCTGGA CGCAGTGCTT
301 CGGACTGCTT CGCAAGGAAG CGGGGCGGCT GCAGCGAGTA GGCGGCGGCG
351 GAGGATCCAA GTATTTTAGA ACATGCTCAA GAGGTGAGCA CTTGACAATA
401 GAGTTTGAGA ATCTAGTAGA AAGTGATGAA GGGGAGAGCC CAGGAAGCAG
451 TCATAGGCCT CTTACIGAGG AAGAAATTGT TGACCTAAGA GAAAGGCATT
501 ATGATTCATG TGCCGAAAAA CAAAAAGATC TTGATGAGAA AATTCAAAAA
551 GAGTTAGCCT TACAAGAAGA GAAGTTAAGA CTAGAAGAAG AAGCTTTATA
601 CGCTGCACAG CGTGAAGCAG CCAGGGCAGC AAAGCAGCGA AAGCTCTTGG
651 AGCAAGAAAG GCAGAGAATT GTGCAGCAAT ATCATCCTTC CAACAATGGA
701 GAATATCAAA GTTCAGGACC AGAAGATGAC TTCGAATCTT GTTGAGAAAA
751 TATGAAGTCA CAGTATGAAG TTTTTCGAAG TAGTAGACTC TCATCAGATG
801 CTACAGTTTT GACACCAAAAT ACAGAAAGCA GTTGTGATTT AATGACCAAA
851 ACTAAATCAA CTAGTGGAAA TGACGACAGC ACATCCTTAG ATCTAGAGTG
901 GGAAGATGAA GAAGGAATGA ATAGAATGCT TCCAATGAGA GAACGTTCCA
951 AAACAGAGGA AGACATTCTA CGGGCAGCAC TTAAGTATAG CAACAAGAAG
1001 ACTGGAAGTA ATCCTACATC AGCCTCTGAT GATTCCAATG GGCTGGAGTG
1051 GGAATAATGAT TTTGTTAGTG CCGAAATGGA TGATAATGGA AATTCGGAGT
1101 ATTCTGGATT TGTAAATCCT GTATTAGAAC TGTCTGATTC TGGCATAAGG
1151 CATTCTGACA CAGATCAACA GACTCGATAG GGTAAATTTG TGTGACCTTG
1201 TTTATCAGTT ATGACCAAAAT GTTAAAAACC AACTAGAATG TATAAGTGAT
1251 TGTGCTTAGC CTTTITGTAA GGGAGATGTG TAAGAAACCA TGCTGTAAAT
1301 GCTTATTTTA TTACAAAGGA GTAGGGATGA TAGGATCTGA ATTGATACAG
1351 AATTAAGTGC AATTTTCATCA TCTGCCCTCT GCTTTTCAAG ACCAATTTAA
1401 TGGTCCGTGC ATGTTACTGA TTAAATTAC TTTGTCTTGT CTTTATAGCA
1451 TTTCTGTTTA CTATGGTAGA TTTCCACTTT CAATTTTTTA AATTAATTTT
1501 ACTTTGAATG ATTTATGAAG CCTATTTTAT TGTCTAACTA TGAAAAATAT
1551 AAGACTTTTT TGTAAATTTT CAGCCGATGT GAAGGAAGCA TGAGGAGGGA
1601 TCGTCAGACT CAGATTTAGA ATAGTGTTCG CGTTTCCAGC ATTATTTATT
1651 TCTATGACTT CTTTGGATTT TATTATCTAA TAGTAAGTAC AGTTGATGTG
1701 GGTAGATGAC TCTAAGAAAT GCTGAAGTAT CGGCATTACA TGTGTTTATT
1751 TACATGTCCT AGTTTGATAA TGTGATTCA ATCTGAACAA AAGATAATAT
1801 AAAAAATAAC CTTTCAGAGT TGGACATTTT AAGTTGGTAA TAATAAAAAA
1851 TAATATTAA GAAGATATAT ATATATATAT ATTTAGTTTT TTCCACTTCA
1901 TTTTACATGC CACTATATTG ACTTTAATTG ATATACAGTA TTAAGTTTTT
1951 AGGTGCCATT ATTTTTAAAA AATTTCTATAT TTCCAATGAA CGATGTTAGA
2001 TTTTACACAG AACATATTCT CTGCATGATT TCAGAAAGA AAATCTAAAA
2051 AGGTAATACG GGTATTTCAA ATAAATCCTT TTCTGGTATG AAAGGCTCCA
2101 TTGATTTTAT TAAGCCTTCC TTTACCTTGT AGTACAAGGT GCTTTAATGG
2151 GATAGATCAA AGCAATATCA TATCTATAAC TGCATTTTGT GCTAGACAAT
2201 TACTGTCTTT TTCTCTAAAA TGTATATGTC AATTTACAAG GCCAGGGATA
2251 GAAAACACTC CATAATTGCT TTCCTTGATT TTGCTGAGGA TTTGGTATGA
2301 TTTTATTAAG AAGACTGTTT TTTGGTTTTT CCTTAATGTT TTTAATTTTT
2351 TTTCTCTTGT CAACAATGAC GGTGCATGTT CTTATAAATA TAGGAAGGTC
2401 CAGATATAAA TAGTAACCTA AAGTTCCTGC TGTGCTTAAA AAAAAAATC
2451 ATGTGCTCTT TCAATATTTT GAACTGCTAA GCAATGACAT CTGTAGTTTT
2501 ATCTCCTTTT TTATGTCATA GAAATTAATA TGATACTTTA AATATGTAAA
2551 TATAATACAT TGGTAATGCT ATTATTTATA TCTGCTTAA CATAATTTAA
2601 GTTGTAGCTG TGTCTTGGAA ATATTTTAA GGTAACTCTAT ATTCACATTG
2651 CCTGTGTTAA TGCTTTTTAA GCTTTGTATA CATCAGATGT ATATTTTTTG
```

2701 TTTGGCATAA GCTACGATTG TAATTTTCT TGGCTTTTG TTCATAAGA
 2751 ATTTTGTGAA GGAATGGTAA CAAATGGTAA TTTACAAATG GTTGTGAATA
 2801 AACACATTTT TACACTTAAA AAAAAAAAAA AAAAA

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 272 bp to 1177 bp; peptide length: 302
 Category: similarity to known protein

1 MGNCWTQCF GLLRKEAGRL QRVGGGGGSK YFRTCSRGEH LTIEFENLVE
 51 SDEGESPGSS HRPLTEEEIV DLRRHYDSI AEKQKDLDEK IQKELALQEE
 101 KLRLEEEALY AAQREAAARA KQRKLEQER QRIVQYHPS NNGEYQSSGP
 151 EDDFESCLRN MKSQYEVFRS SRLSSDATVL TPNTSSCDL MTKTKSTSGN
 201 DDSTSLDLEW EDEEGMNRML PMRERSKTEE DILRAALKYS NKKTGSNPTS
 251 ASDDSNGLEW ENDFVSAEMD DNGNSEYSGF VNPVLELSDS GIRHSDTDQO
 301 TR

BLASTP hits

Entry A55817 from database PIR:
 cyclin-dependent kinase p130-PITSLRE - mouse
 Length = 783
 Score = 123 (43.3 bits), Expect = 0.00013, P = 0.00013
 Identities = 53/197 (26%), Positives = 96/197 (48%)

Alert BLASTP hits for DKFZphfbr2_2c18, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2c18, frame 2

Report for DKFZphfbr2_2c18.2

[LENGTH] 302
 [MW] 34281.39
 [pI] 4.73
 [PROSITE] MYRISTYL 5
 [PROSITE] CK2_PHOSPHO_SITE 12
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 3
 [KW] All_Alpha
 [KW] LOW_COMPLEXITY 13.58 %
 [KW] COILED_COIL 13.58 %

SEQ MGNCWTQCFGLLRKEAGRLQRVGGGGGSKYFRTCSRGEHLTIEFENLVESDEGESPGSS
 SEGxxxxx.....
 PRD cccccccchhhhhhhhhheeeccccccccceccccccchhhhhhhcccccccccc
 COILS
 SEQ HRPLTEEEIVDLRRHYDSIAEKQKDLDEKIQKELALQEEKLRLEEEALYAAQREAAARA
 SEGxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
 PRD ccchhhhhhhhhhhccchhh
 COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
 SEQ KQRKLEQERQRIVQYHPSNNGEYQSSGPEDDFESCLRNKMSQYEVFRSSRLSSDATVL
 SEGxxxxxxx.....
 PRD hhhhhhhhhhhhhhhccccccccccccccchhhhhhhhhhhheeeccccccccce
 COILS CCCCCCCC.....

Prosites for DKFZphfbr2_2c18.2

(No Pfam data available for DKF2phfbr2_2c18.2)

DKFZphfbr2_2d15

group: differentiation/development

DKFZphfbr2_2d15 encodes a novel 438 amino acid protein similarity to Mus musculus testis-specific Y-encoded-like protein (Tspyl1).

The TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. The novel protein is a new member of the TSPY-SET-NAP1L1 family, which represents proteins closely related to TSPY. Therefore, the new protein seems to be involved in early spermatogenesis.

The new protein can find application in modulating early spermatogenesis.

strong similarity to testis-specific Y-encoded-like protein

complete cDNA, complete cds, EST hits
localisation: primer B does not match perfect

Sequenced by Qiagen

Locus: /map="729.2 cR from top of Chr6 linkage group"

Insert length: 3229 bp

Poly A stretch at pos. 3206, polyadenylation signal at pos. 3184

```
1 GGAGACTGTA GGGTGGGCGG TGCGAGCGGC GGTTAGCTCC CAGTTCGGCC
51 TCTGAGGAAA ACGGGCGTTC GCCTGCGGTT GGTCCGACTG TTAGCAACAT
101 GAGCGCCCTG GATGGGCTCA AGAGGACCAC TCCCCTCCAA ACCCACAGCA
151 TCATTATTTC TGACCAAGTC CCGAGCGACC AGGACGCACA CCAGTACCTG
201 AGGCTCCGCG ACCAAAGCGA GCGACACAG GTGATGGCGG AGCCGGGTGA
251 GGGAGGCTCG GAGACCGTCG CGCTCCCGCC TTCACCGCCT TCAGAGGAGG
301 GGGGCGTACC CCAGGATCCC GCGGGCCGTG GCGGTACTCC CCAGATCCGA
351 GTTGTGGGGG GTCGCGGTCA TGTGCGATC AAAGCCGGGG AGGAAGAGGG
401 CCAGCCTCCC GCCGAAGGCC TGGCAGCCGC TTCTGTGGTG ATGGCAGCCG
451 ACCGCAGCCT GAAAAAGGGC GTTCAGGGTG GAGAGAAGGC CCTAGAAATC
501 TGTGGCGCCC AGAGATCCGC GTCTGAGCTG ACGGCGGGGG CGGAGGCTGA
551 GGCGGAGGAG GTGAAGACAG GAAAGTGCGC CACCGTCTCA GCAGCCGTGG
601 CTGAGAGGGA AGCGCTGAG GTGGTGGTGA AGGAAGGCCT GGCGGAGAAG
651 GAGGTAATGG AGGAGCAGAT GGAGGTAGAG GAGCAGCCGC CAGAAGGTGA
701 AGAAATAGAA GTGGCGGAGG AGGATAGATT GGAGGAGGAG GCGAGGGAGG
751 AAGAAGGGCC CTGGCCTTTG CATGAGGCTC TCCGCATGGA CCCTCTGGAG
801 GCCATCCAGC TGGAACTGGA CACTGTGAAT GCTCAGGCCG ACAGGGCCTT
851 CCAACAGCTG GAGCACAAGT TTGGGCGGAT GCGTCGACAC TACCTGGAGC
901 GGAGGAAC TAATCATTAG AATATCCCGG GCTTCTGGAT GACTGCTTTT
951 CGAAACCACC CCCAGTTGTC CGCCATGATT AGGGGCCAAG ATGCAGAGAT
1001 GTTAAGGTAC ATAACCAATT TAGAGGTGAA GGAAC TCAGA CACCCTAGAA
1051 CCGTTGCAA GTTCAAGTTC TTCTTTAGAA GAAACCCCTA CTTCAGAAAC
1101 AAGCTGATTG TCAAGGAATA TGAGGTAAGA TCCTCCGGCC GAGTGGTGTG
1151 TCTTTCTACT CCAATTATAT GCGCAGGGGG GCATGAACCC CAGTCCTTCA
1201 TTCCGAGAAA CCAAGACCTC ATCTGCAGCT TCTTCACTTG GTTTTCAGAC
1251 CACAGCCTTC CAGAGTCCGA CAAAATTGCT GAGATTATTA AAGAGGATCT
1301 GTGGCCAAAT CCACTGCAAT ACTACCTGTT GCGTGAAGGA GTCCGTAGAG
1351 CCCGACGTCG CCCGCTAAGG GAGCCTGTAG AGATCCCCAG GCCCTTTGGG
1401 TTCCAGTCTG GTTAACATTT GCCCTTGGGA ATACTCCTGC ACAAGGTCTC
1451 CTACCACCTT CTGCTGGACC TGTGCTTGGG CATCAGCAAT GAGTATGCCT
1501 TCTATTGTGC TTTGTTTTTG CTGACTTTTC TGCACCCTGT TTCCTTTGGA
1551 TATTCACTTC TCTCAACCTC AAGATTGAGA CCGTGGTGGG TATGCTTCTC
1601 CACTTCCATA TGACCTTCAT GCTGTTCTGG AATATCACAT GCTACGAGGT
1651 CATCCTTCAC ACTACTTGTA AGCCAAGCAA ATGATACTGT AGATTGTACT
1701 GCCTTTATCT GCAGTCTTG GACCCTGTTT ATTCCCAGGG CCTCTGAACT
1751 GGTGTGCTGC ACTTGGATT CTAGCTTTGG GAGCCTGTTC CACCTACTCA
1801 GCTCTGCATT GAGCAGTATG GGCACATGCC CTGTGGACAG TTAGTGACG
1851 TTAATGAAC TACAGGAGAA AAGCAGTGAG CCACTTGTTC TGTGTGATT
1901 ATGGTACTTC ATTGCTCTTC CTTACCTCT AGTCACTTTC TATTGCTACC
1951 TGCCCTACAT TGCTCTCTGC CAAGGTCCCT CTCTCTCCCT GTTTTCCTTT
2001 TTTTTTTTTT TTTTTTTTTT TTTTGTAGAC GAGGACGGAG TCTTGCTCTG
2051 TCGCCCAGGT TGGAGTGCAG TGGCGCGATC TCGGCTCACT GCAACCTCCA
2101 CCTCCCGGGT TCAGCGGATT CTCTGCTC AGCCTCCCGA GTAGCTGGGA
2151 CTACAGGCGC GCGCGGCTAA TTTTATATT TTTAGTAGAG
2201 ACGGGGTTTC ACCATGCTGG CCAGGCTGGT CTCGAACCCC GACCTCGTGA
2251 TCCGCCCTCC TTAGCCTCCC AATCCTCTCT TAAAAAGTG ATAGCTCAGA
2301 AATATTGTGA AAAGCAAGGT TTTTATTTC TTTTGGCTCT GTCATTTTCA
2351 GAGGCAAAGA AGTTGGCCTG TAAAATAGAG TGCTAGAGCT CTTACGCCCC
2401 TCCCTTCTTT CCCAACTTCC TACTTCCTAG CCCTTTTATC AACTCCTAGA
2451 ATAGTTAAAG AGAGACACAT CTAGATGGGA TGAAAGGTGC CCTAAGCAGG
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2501 AGAACTGAA CAAAAGGCTA GAGGCATGGG CCAGGTAAAA ATTGGGCCTA
2551 GAGTGAAGAC TGTGCTGCCG TTAAGAGCTT TCGAGGAAGG AGTACTTACT
2601 CCCCAATGAT GATGAATGGA GAAATACTTT TCAGGGAGAA TTGAAGGGGT
2651 TAAAGTGTTA AATATGTTGC CTAGACAAGG GTTCTTTAAA GAAAGACAGC
2701 GCAACTTTGA ATGCTTTCTT ACTTGTTTTG TGACCTAATT TATGTGGAAG
2751 ATTGTTATTT CATTAGGATT TAGTAAAATT TTTTCTCTG ATTCTAACT
2801 TATTGTGAAA ATTGAGCTGT ACAGATATTC TTTTGATTTC AATTGGGAAC
2851 ATTTGGAAGA ACAACAGTCT TACTTGCCTG TACAATATAG AGACATATGA
2901 ATAGTCATAA CAGTTTTCAA CTTGTTCTTG TTTCTGTAA ACTATATTCC
2951 TAGAAACATA GTTTGAACAA CTTGGTCTTT GTTAGGCTTG TCAAATTGCC
3001 TTCATGGAAA AATAATCTAC AAAAGTATGG TTTAATTGAT TGTCTTACAT
3051 GATAATTTTC CCTGGCAACA ACTTAGTAAG TGATATATCT TTTTCTCTAA
3101 ATTGCTTAAA TACTGTGAAA TGCTCTGAC AAATTGGAAG TGTACCATTG
3151 GCATATTGT CTTCCTTTT ATGCATGATG GTAAATAAA AGCATGTTGT
3201 TCTGCTAAGA AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

Entry AF042181 from database EMBLNEW:
Homo sapiens testis-specific Y-encoded-like protein (TSPYL) mRNA,
partial cds.

Score = 3411, P = 6.9e-148, identities = 685/687

Entry HS938343 from database EMBL:
human STS WI-11947.
Score = 1195, P = 2.1e-46, identities = 273/299

Medline entries

98399864:
Murine and human TSPYL genes: novel members of the TSPY-SET-NAP1L1 family

Peptide information for frame 3

ORF from 99 bp to 1412 bp; peptide length: 438
Category: strong similarity to known protein
Classification: Differentiation/Development

```

1 MSGLDGVKRT TPLQTHSIII SDQVPSDQDA HQYLRRLRDS EATQVMAEPG
51 EGGSETVALP PSPPSEEGGV PQDPAGRGGT PQIRVVGGRG HVAIKAGQEE
101 QPPAEGGLAA ASVUMAADRS LKXGVQGGKE ALEICGAQRS ASELTAGAEA
151 EAEEVKTGKC ATVSAAVAER ESAEVVVKEG LAEKEVMEEQ MEVEEQPPEG
201 EEIEVAEEDR LEEEAAREEG PWPLHEALRM DPLEAIQLEL DTVNAQADRA
251 FQQLHEHKFGR MRRHYLFERN YIIQNIPGEW MTAFRNHQOL SAMIRGQDAE
301 MLRYITNLEV KELRHPRTGC KFXFFFRNP YFRNKLVKE YEVRSSGRV
351 SLSTPIIWRG GHEPQSFIRR NQDLICSFET WFSHSLPES DKIAEIIKED
401 LWPNPLOYYL LREGVRRARR RPLREPVEIP RPFQFQSG

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2d15, frame 3

TREMBL:AF042180_1 gene: "Tspyl1"; product: "testis-specific Y-encoded-like protein"; Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds., N = 1, Score = 1202, P = 3.1e-122

TREMBL:AB018264_1 gene: "KIAA0721"; product: "KIAA0721 protein"; Homo sapiens mRNA for KIAA0721 protein, partial cds., N = 1, Score = 798, P = 2e-79

TREMBL:AB015345_1 gene: "HRIHF2216"; Homo sapiens HRIHF2216 mRNA, partial cds., N = 1, Score = 570, P = 2.9e-55

>TREMBL:AF042180_1 gene: "Tspyl1"; product: "testis-specific Y-encoded-like protein"; Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.
Length = 379

HSPs:

Score = 1202 (180.3 bits), Expect = 3.1e-122, P = 3.1e-122
Identities = 258/377 (68%), Positives = 283/377 (75%)

```

Query:   62 SPPSEEGGVQDPAGR-----GGTPQIRVVGGRGHVAIKAGQEE--GQP-P---AEGLAA 110
          SP +EG D G GTP R + G G+ G P P EGL
Sbjct:   3 SPERDEGTPVPDSRGHCADTVSGTPDPRRPLLGEKAVTGEGRAGIVGSPAPRDVEGLVP 62

Query:  111 ASVVMADRSCLKK-GVQGGKALEICGAQRSASELTAGAEAEAEVKTGKCATVSAVAE 169
          V AA + V+G A+ + ++ T GAE++A +VKT + TV+AA
Sbjct:  63 QIRVAAARQGESPPSVRGPAAAVFVTPKYVEKAQETRGAESEQARDVKT-EPGTVA AAA-- 119

Query:  170 RESAEVVVKEGLAEKEVMEEQMEVEEQPPEGEEIEVAEEDRLEEEAREEEGWPWLHEALR 229
          E +EV EE MEVE Q P GEE+E+ E EA EE GPW L LR
Sbjct:  120 -EKSEVATPGS-----EEVMEVE-QKPAGEEMEMLEASGGVREAPPEAGPWHLGIDLR 170

Query:  230 MDPLEAIQLELDTVNAQADRAFAQLEHKFGRMRHYLERNNYIIQNIPGEFWMTAFRNHPQ 289
          +PLEAIQLELDTVNAQADRAFO LE KFGMRMRHYLERNNYIIQNIPGEFWMTAFRNHPQ
Sbjct:  171 RNPLEAIQLELDTVNAQADRAFOHLEQKFGMRMRHYLERNNYIIQNIPGEFWMTAFRNHPQ 230

Query:  290 LSAMIRGQDAEMLRITNLEVKELRHPRTGCKFKFFFRNPNPYFRNKLIVKEYEVRSSGRV 349
          LSAMIRG+DAEMLRIT+LEVKELRHP+TGCKFKFFFRNPNPYFRNKLIVKEYEVRSSGRV
Sbjct:  231 LSAMIRGRDAEMLRIVTSLEVKELRHPRTGCKFKFFFRNPNPYFRNKLIVKEYEVRSSGRV 290

Query:  350 VSLSTPIIWRRGHEPQSFIRRNQDLICSFFTWFSHDLSLPESDKIAEIIKEDLWPNPLQYY 409
          VSLSTPIIWRRGHEPQSFIRRNQDLICSFFTWFSHDLSLPESD+IAEIIKEDLWPNPLQYY
Sbjct:  291 VSLSTPIIWRRGHEPQSFIRRNQDLICSFFTWFSHDLSLPESDRIAEIIKEDLWPNPLQYY 350

Query:  410 LLREGVRRARRRPLREPVEIPRPFQSG 438
          L REG+RR RRRP+REPVEIPRPFQSG
Sbjct:  351 LCREGIRRRRRPIREPVEIPRPFQSG 379

```

Pedant information for DKFZphfbr2_2d15, frame 3

Report for DKFZphfbr2_2d15.3

```

[LENGTH]      438
[MW]           49307.65
[pI]           5.36
[HOMOL]        TREMBL:AF042180_1 gene: "Tspyl1"; product: "testis-specific Y-encoded-like
protein"; Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds. 1e-
107
[FUNCAT]       06.10 assembly of protein complexes [S. cerevisiae, YKR048c] 1e-07
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YKR048c] 1e-07
[FUNCAT]       03.04 budding, cell polarity and filament formation [S. cerevisiae, YKR048c]
1e-07
[FUNCAT]       09.13 biogenesis of chromosome structure [S. cerevisiae, YKR048c] 1e-07
[FUNCAT]       30.10 nuclear organization [S. cerevisiae, YKR048c] 1e-07
[BLOCKS]       BL00376F
[PIRKW]        nucleus 6e-39
[PIRKW]        DNA binding 3e-06
[PIRKW]        phosphoprotein 6e-39
[PIRKW]        alternative splicing 6e-39
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY 22.83 %

```

```

SEQ  MSGLDGVKRTTPLQTHSIIISDQVPSDQDAHQYLRLRDQSEATQVMAEPGEGGSETVALP
SEG  .....x
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  PSPPEEGGVQDPAGRGTPQIRVVGGRGHVAIKAGQEEGQPPAEGLAAASVVMADRS
SEG  xxxxxxxx
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  LKKGVQGGKALEICGAQRSASELTAGAEAEAEVKTGKCATVSAVAERESAIEVVVKEG
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  LAEKEVMEEQMEVEEQPPEGEEIEVAEEDRLEEEAREEEGWPWLHEALRMDPLEAIQLEL
SEG  .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  DTVNAQADRAFAQLEHKFGRMRHYLERNNYIIQNIPGEFWMTAFRNHPQLSAMIRGQDAE
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  MLRYITNLEVKELRHPRTGCKFKFFFRNPNPYFRNKLIVKEYEVRSSGRVSVSLSTPIIWR

```

```
SEG .....
PRD hhhhhhhhhhhhhccccceeeeeccccccchhhhhccccccccccccceeeec

SEQ GHEPQSFIRRNDLICSFFTWFSDSLPEKDIAEIIKEDLWPNPLQYYLLREGVRRARR
SEG .....XXXXXXXXXX
PRD cccchhhhhccccceeeeeccccccchhhhhhhccccceeeeeccccchhhh

SEQ RPLREPVEIPRPFQSG
SEG xxxxxxxx.....
PRD hcccccccccccccccc
```

(No Prosite data available for DKFZphfbr2_2d15.3)

(No Pfam data available for DKFZphfbr2_2d15.3)

DKFZphfbr2_2d17

group: transmembrane proteins

DKFZphfbr2_2d17 encodes a novel 292 amino acid protein with similarity to a C.elegans hypothetical protein.

One transmembrane region is predicted for the protein.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to C.elegans hypothetical protein

TRANSMEMBRANE 1

Sequenced by Qiagen

Locus: unknown

Insert length: 1009 bp

Poly A stretch at pos. 990, polyadenylation signal at pos. 969

```

1 TGGGCCTGTG GCTGGGGGCA GAGCTCAGAC TGTCTTCTGA AGATTGATGT
51 CTATTTCCTT GAGCTCTTTA ATTTTGTTCG CAATTGGGAT AAACATGGCA
101 CAAATCCAGC AGGGAGGTCC AGATGAAAAA GAAAAGACTA CCGCACTGAA
151 AGATTTATTA TCTAGGATAG ATTTGGATGA ACTAATGAAA AAAGATGAAC
201 CGCCTCTTGA TTTTCCTGAT ACCCTGGAAG GATTGAATA TGCTTTTAAT
251 GAAAAGGGAC AGTTAAGACA CATAAAAACT GGGGAACCAT TTCTTTTAA
301 CTACCGGGAA GATTACACA GATGGAACCA GAAAAGATAC GAGGCTCTAG
351 GAGAGATCAT CACGAAGTAT GTATATGAGC TCCTGGAAAA GGATTGTAAT
401 TTGAAAAAAG TATCTATTCC AGTAGATGCC ACTGAGAGTG AACCAAAGAG
451 TTTTATCTTT ATGAGTGAGG ATGCTTTGAC AAATCCACAG AAAGTATGG
501 TTTTAATTCA TGGTAGTGGT GTTGTGAGG CAGGGCAGTG GGCTAGAAGA
551 CTTATTATAA ATGAAGATCT GGACAGTGGC ACACAGATAC CGTTTATTAA
601 AAGAGCTGTG GCTGAAGGAT ATGGAGTAAT AGTACTAAAT CCCAATGAAA
651 ACTATATTGA AGTAGAAAAG CCGAAGATAC ACGTACAGTC ATCATCTGAT
701 AGTTCAGATG AACGACGAGA AAAACGGGAA AGAAAAGATA AAGTTTCTAA
751 AGTAACAAAG AAGCGACGTG ATTTCTATGA GAAGTATCGT AACCCCAAAA
801 GAGAAAAAGA AATGATGCAA TTGTATATCA GAGTGAGTGA GATCACTACT
851 TTCTTTTACT ATTTTCTTTA CCTTGTATAT ATTTTATTAT ATGTAGATTG
901 TTTTGTTTTT CTTCAAGAAT ATTAATTTCT TTATTGTGTA TCATTATTT
951 CCCATGGTGC TCTACTTGGA TTAAATGGGT TTTTAAATTC AAAAAAATAA
1001 AAAAAAATAA

```

BLAST Results

Entry I89937 from database EMBL:
Sequence 11 from patent US 5723315.
Score = 1083, P = 2.2e-42, identities = 223/231

Entry I89938 from database EMBL:
Sequence 12 from patent US 5723315.
Score = 875, P = 7.4e-33, identities = 175/175

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 47 bp to 922 bp; peptide length: 292
Category: similarity to unknown protein
Classification: unset

1 MSISLSSLIL LPIWINMAQI QQGGPDEKEK TTALKDLLSR IDLDELMKKD

```

51 EPPLDFPDTL EGFEYAFNEK QLRHIKTGE PFVFNREDL HRWNQKRYEA
101 LGEIITKYVY ELLEKDCNLK KVSIPVDATE SEPKSFIEMS EDALTNPQKL
151 MVLINGSGVV RAGQWARRLI INEDLDSGTQ IPFIKRAVAE GYGIVVLNPN
201 ENYIEVEKPK IHVQSSSDSS DEPAEKREK DKVSKVTKR RDFYEKYNRP
251 QREKEMMQLY IRVSEITTFLL YFFLYLVYIL LYVDCFVFLQ EY

```

BLASTP hits

Entry S67436 from database PIR:
 hypothetical protein - fission yeast (*Schizosaccharomyces pombe*)
 Length = 266
 Score = 112 (39.4 bits), Expect = 0.00037, P = 0.00037
 Identities = 33/147 (22%), Positives = 69/147 (46%)

Entry CEY75B8A.12 from database TREMBLNEW:
 gene: "Y75B8A.31"; *Caenorhabditis elegans* cosmid Y75B8A
 Score = 327, P = 1.5e-29, identities = 72/140, positives = 93/140

Alert BLASTP hits for DKFZphfbr2_2d17, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2d17, frame 2

Report for DKFZphfbr2_2d17.2

```

[LENGTH]      292
[MW]           34260.50
[pI]           5.50
[HOMOL]        TREMBLNEW:AF064782_1 product: "unknown"; Mus musculus clone pEN87 unknown mRNA,
partial cds. 1e-119
[KW]           SIGNAL PEPTIDE 19
[KW]           TRANSMEMBRANE 1
[KW]           LOW_COMPLEXITY 10.96 %

```

```

SEQ  MSISLSSLILLPIWINMAQIQGGPDEKEKTTALKDLLSRIDLDELMKKDEPPLDFPDTL
SEG  .XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD  ccchhhhhhhchhhhhhhccccccccccccchhhhhhhhhhhhhchhhhhhhcccccccccc
MEM  .....

SEQ  EGFEYAFNEKGQLRHIKTGEPFVFNREDLHRWNQKRYEALGEIITKYVYELLEKDCNLK
SEG  .....
PRD  hhhhhhccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM  .....

SEQ  KVSIPVDATESEPKSFIEMSEDALTNPQKLMVLINGSGVVVRAGQWARRLIINEDLDSGTQ
SEG  .....
PRD  eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeccccchhhhhcccccccccccccccccc
MEM  .....

SEQ  IPFIKRAVAEGYGIVVLNPNENYIEVEKPKIHVQSSSDSSDEPAEKREKDKVSKVTKR
SEG  .....
PRD  chhhhhhhccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhh
MEM  .....

SEQ  RDFYEKYNRPQREKEMMQLYIRVSEITTFLLYFFLYLVYILLYVDCFVFLQY
SEG  .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD  hhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

```

(No Prosite data available for DKFZphfbr2_2d17.2)

(No Pfam data available for DKFZphfbr2_2d17.2)

DKFZphfbr2_2d20

group: brain derived

DKFZphfbr2_2d20 encodes a novel 197 amino acid protein with similarity to *Synechocystis* sp. P74594 hypothetical 32.8 kD protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to *Synechocystis* sp. (PCC 6803)

complete cDNA, complete cds, EST hits
potential start at bp 67 matches kozak consensus ANCatgG

Sequenced by Qiagen

Locus: unknown

Insert length: 1787 bp
Poly A stretch at pos. 1768, polyadenylation signal at pos. 1743

```
1 TGGGGCGGCC CCGGGCCGAA CATGGAGGAG CTGCTGAGGC GCGAGCTGGG
51 CTGCAGCTCT GTCAGGGCCA CGGGCCACTC GGGGGCGCGG TGCATCAGCC
101 AGGGCCGGAG CTACGACACG GATCAAGGAC GAGTGTTCGT GAAAGTGAAC
151 CCCAAGGCGG AGGCCAGAAG AATGTTTGAA GGTGAGATGG CAAGTTTAAC
201 TGCCATCCTG AAAACAAACA CGGTGAAAGT GCCCAAGCCC ATCAAGGTTT
251 TGGATGCCCC AGGCGGCGGG AGCGTGCTGG TGATGGAGCA CATGGACATG
301 AGGCATCTGA GCAGTCATGC TGCAAAGCTT GGAGCCAGC TGGCCGATTT
351 ACACCTTGAT AACAGAAGC TTGGAGAGAT GCGCCTGAAG GAGGCGGGCA
401 CAGTGTGGAG AGGAGGTGGG CAGGAGGAAC GGCCCTTTGT GGCCCGGTTT
451 GGATTTGACG TGGTGACGTG CTGTGGATAC CTCCCCAGG TGAATGACTG
501 GCAGGAGGAC TGGGTGCTGT TCTATGCCCC GCAGCGCATT CAGCCCCAGA
551 TGGACATGGT GGAGAAGGAG TCTGGGGACA GGGAGGCCCT CCAGCTTTGG
601 TCTGCTCTGC AGTAAAAGAT CCCTGACCTG TTCCGTGACC TGGAGATCAT
651 CCCAGCCTTA CTCCACGGGG ACCTCTGGGG TGGAACGTA GCAGAGGATT
701 CCTCTGGGCC GGTGATTTT GACCCAGCTT CTTTCTACGG CCACTCGGAA
751 TATGAGCTGG CAATAGCTGG CATGTTTGGG GGCTTTAGCA GCTCCTTTTA
801 CTCGCCTTAC CACGGCAAAA TCCCCAAGGC CCCAGGATTG GAGAAGCGCC
851 TTCACTTGTA TCAGCTCTTT CACTACTTGA ACCACTGGAA TCATTTTGA
901 TCGGGGTACA GAGGATCCTC CCTGAACATC ATGAGGAATC TGGTCAAGTG
951 AGCGGGCCTT ACTCTGGAAG GAGGTCTCAG AGGTTTCTCC ACAGTCTCT
1001 TCTGGGCAAA TTCTTGTTT TCACATGCC GGAAGTCTT AAGACCAATG
1051 CAGTAGCTTA TTTCCAAGCC TTGCAAAGTA TATAATATCT AAGAGGAAAG
1101 GTTTGTGTCG CCCAGCGTTG TCCACTTTGT GGGGCTTTGT AGGTAGACGG
1151 AGCCACACTA CAGGCAGGGT ATGAGCAGAG GGATGTATGG AGTGTGGGCG
1201 ACTCTGAGCG TCACTGCTGC TGCAAGGTGG GGAACTGTA AGTGAACCCC
1251 TGTGGGTGCG GGGGAGGTA TCCGGTGCGC AGGGAGGTGG CCAGCGCCCC
1301 CGGGCACTGC TGCTCATAGG TACCTTTCCG CTGCTCTCTC CCTGCTCTCC
1351 TGTGCAGGAA TGCTCTGAG CTGTTACAGT TGATGCTTCT TGGTTGGCAA
1401 GACTTGGGTG TAGACATGAA ACCACCTTAC TAAAAGCGTC TTAATATGAC
1451 CAATTCCAGA ATCAAGCGTA TTCCGTTTTT CTCCTGCATG ATCCCTGGGC
1501 CCTCCCGCAG GCTGAGCAAG TCTGTAAACT GATTCTGGGA GAAACCAAGC
1551 TGCTGGCCGT AGGATGTCCT TGGGTACATC CAGGAGTCTT CATTGCTTCT
1601 GTTATTACCC CGTCTCTCTT GCCATTTTCT ACAGCTTGCT GAGTTGTCAT
1651 TCCTTTGCAA CATTAATAAATA CATGCTGAAC TCATATTTTT CCTTCTTCA
1701 CTGTTGTAGT AAAGAGACAT ATTTTCATGAA TGGCATTGAT GCTAATAAAC
1751 CCTTTGCCCA AAAATTTGAA AAAAAAAAAA AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

```

1 MEELLRRELG CSSVRATGHS GGCISQGRS YDTDQGRV FV KVPKAEARR
51 MFEGEMASLT AILTKNTVKV PKPIKVLDA GGSVLVMEH MDMRHLSSHA
101 AKLGAQLADL LHNKKNLGM RLKEAGTVWR GGSQEERFV ARFGEDVUTC
151 CGYLPQVNDW QEDWVVFYAR QRIQPMDMV EKESGDREAL QLSWALQ

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2d20, frame 1

No Alert BLASTP hits found

Pedant information for DKF2phfbr2 2d20, frame 1

Report for DKFZphfbr2 2d20.1

```
[LENGTH]          197
[MW]               21963.25
[pI]               6.96
[HOMOL]            PIR:S76790 hypothetical protein - Synechocystis sp. (strain PCC 6803) 9e-12

[SUPFAM]           hypothetical protein b1725 1e-06
[PROSITE]          LEUCINE ZIPPER 1
[PROSITE]          MYRISTYL 2
[PROSITE]          GLYCOSAMINOGLYCAN 1
[PROSITE]          PKC_PHOSPHO_SITE 2
[KW]               Alpha Beta
```

```

SEQ      MEELLRLRELGCSSVRATGHSGGGCISQGRSYDTDQGRVFKVKNPKAEARRMFEGEMASLT
PRD      ccchhhhhccccceeeccccceeeccccccceeeeeeccchhhhhhhhhhhhhhhhh

SEQ      AILKTNTVKVPKPIKVLDPAGGGSVLVMEHMDMRHLSSHAAKLGAQLADLHLDNKKLGEM
PRD      hhhhhhheeeccccccccceeeccccceeeccccccccchhhhhhhhhhhhhhhccccchhh

SEQ      RLKEAGTVWRGGGQEERPFVARFGFDVVTCCGYLPQVNDWQEDWVVFYARQRIQPQMDMV
PRD      hhhhhccccccccccccceccccceeeccccccccccccchhhhhhhhhhhhhhhhhhhhh

SEQ      EKESGDREALQLWSALO
PRD      hhccchhhhhhhhhccccc

```

Prosites for DKFZphfbr2 2d20.1

PS00002	20->24	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	13->16	PKC_PHOSPHO_SITE	PDOC00005
PS00005	67->70	PKC_PHOSPHO_SITE	PDOC00005
PS00008	22->28	MYRISTYL	PDOC00008
PS00008	104->110	MYRISTYL	PDOC00008
PS00029	96->118	LEUCINE ZIPPER	PDOC00029

(No Pfam data available for DKFZphfbr2 2d20.1)

DKF2phfbr2_2g18

group: brain derived

DKF2phfbr2_2g18 encodes a novel 229 amino acid protein with partial similarity to the humane dJ30M3.2 gene product.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

J30M3.2 extension of genmodel

complete cDNA, complete cds, EST hits
(mouse ESTs with >90% Identities)

Sequenced by Qiagen

Locus: /map="6p22.1-22"

Insert length: 2444 bp

Poly A stretch at pos. 2425, no polyadenylation signal found

```
1 TGGTCGAGGG TCGACGGTAT CGATAAGTTT TTTTTTTTTT TTTTTTTTTT
51 TGGAAAGCAA GGATCACACT TCCCCCTCCC TGTCCTTAA TCCCTTTTCT
101 AAAAAGGGGG GAAAATCCGG ATGGATTTTA GGGATTGGTC TGGTGTGACG
151 TGTGTCTTAT TGCACACCTA AATCCTGATT ATAGGCTTTT CATTTCTCCG
201 CAAAGCCTTT ATTTTGGCAG TTAAGCCAAA TGTGTTTTCC AGAAAGTTAG
251 TTATTTTCTC CTCTTTCTTT CTTTCTTTT CTCCCTTTT CCCGTCTGAC
301 CCCAAACGTT ATTGTCCAAA CATGACTGGA CAGCAGCTTT TGTTCCTTGA
351 CCCTGTAATA TGACAGTCTG CTAATATTGA CAGAAGGTGC AGTTTTTGGG
401 TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA AAAAAATGA
451 CTTGTTTCTG TTGTACTTGA GTCTTAAGAA AAAGTGCCCA TAGTTTAGTG
501 ACAATTTCCA AAGGCTTTAG TACCACCTGT ATTTCAAAAT GGGGGACCCA
551 AACTCCCGGA AGAAACAAGC TCTGAACAGA CTACGTGCTC AGCTTAGAAA
601 GAAAAAAGAA TCTCTAGCTG ACCAGTTTGA CTTCAAGATG TATATTGCCT
651 TTGTATTCAA GGAGAAGAAG AAAAAGTCAG CACTTTTTGA AGTGTCTGAG
701 GTTATACCAG TCATGACAAA TAATTATGAA GAAAATATCC TGAAAGGTGT
751 GCGAGATTCC AGCTATTCTT TGGAAAGTTC CCTAGAGCTT TTACAGAAGG
801 ATGTGGTACA GCTCCATGCT CCTCGATATC AGTCTATGAG AAGGGATGTA
851 ATTGGCTGTA CTCAGGAGAT GGATTTTCATT CTTTGGCCTC GGAATGATAT
901 TGAAAAAATC GTCTGTCTCC TGTTTTCTAG GTGGAAGAA TCTGATGAGC
951 CTTTTAGGCC TGTTTCAGGC AAATTTGAGT TTCATCATGG TGAATATGAA
1001 AAACAGTTTC TGCATGTACT GAGCCGCAAG GACAAGACTG GAATCGTTGT
1051 CAACATCCTT AACCAGTCAG TGTTCCTCTT CATTGACAGA CAGCACTTGC
1101 AGACTCCAAA AAACAAGCTT ACAATCTTCA AGTTATGCAG CATCTGCCTC
1151 TACCTGCCAC AGGAACAGCT CACCCACTGG GCAGTTGGCA CCATAGAGGA
1201 TCACCTCCGT CCTTATATGC CAGAGTAGAG TACTGACCAG CAAAATGGAG
1251 AAGATCAGAG AATGCAGCAG CAGTTTTTTT TCTTGTTTTT TTACCACTTT
1301 ATTCTTTTCA AGTTTAAAGA AAATGGACTC ATGCACAGAA CACTATGCAT
1351 TTTGAACTTT GTTCATCCTG GATTTTTTTA AATCATTTTT ATCTCAGAAC
1401 TTAACAACAA ATTAGATGTC GTGCACGGAC TGTGTGAAAG AAGATGCTTT
1451 GCATATTTGC TGCATGTCAT CAGTATCTTA CTAAAAATGT GAAATGAAAG
1501 CACTATTGTA CACTGAAATC CTTAAATGTA TCTGAAAGCA CAAGGTGATA
1551 CTCATTTTTT TGGTCTTCCC ATTTGTGCTG GTTTTGCCTT CTTTGACATC
1601 TGTCATCAGT ATTTAGAGGG TGAGAAGTGA ATGTAACAGG TATAAATAAC
1651 ATTTTAAAAA ACAATAACTT TGCTATAATC ACAGTTGTTC CAGAGCACTG
1701 TCAGATACAT TCTAATGACC AGAAGTGGTT TAAAAAAGA AAATACAACC
1751 ATGGGAAAGA AATCTTAAAT GAAAAACGCA TCTCATGTGA GGCATTTTTG
1801 CCTCATATTT TACTGGGCCA TGTTTGTTC CTGGTACTCA TGTATTTTTT
1851 TTTTTCAG AGTCTTTTCC CCAAGTTGCT ATTGTAACAG TATTCTGCTG
1901 CGTGTGGATG CAGTTATACA CATTAAAGCA GATCTGGAGT CTGAAGTAGC
1951 TATAAAGCAG CTATAAACA GAAATACATG CATAGCTGCA GAAACCATGA
2001 TAGGTAGAGG ACTTTTCTTT TGGTTTGTGTT TGTTTGTGTT TGTTTGTGTT
2051 TTTGGTTTTA CAGAGAAGAG ATTTTATTA CAAAGAAAAA AATTCCAGTG
2101 AATTGTGCAG AAATGCTGGT TTTTACACCA TCCTAAAGAA AAACCTTTACA
2151 AGGGTGTTTT GGAGTAGAAA AAAGGTATA AAGTTGGAAT CTTAAATTGT
2201 AAAATTAACC ATTGAGTGTC AAAGTTCTAA AAGCAGAACT CATTTCTGTC
2251 AATGAACATA AGGAAAGACT ACTGTATAGG TTTTTTTTTT TCTCCTTTTA
2301 AATGAAGAAA AGCTTGCTT AAGGGTTGCA TACTTTTATT GGAGTAAATC
2351 TGAATGATCC TACTCCTTTG GAGTAAGACT AGTCCTTACC AGTTTCCAAT
2401 TGTATTTAGC TTCTGTTGGA ATTTGAAAAA AAAAAAAAAA AAAA
```

BLAST Results

Entry HS338352 from database EMBL:
human STS EST171398.
Score = 1747, P = 3.0e-74, identities = 359/365

Entry HS447255 from database EMBL:
human STS SHGC-10143.
Score = 1717, P = 6.5e-73, identities = 365/383

Entry HS30M3 from database EMBLNEW:
Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands.
Score = 6646, P = 0.0e+00, identities = 1344/1355

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 539 bp to 1225 bp; peptide length: 229
Category: putative protein

```
1 MGDPNRKKQ ALNRLRAQLR KKKESLADQF DFKMYIAFVF KEKKKKSALF
51 EVSEVIPVMT NNYEENILKG VRDSSYSLES SLELLQKDVV QLHAPRYQSM
101 RRDVIGCTQE MDFILWPRND IEKIVCLLFS RWKESDEFFR PVQAKFEFHH
151 GDYEKQFLHV LSRKDKTGIV VNNPNQSVFL FIDRQHLQTP KNKATIFKLC
201 SICLYLPQEQ LTHWAVGTIE DHLRPYMPE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phfbr2_2g18, frame 2

TREMBLNEW:HS30M3_2 gene: "dJ30M3.2"; product: "dJ30M3.2 (novel protein)"; Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands., N = 1, Score = 470, P = 1.1e-44

>TREMBLNEW:HS30M3_2 gene: "dJ30M3.2"; product: "dJ30M3.2 (novel protein)"; Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands.
Length = 86

HSPs:

Score = 470 (70.5 bits), Expect = 1.1e-44, P = 1.1e-44
Identities = 86/86 (100%), Positives = 86/86 (100%)

```
Query: 144 AKFEFHG DY EKQFLHVL SRKDKTGIV VNNPNQSVFL FIDRQHLQTPKNKATIFKLCSIC 203
      AKFEFHG DY EKQFLHVL SRKDKTGIV VNNPNQSVFL FIDRQHLQTPKNKATIFKLCSIC
Sbjct: 1 AKFEFHG DY EKQFLHVL SRKDKTGIV VNNPNQSVFL FIDRQHLQTPKNKATIFKLCSIC 60

Query: 204 LYLPQEQ LTHWAVGTIEDHLRPYMPE 229
      LYLPQEQ LTHWAVGTIEDHLRPYMPE
Sbjct: 61 LYLPQEQ LTHWAVGTIEDHLRPYMPE 86
```

Pedant information for DKF2phfbr2_2g18, frame 2

Report for DKF2phfbr2_2g18.2

```
SEQ      MGDPNRSKKQALNRLRAQLRKKEESLADQDFDKMYIAFVFKEKKESSALFEVSEVIPVMT  
SEG      .....  
PRD      cccccchhhhhhhhhhcccccccccchhhhhhhhhhhhhhhhhhhheeeec
```

```
SEQ      NNYEENILKGVRDSSYSLESSLELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRND  
SEG      .....xxxxxxxxx.....  
PRD      cchhhhhhhccccccccccchhhhhhhhhhhhhccccccccceeeeecccccceccccch
```

```
SEQ      IEKIVCLLSRWKESDEPFRPVQAKFEFHHG DYEQFLHVLSRKDKTGIVNNPNQSVFL  
SEG      .....  
PRD      hhhhhhhhhhhccccccccccccccccccchhhhhhhhhhhccccceeeeccccceeee
```

```
SEQ      FIDRQH LQT PKN KATIFKLCSICLYLPQEQLTHWAVGTIEDHLRPYMP E  
SEG      .....  
PRD      eeeeeccccccccceeeeeeeeeeeeeccccccccceeecccccccccc
```

PS000001	175->179	ASN_GLYCOSYLATION	PDOC000001
PS000004	22->26	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	44->48	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	6->9	PKC_PHOSPHO_SITE	PDOC000005
PS000005	99->102	PKC_PHOSPHO_SITE	PDOC000005
PS000005	162->165	PKC_PHOSPHO_SITE	PDOC000005
PS000005	189->192	PKC_PHOSPHO_SITE	PDOC000005
PS000006	25->29	CK2_PHOSPHO_SITE	PDOC000006
PS000006	80->84	CK2_PHOSPHO_SITE	PDOC000006
PS000006	162->166	CK2_PHOSPHO_SITE	PDOC000006
PS000006	218->222	CK2_PHOSPHO_SITE	PDOC000006
PS000007	69->77	TYR_PHOSPHO_SITE	PDOC000007
PS000008	70->76	MYRISTYL	PDOC000008
PS000008	168->174	MYRISTYL	PDOC000008

227

DKFZphfbr2_2h1

group: brain derived

DKFZphfbr2_2h1 encodes a novel 180 amino acid protein with weak similarity to C.elegans D2007.4 protein

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to C.elegans D2007.4 protein

CpG island in 5' region, complete cDNA

Sequenced by Qiagen

Locus: unknown

Insert length: 957 bp

Poly A stretch at pos. 939, polyadenylation signal at pos. 916

```
1 GGGGGTCCCT GACTTTATAT GGCTGCTCCT GGCGAGCGAC TGAGTCGTCC
51 GTGAGGAAAA ACAGCGGAGG CTTTCCGAG ATCGTCTCAG CGATGCCGCT
101 TCGGTCCGCG TTTTGGGGGT TGTTCTCGGT TTGCAGGAAC CCTGGGTGCA
151 GGTTCCGAGC CCGTCAACC AGCTCCGAGC CGGCAGCGAA ACCTGAAGTG
201 GACCCTGTGG AAAATGAAGC TGTCGCCCA GAATTCACCA ACCGGAACCC
251 CCGGAACCTG GAGCTTTTGT CTGTAGCCAG GAAAGAGCGG GGCTGGCGGA
301 CGGTGTTTCC CTCCCGTGAG TTCTGGCACA GGTGCGAGT TATAAGGACT
351 CAGCATCATG TAGAAGCACT TGTGGAGCAT CAGAATGGCA AGGTTGTGGT
401 TTCGGCCCTC ACTCGTGAGT GGGCTATTAA AAAGCACCTT TATAGTACCA
451 GAAATGTGGT GGCTTGTGAG AGTATAGGAC GAGTGTGCGC ACAGAGATGC
501 TTAGAGGCGG GAATCAACTT CATGGTCTAC CAACCAACCC CGTGGGAGGC
551 AGCCTCAGAC TCGATGAAAC GACTACAAAG TGCCATGACA GAAGGTGGTG
601 TGGTTCTACG GGAACCTCAG AGAATCTATG AATAAATGGA AGCATTAAAT
651 GTTTTGAACA TGTAATATA AATCTGTCAG CCACTACAGC CATCAAAGA
701 GAGCATCTGG AAGAACAGCC AGCTTGGAAG TTTTACAGCA ATAATGTTGC
751 AGTGGAAATAT TATTTGTAGT TAAGGTCAAT CTCCTCCCTT TTCTGTTTT
801 TTAAATCAAG AACTACGTTT TGCCCTCTC TTGGGCTTCA GAAGCATCTA
851 AGAAAAGCAG CATCAATTA TAATTAACCT TCAAAGGGCA AGTCAGAAGT
901 TGTTTATAAA TTACAAAATA AAGGCATATT ATGAACCTTA AAAAAAAAAA
951 AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 93 bp to 632 bp; peptide length: 180
Category: similarity to known protein
Classification: unset

```
1 MALRSRFWGL FSVCRNPGCR FAALSTSSEP AAKPEVDPVE NEAVAPEFTN
51 RNFRNLELLS VARKERGWRT VFPSREFWHR LRVIRTQHHV EALVEHQNGK
101 VVVSASTREW AIKKHLYSTR NVVACESIGR VLAQRCLFAG INFMVYQPTP
151 WEAASDSMKR LQSAMTEGGV VLREPQRIYE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2h1, frame 3

PIR:S44789 D2007.4 protein - *Caenorhabditis elegans*, N = 1, Score = 194, P = 2e-15

PIR:JC5753 ribosomal protein L18 - *Vibrio proteolyticus*, N = 1, Score = 121, P = 1.1e-07

>PIR:S44789 D2007.4 protein - *Caenorhabditis elegans*
Length = 170

HSPs:

Score = 194 (29.1 bits), Expect = 2.0e-15, P = 2.0e-15
Identities = 51/134 (38%), Positives = 78/134 (58%)

Query: 48 FTNRNPRNLELLSVARKERGWRVFP--SREFWHRLRVIRTQHHVEA-LVEHQNGKVVVS 104
F NRNPRN EL+ G++ +R + +++ ++ + H E LV +Q+G VV+S
Sbjct: 9 FVNRNPRNNELMGRQAPNTGYQFEKDRAARSYIYKVELVEGKSHREGRLVHYQDG-VVIS 67

Query: 105 ASTREWAIAKKHLYSTRNVVACESIGRVLAQRCL EAGINFMVYQPTPWEAASDSMKRLQ-- 162
AST+E +I LYS + A +IGRVLA RCL++GI+F + T EA S +
Sbjct: 68 ASTKEPSIASQLYSKTDTSAALNIGRVLALRCLQSGIH FAMPGATK-EAIEKSQHQT HFF 126

Query: 163 SAMTEGGVVLREPQRI 178
A+ E G+ L+EP +
Sbjct: 127 KALEEEGLTLKEPAHV 142

Pedant information for DKFZphfbr2_2h1, frame 3

Report for DKFZphfbr2_2h1.3

[LENGTH] 180
[MW] 20576.57
[pI] 9.63
[HOMOL] PIR:S44789 D2007.4 protein - *Caenorhabditis elegans* 2e-13
[FUNCAT] j mrna translation and ribosome biogenesis [H. influenzae, HI0794] 2e-04
[SUPFAM] Escherichia coli ribosomal protein L18 8e-06
[KW] Alpha_Beta

SEQ MALRSRFWGLFSVCRNPGCRFAALSTSSEPAAKPEVDPVENEAVAPEFTNRNPRNLELLS
PRD cccccceeeeeccccceeeeeccccccccccccccccccccccccccccccccchhhh

SEQ VARKERGWRVFP SREFWHRLRVIRTQHHVEALVEHQNGKVVVSASTREWAIAKKHLYSTR
PRD hhhhccccccccchhhhhhhhhccccchhhhhhhhhccccceeeechhhhhhhhhhhcc

SEQ NVVACESIGRVLAQRCL EAGINFMVYQPTPWEAASDSMKRLQSAMTEGGVVLREPQRIYE
PRD ccceehhhhhhhhhhhhhccccceeeccccchhhhhhhhhhhhhhhhhccceeeccccccc

(No Prosite data available for DKFZphfbr2_2h1.3)

(No Pfam data available for DKFZphfbr2_2h1.3)

DKFZphfbr2_2h10

group: brain derived

DKFZphfbr2_2h10 encodes a novel 220 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 2176 bp

Poly A stretch at pos. 2161, polyadenylation signal at pos. 2143

```
1 TGGGGAGTAT TCTAATTATA TTTTATATTT AATAAATTAT TTTTCTATTT
51 CTTTGTTTATA TTAAGTTGCA CACTTGTTTC TTTTATCCAG AAAGTTTAGT
101 ATAATAAAAA TAGTTTTAAG ATTAAGTGTG AATGTAAAGG AAAAGTATTA
151 TTAATTATTT CAGGAAATTG CAAGACCTAA CATGGCTGAA AGAGAAACAG
201 AAACATCAAA TTCTGAAAGT AAACAAGATA AAGCTGCTTC TTCAAAAGAA
251 AAAAATGGAT GTAATGCAAA TTCAATTTGAA GGCTCATCAA CAACAAAAAG
301 TGAAGAAAGC ATAACAGTTT CAGATAAGGA AAATGAAACC TGTCTGCAG
351 ACCAGGAAAC TGGCTCAAAA AACATCGTCA GTTGTGATTC AAATATTGGT
401 GCAGATAAAG TGGAAAAGAA AAAACAAATA CAACACGTTT GTCAGGAAAT
451 GGAGTTGAAG ATGTGCCAGA GTTCAGAAAA CATAATCTTA TCTGATCAGA
501 TTAAAGATCA CAACTCCAGT GAAGCCAGAT TTTCTTCAAA GAATATTAAG
551 GATTTGCGAT TAGCATCAGA TAATGTAAGC ATTGATCAGT TTTTGAGAAA
601 AAGACATGAA CCTGAATCTG TTAGTTCTGA TGTAGCGAG CAAGGCAGTA
651 TTCATTTGGA ACCTCTGACT CCATCCGAGG TACTTGAGTA TGAAGCCACA
701 GAGATTCTTC AGAAAGGTAG TGGTGATCCT TCAGCCAAGA CTGATGAAGT
751 AGTGTCTGAT CAAACAGATG ACATTCCCTGG AGGAAATAAC CCTAGCACAA
801 CAGAGGCAAC AGTAGACCTG GAAGATGAAA AAGAAAGAAG TTGAATTAG
851 TCATTTTAAAG TTTCAAGTGA CCAACGATAA GGGCATTGGG AACAGTGCTA
901 TCAGGTGAGC TCAGTGCTGC TGTGTAGGT TCAGAAATGG AAATATGTAA
951 GGGAGGTCAC ACATACACTT TACCTGTATG TTCAACCTAT GTTATCAAAC
1001 AAACCAATTC ACCAATAATA GCATGATTAG TAGGGATTCC CAAAAAGTTT
1051 TTAATAAACAC GAACAGGATT TTAATGATAA TTAATTTGTC AGTGGAAAGG
1101 TCTCATTTAA TGGTTTTCAG GGAATGGGA TTTGGTTGCT GACATGAATT
1151 GATGATATTA GTAATATTTA TAAAGCCTTT CAACTTCCA TCAATCCTAA
1201 GCTAAAAATC TTTATTACCT GTATATCCTT TTCAGTTAAC TGAGAGGAAG
1251 GGATTGGGAA ACCATGTACT TTTGGGGAGT AATTGATTAA AAACATGGC
1301 TGATTGGCAT TGTTAATGAA GGCTTTATTT GTGAGGATGA TGTGGTAA
1351 TGGAGCATGC TTAGAGTACT AAATGATCT AATGAGAATT TGGATGAACA
1401 TAACTTAAT TTTGGATTTA ATATAACATT CCAGTCAGAC GCATGTAAAC
1451 AGAATATTTG AATCTTTGTA CCTCCATACA AGTGTAGCC TGCCAGGCTG
1501 TAAGCTTACC TTAATTAAAC TTTCAAGTGA AGTGGAAATTA TTAAGATATA
1551 AATTTATATT TGTGCTTTTT GTCAGTGTGT AAGCTGTGTA GAAATTCCTT
1601 GATGTATTAG TTGTATTAAT GTAAAGTAGA AACCATTGT TGAACTCCT
1651 GTAGCTATTA TGCTTTTAAT ATTGTTTAA TGTCTTCCT TAGAATAGG
1701 CCCATAAAAA TGGTCTGGAA GCCAAACCAA AGTATGGTAT AATGTAGATA
1751 TTGTAAGACA GTAACTGAA AACATGTCCT GCCATGATT CAGCCATGTT
1801 TAAGTGACTT TTCTGAATT GTAAAATAAA AACTTCAAT GGGACCTAAA
1851 ACAGTGATGT AAAAGAAGT GTTTTGGAAA TTTAGCCTAA TTTATCTATA
1901 AGATGGCTGC TAAATTGATT TTTCAAGTCT TTTTATCATC TAAAATATA
1951 TAGATATAGA AATGAATAAT ATGAAGAACA GTAGTTTGCT TTGAATACT
2001 AATAAACTTT TATTTAAGAT GCTTCATTTT TACTTCTTAA AACGTGCTTT
2051 GGATTCTTAA ATTTGTTC ACTGAATGTT CAATGTTTAA AATGGCGATT
2101 AAAAATACTCT GCTGTATATA GTAGTTTTTG AGTAAATATT TGCAATAAAA
2151 ATCTGCCCCC GAAAAAATAA AAAAAA
```

BLAST Results

Entry G35287 from database EMBL:

human STS SHGC-37375.

Score = 2163, P = 2.8e-91, identities = 437/441

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 182 bp to 841 bp; peptide length: 220
Category: putative protein

```

1 MAERETETSN SESKQDKAAS SKEKNGCNAN SFEGSSSTKS EESITVSDKE
51 NETCLADQET GSKNIVSCDS NIGADKVEKK KQIQHVQCQM ELKMCQSSN
101 IILSDQIKDH NSSEARFSSK NIKDLRLASD NVSIDQFLRK RHEPESVSSD
151 VSEQSGSIHE PLTPSEVLEY EATEILQKGS GDPSAKTDEV VSDQTDDIPG
201 GNNPQSTEAT VLDDEFKERS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2 2h10, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2 2h10, frame 2

Report for DKFZphfbr2 2h10.2

```
[LENGTH]      220
[MW]           24109.02
[pI]           4.51
[FUNCAT]      04.99 other transcription activities [S. cerevisiae, YKR092c] 4e-05
[FUNCAT]      30.10 nuclear organization [S. cerevisiae, YKR092c] 4e-05
[PROSITE]     MYRISTYL 3
[PROSITE]     CK2_PHOSPHO_SITE 8
[PROSITE]     PKC_PHOSPHO_SITE 5
[PROSITE]     ASN_GLYCOSYLATION 3
[PFAM]        TNFR/NGFR cysteine-rich region
[KW]          Alpha Beta
```

```
SEQ      MAERETETSNSSESKQDKAASSKEKNGCNANSFEGSSTTKSEESITVSDKENETCLADQET  
PRD      ccccccccccccccchhhhhhhhccccccccccccccccceeeeeeecccccccccccccc  
  
SEQ      GSKNIVSCDSNIGADKVEKKKIQIHVCQEMELKMCQSSENIILSDQIKDHNSSEARFSSK  
PRD      cccceeeeccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhccceeecccccccccccccccccc  
  
SEQ      NIKDLRLASDNVSIDQFLRKRHEPESVSSDVSEQGSIHLEPLTPSEVLEYEATEILQKGS  
PRD      cchhhhhhccccchhhhhhhhccccccccccccccccceeeccccccccchhhhhhhcccccc  
  
SEQ      GDPSAKTDEVVSDQTDDIPGGNNPSTTEATVLDSEKERS  
PRD      ccccccccccccccccccscggcgccgacgaehhhhhhhccc
```

Prosites for DKFZphfbr2 2h10.2

PS00001	51->55	ASN_GLYCOSYLATION	PDOC00001
PS00001	111->115	ASN_GLYCOSYLATION	PDOC00001
PS00001	131->135	ASN_GLYCOSYLATION	PDOC00001
PS00005	20->23	PKC_PHOSPHO_SITE	PDOC00005
PS00005	37->40	PKC_PHOSPHO_SITE	PDOC00005
PS00005	47->50	PKC_PHOSPHO_SITE	PDOC00005
PS00005	118->121	PKC_PHOSPHO_SITE	PDOC00005
PS00005	184->187	PKC_PHOSPHO_SITE	PDOC00005
PS00006	9->13	CK2_PHOSPHO_SITE	PDOC00006
PS00006	13->17	CK2_PHOSPHO_SITE	PDOC00006
PS00006	20->24	CK2_PHOSPHO_SITE	PDOC00006
PS00006	38->42	CK2_PHOSPHO_SITE	PDOC00006
PS00006	45->49	CK2_PHOSPHO_SITE	PDOC00006
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	163->167	CK2_PHOSPHO_SITE	PDOC00006
PS00006	205->209	CK2_PHOSPHO_SITE	PDOC00006
PS00008	26->32	MYRISTYL	PDOC00008

PS00008 34->40 MYRISTYL
PS00008 201->207 MYRISTYL

PDOC00008
PDOC00008

Pfam for DKFZphfbr2_2h10.2

HMM_NAME TNFR/NGFR cysteine-rich region

HMM *CpeG.tYtD.WNHvpqClpCtrCePEMGQYMvgPCTWTQNTVC*
+E+ T +D +N ++C E G+ + +C+++ +

Query 40 SEESITVSDKEN--ETC--LADQET--GSKNIVSCDSNIGADK 76

DKFZphfbr2_2i17

group: intracellular transport and trafficking

DKFZphfbr2_2i17.3 encodes a novel 201 amino acid putative GTP-binding protein related to Rab1B.

Rab proteins are members of the Ras superfamily of GTPases. Rab proteins are localised to the cytoplasmic side of organelles and vesicles involved in the secretory (biosynthetic) and endocytotic pathways in eukaryotic cells. Rab proteins direct the targeting and fusion of transport vesicles to their acceptor membranes. Rab1B is essential for the intracellular transport of nascent low density lipoprotein (LDL) receptor. It is discussed as a universal mediator of endoplasmatic reticulum to Golgi transport of membrane glycoproteins in mammalian cells.

The new protein can find clinical application in modulating the transport of glycoproteins inside cells, especially of the LDL receptor.

Medline

96245776: Intracellular transport and maturation of nascent low density lipoprotein receptor is blocked by mutation in the Ras-related GTP-binding protein, Rab1B

strong similarity to rab1

complete cDNA, complete cds, start at 47, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 1985 bp

Poly A stretch at pos. 1901, polyadenylation signal at pos. 1859

```

1 GGGAGCAGAG TCGACTGGGA GCGACCGAGC GGGCCGCCGC CGCCGCCATG
51 AACCCCGAAT ATGACTACCT GTTAAAGCTG CTTTGTATG GCGACTCAGG
101 CGTGGGCAAG TCATGCCTGC TCCTGCGGTT TGCTGATGAC ACGTACACAG
151 AGAGCTACAT CAGCACCATC GGGGTGGACT TCAAGATCCG AACCATCGAG
201 CTGGATGGCA AACTATCAA ACTTCAGATC TGGGACACAG CGGGCCAGGA
251 ACGGTTCGGG ACCATCACTT CCAGCTACTA CCGGGGGGCT CATGGCATCA
301 TCGTGGTGTG TGACGTCACT GACCAGGAAT CCTACGCCAA CGTGAAGCAG
351 TGGCTGCAGG AGATTGACCG CTATGCCAGC GAGAACGTCA ATAAGCTCCT
401 GGTGGGCAAC AAGACGACC TCACCACCAA GAAGGTGGTG GACAACACCA
451 CAGCCAAGGA GTTTGCAGAC TCTCTGGGCA TCCCCTTCTT GGAGACGAGC
501 GCCAAGAATG CCACCAATGT CGAGCAGGCG TTCATGACCA TGGCTGCTGA
551 AATCAAAAAG CGGATGGGCG CTGGAGCAGC CTCTGGGGCC GAGCGGCCCA
601 ATCTCAAGAT CGACAGCACC CCTGTAAAGC CGGCTGGGCG TGGCTGTTGC
651 TAGGAGGGGC ACATGGAGTG GGACAGGAGG GGGCACCTTC TCCAGATGAT
701 GTCCCTGGAG GGGGAGGAG GTACCTCCCT CTCCTCTCTT TGGGGCATT
751 GAGTCTGTGG CTTTGGGGTG TCCTGGGCTC CCCATCTCCT TCTGGCCCAT
801 CTGCCTGCTG CCCTGAGCCC CGGTTCTGTC AGGGTCCCTC AGGGAGGACA
851 CTCAGGGCCT GTGGCCAGGC AGGGCGGAGG CCTGCTGTGC AGTTGCCTCT
901 AGGTGACTTT CCAAGATGCC CCCCTACACA CCTTTCTTTG GAACGAGGGC
951 TCTTCTGTCG GTGTCCCTCC CACCCCATG TATGCTGCAC TGGGTCTCT
1001 CTTTCTTCTT CTTGCTGTCC TGCCCAAGAA CTGAGGTCTC CCGGCGCTC
1051 TACTGCCCTG GCTGCAGTCA GTGCCAGGG CGAGGAATGT GGCCAGGGGA
1101 TCCAGGACCT GGGATCCAGG GCCCTGGGCT GGACCTCAGG ACAGGCATGG
1151 AGGCCACAGG GGGCCAGCAG CCCACCTTTT CCTCTCCCCA CTGCCTCCTC
1201 TCCCTTCTTA CACTCCAGC TCGAGCCGTC CAGCTGCGGT GGGATCTGAG
1251 TATATCTAGG GCGGGTGGGC GGGTAGCAGT GCTGGGCTG TGTCTTGAGC
1301 CTGGAGGGAG ACTGCTCCTG CCGCCCTCTG CCTGCCGGA GACAGACCCA
1351 TGGCTGCTCT GCCACCCTG CCCCTTTGTC CCCATGTGAG GCGGAGGCGG
1401 AAGGCCACCC GTGCCAGAGG CTGGGCACCA GCCTTAACCC TCACTCTGCT
1451 AGCACCTCCT CCTTTTCCCC AAGGTAGCAC ATCTGGCTCA CTCCCCACTC
1501 CGTCTCTGGA GCCCACCAGG GAAGGCCCTC ATCCCCTGCC GCTACTTCTC
1551 TGGGGAATGT GGGTTCCATC CAGGATTGGG GGCCTCTCTG CTCACCCACT
1601 CTGCACCCAG GATCCTAGTC CCCTGCCCTC TGGCACAGCT GCTTCTGCA
1651 AGAAAGCAAG TCTTTGGTCT CCCTGAGAAG CCATGTCCCT CGTGCTGTCT
1701 CTTGCCCTGC CCACCTGTGC CCTGCCCTCC AGCTTGATTT TAAGTCCCTG
1751 GGCTGCCCCC TTGGGGTGCC CCCGCTCCC AGGTTCCCTC CTGGTGTGAT
1801 GTCAGGCATT TTGCAAGGAA AAGCCACTTG GGGAAAGATG GAAAAGGACA
1851 AAAAAAATTA ATAAATTTCC ATTGGCCCTC GGGTGAGCTG AGGGTTTTTG
1901 CAAGGAAAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA
1951 AAAAAAATAA AAAAGAAAAA AAAAAAATAA AAAAAAATAA

```


BLAST Results

No BLAST result

Medline entries

91115900:

A family of ras-like GTP-binding proteins expressed in electromotor neurons.

Peptide information for frame 3

ORF from 48 bp to 650 bp; peptide length: 201
Category: strong similarity to known protein

```
1 MNPEYDYLFK LLLIGDSGVG KSCLLLRFD DTYTESYIST IGVDFKIRTI
51 ELDGKTIKIQ IWDTAGQERF RTITSSYYRG AHGIIVVYDV TDQESYANVK
101 QWLQEIIDRYA SENVNKLLVG NKSDLTTKKV VDNTAKEFA DSLGIPFLET
151 SAKNATNVEQ AFMTMAAEIK KRMGPGAASG GERPNLKIDS TPVKPAGGGC
201 C
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2117, frame 3

SWISSPROT:RB1B_RAT RAS-RELATED PROTEIN RAB-1B., N = 1, Score = 1023, P = 2.7e-103

PIR:S06147 GTP-binding protein rab1B - rat, N = 1, Score = 1013, P = 3.2e-102

SWISSPROT:RAB1_DISOM RAS-RELATED PROTEIN ORAB-1., N = 1, Score = 967, P = 2.4e-97

PIR:TVHUYP GTP-binding protein Rab1 - human, N = 1, Score = 966, P = 3e-97

>SWISSPROT:RB1B_RAT RAS-RELATED PROTEIN RAB-1B.
Length = 201

HSPs:

Score = 1023 (153.5 bits), Expect = 2.7e-103, P = 2.7e-103
Identities = 197/201 (98%), Positives = 199/201 (99%)

```
Query: 1 MNPEYDYLFKLLIGDSGVGKSCLLLRFD DTYTESYISTIGVDFKIRTI ELDGKTIKIQ 60
      MNPEYDYLFKLLIGDSGVGKSCLLLRFD DTYTESYISTIGVDFKIRTI ELDGKTIKIQ 60
Sbjct: 1 MNPEYDYLFKLLIGDSGVGKSCLLLRFD DTYTESYISTIGVDFKIRTI ELDGKTIKIQ 60

Query: 61 IWDTAGQERFRTITSSYYRG AHGIIVVYDV TDQESYANVK QWLQEIIDRYA SENVNKLLVG 120
      IWDTAGQERFRT+TSSYYRG AHGIIVVYDV TDQESYANVK QWLQEIIDRYA SENVNKLLVG
Sbjct: 61 IWDTAGQERFRTVTSSYYRG AHGIIVVYDV TDQESYANVK QWLQEIIDRYA SENVNKLLVG 120

Query: 121 NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG 180
      NKSDLTTKKVVDNTTAKEFADSLG+PFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG
Sbjct: 121 NKSDLTTKKVVDNTTAKEFADSLGVFPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG 180

Query: 181 GERPNLKIDSTPVKPAGGGCC 201
      GERPNLKIDSTPVK A GGCC
Sbjct: 181 GERPNLKIDSTPVKSASGGCC 201
```

Pedant information for DKFZphfbr2_2117, frame 3

Report for DKFZphfbr2_2117.3

{LENGTH} 201

[MW] 22171.25
 [pI] 5.56
 [HOMOL] SWISSPROT:RB1B_RAT RAS-RELATED PROTEIN RAB-1B. 1e-112
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YFL038c] 2e-77
 [FUNCAT] 30.08 organization of golgi [S. cerevisiae, YFL038c] 2e-77
 [FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YFL005w] 4e-57
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YFL005w] 4e-57
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL005w] 4e-57
 [FUNCAT] 08.19 cellular import [S. cerevisiae, YER031c] 8e-46
 [FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YER031c] 8e-46
 [FUNCAT] 09.09 biogenesis of intracellular transport vesicles [S. cerevisiae, YGL210w] 1e-44
 [FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YOR089c] 1e-30
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 11.01 stress response [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 03.99 other cell growth, cell division and dna synthesis activities [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 01.03.13 regulation of nucleotide metabolism [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 10.04.07 g-proteins [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YNL098c] 3e-25
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR101w] 9e-24
 [FUNCAT] 11.10 cell death [S. cerevisiae, YOR101w] 9e-24
 [FUNCAT] 04.07 rna transport [S. cerevisiae, YOR185c] 4e-23
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YOR185c] 4e-23
 [FUNCAT] 08.01 nuclear transport [S. cerevisiae, YOR185c] 4e-23
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YPR165w] 7e-17
 [FUNCAT] 10.02.07 g-proteins [S. cerevisiae, YPR165w] 7e-17
 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YCR027c] 1e-16
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR229c] 1e-11
 [FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YLR229c] 1e-11
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YDL192w] 4e-10
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YNL180c] 9e-09
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YPL051w] 3e-08
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YAL048c] 5e-05
 [BLOCKS] BL01019A ADP-ribosylation factors family proteins
 [BLOCKS] BL01115A GTP-binding nuclear protein ran proteins
 [SCOP] dlplk_ 3.25.1.3.1 cH-p21 Ras protein [human (Homo sapiens)] 2e-41
 [SCOP] dlguaa_ 3.25.1.3.10 Rap1A [Human (Homo sapiens)] 5e-60
 [SCOP] dlrrga_ 3.25.1.3.5 ADP-ribosylation factor 1 (ARF1) [rat (Rattus)] 2e-30
 [SCOP] dlhura_ 3.25.1.3.4 ADP-ribosylation factor 1 (ARF1) [human (Homo sapiens)] 2e-33
 [PIRKW] nucleus 1e-21
 [PIRKW] membrane trafficking 1e-110
 [PIRKW] oncogene 1e-25
 [PIRKW] endoplasmic reticulum 1e-105
 [PIRKW] phosphoprotein 1e-105
 [PIRKW] glycoprotein 3e-25
 [PIRKW] prenylated cysteine 1e-110
 [PIRKW] signal transduction 4e-23
 [PIRKW] transforming protein 1e-105
 [PIRKW] purine nucleotide binding 2e-24
 [PIRKW] alternative splicing 5e-26
 [PIRKW] P-loop 1e-110
 [PIRKW] lipoprotein 1e-110
 [PIRKW] proto-oncogene 3e-27
 [PIRKW] methylated carboxyl end 3e-27
 [PIRKW] hydrolase 7e-25
 [PIRKW] membrane protein 1e-105
 [PIRKW] GTP binding 1e-110
 [PIRKW] thiolester bond 5e-76
 [PIRKW] Golgi apparatus 1e-105
 [SUPFAM] ras transforming protein 1e-110
 [PROSITE] ATP_GTP_A 1
 [PROSITE] MYRISTYL 2
 [PROSITE] CK2_PHOSPHO_SITE 5
 [PROSITE] SIGMA54_INTERACT_1 1
 [PROSITE] TYR_PHOSPHO_SITE 1
 [PROSITE] GLYCOSAMINOGLYCAN 1
 [PROSITE] PKC_PHOSPHO_SITE 4
 [PROSITE] ASN_GLYCOSYLATION 3
 [PFAM] Ras family (contains ATP/GTP binding P-loop)
 [KW] Alpha_Beta
 [KW] 3D

```

SEQ      MNPEYDYLFKLLIGDSGVGKSCLLLRFAADTYTESYISTIGVDFKIRTIELDGKTIKIQ
221p-    .....EEEEEEETTTCHHHHHHHHHHCCCCCCCCCTTEEEE-EEEEETEEEEEE

SEQ      IWDTAGQERFRTITSSYYRGAGHIIVVYDVTQESYANVKQWLQEI DRYASENVNKLVLG
221p-    EEECTTTTTTCGGGHHHHHHHCCCCEEEEETTBHHHHHHHHHHHHHHHHHTTTTCEEEEE

SEQ      NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG
221p-    ETTTTCCTCC-CCCHHHHHHHHHHCCCCEEEEETTTTTTTHHHHHHHHHHHHHHH.....

SEQ      GERPNLKIDSTPVKPAGGGCC
221p-    .....

```

Prosites for DKFZphfbr2_2i17.3

PS00001	121->125	ASN_GLYCOSYLATION	PDOC00001
PS00001	133->137	ASN_GLYCOSYLATION	PDOC00001
PS00001	154->158	ASN_GLYCOSYLATION	PDOC00001
PS00002	17->21	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	56->59	PKC_PHOSPHO_SITE	PDOC00005
PS00005	126->129	PKC_PHOSPHO_SITE	PDOC00005
PS00005	135->138	PKC_PHOSPHO_SITE	PDOC00005
PS00005	151->154	PKC_PHOSPHO_SITE	PDOC00005
PS00006	32->36	CK2_PHOSPHO_SITE	PDOC00006
PS00006	91->95	CK2_PHOSPHO_SITE	PDOC00006
PS00006	135->139	CK2_PHOSPHO_SITE	PDOC00006
PS00006	156->160	CK2_PHOSPHO_SITE	PDOC00006
PS00006	179->183	CK2_PHOSPHO_SITE	PDOC00006
PS00007	27->34	TYR_PHOSPHO_SITE	PDOC00007
PS00008	18->24	MYRISTYL	PDOC00008
PS00008	176->182	MYRISTYL	PDOC00008
PS00017	15->23	ATP_GTP_A	PDOC00017
PS00675	11->25	SIGMA54_INTERACT_1	PDOC00579

Pfam for DKFZphfbr2_2i17.3

HMM_NAME	Ras family (contains ATP/GTP binding P-loop)		
HMM	*KLVLIGDSGVGKSCLLIRFTQNeFnEeYIPTIGvDFYtKTIEIDGKtIK		
Query	10	KL+LIGDSGVGKSCLL+RF +++++E+YI+TIGVDF+++TIE+DGKTIK	58
HMM	LQIWDTAGQERYRrMRPMYYRGAMGFMLVYDITNRqSFENIrNWweEIrR		
Query	59	LQIWDTAGQER+r++++YYRGA+G+++VYD+T+++S+ N+++W+++EI+r	108
HMM	HCDrDENVPIMLVGNKCDLEDQRQVStEEGQeFAREWGAIPFMETSAKTN		
Query	109	+++ ENV ++LVGNK+DL +++V+ +++EFA+++G IPF+ETSAK++	155
HMM	inVEEAFMEIvReIlqrMqe.q.NqteNinidQpsrnrk...rCCCIM*		
Query	156	+NVE+AFM+++ EI++RM+ +++E +N+++S+++ K +CC	201

DKFZphfbr2_2k19

group: brain derived

DKFZphfbr2_2k19 encodes a novel 303 amino acid protein with similarity to human KIAA0378 product.

The protein contains a leucine zipper, which can mediate protein-protein-interaction. No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to KIAA0378

encoded by the genomic clones HS147M19/HS608E8

Sequenced by Qiagen

Locus: unknown

Insert length: 1931 bp

Poly A stretch at pos. 1866, no polyadenylation signal found

```
1 GGGGGGGGCG CGCGGTGACA GCGCGGGGTT GCGGCGGTGG GACCCAGGGG
51 GCGACAGAGG CAGCAGCAGC CCGAGGCCCTG AGGAGAGGAG ACCGGCGGCG
101 GCGGCAATGC TGGAGACCCT TCGCGAGCGG CTGCTGAGCG TGCAGCAGGA
151 TTTCACCTCC GGGCTGAAGA CTTTAAGTGA CAAGTCAAGA GAAGCAAAAG
201 TGAAAGCAA ACCCAGGACT GTTCCATTTT TGCCAAAGTA CTCTGCTGGA
251 TTAGAATTAC TTAGCAGGTA TGAGGATACA TGGGCTGCAC TTCACAGAAG
301 AGCCAAAGAC TGTGCAAGTG CTGGAGAGCT GGTGGATAGC GAGGTGGTCA
351 TGCTTTCTGC GCACTGGGAG AAGAAAAAGA CAAGCCTCGT GGAGCTGCAA
401 GAGCAGCTCC AGCAGCTCCC AGCTTTAATC GCAGACTTAG AATCCATGAC
451 AGCAAATCTG ACTCATTTAG AGGCGAGTTT TGAGGAGGTA GAGAACAACC
501 TGCTGCATCT GGAAGACTTA TGTGGGCAGT GTGAATTAGA AAGATGCAAA
551 CATATGCAGT CCCAGCAACT GGAGAATTAC AAGAAAAATA AGAGGAAGGA
601 ACTTGAACCC TTCAAAGCTG AACTAGATGC AGAGCACGCC CAGAAGGTCC
651 TGGAATGGA GCACACCCAG CAAATGAAGC TGAAGGAGCG GCAGAAGTTT
701 TTTGAGGAAG CCTTCCAGCA GGACATGGAG CAGTACCTGT CCACTGGCTA
751 CCTGCAGATT GCAGAGCGGC GAGAGCCCAT AGGCAGCATG TCATCCATGG
801 AAGTGAACGT GGACATGCTG GAGCAGATGG TCCTGATGGA CATATCGGAC
851 CAGGAGGCC TGGACGTCTT CCTGAACTCT GGAGGAGAAG AGAACACTGT
901 GCTGTCCCCC GCCTTAGGTA GGGTTGACAA ACTTGCATTA GCTGAACCCG
951 GGCAGTATCG ATGCCACTCC CCTCCAAAGG TGAGACGTGA GAACCATCTG
1001 CCAGTCACTT ACGCATAAAC CCCCAGCTC ACAGCCAGCT CCTGGCTCCC
1051 TAACCCACAG GTTCCACACG GCTGTGTGGC AGCTGCAACA GTGGTGTGGT
1101 TCCGTCATGA ATTCTCTCA AAGATTGAC ATGCTCCACT CCGGTAACCT
1151 TGGTGAGTTG AGAGCTTTCT TGTGTTGTTT CCCTCCTTTA CCATCCAGAA
1201 ATCCATTTGA GTCTGCTCCT TGTGGTTAAG GACTGGCGTT TGCAGGGAGG
1251 TGCGGACTCT CCTGCGGGGC TCACGGGAAA CTCTTCCCTC TTCGTGCGAC
1301 AGGCATTTAG GGGCGTGCCT GCCATGGGCA AAGCCATGGT GTGTGTTTCA
1351 CTCTTGGCCT GTGTTGTAAA CTTAGTTGCA CTTCACTTCC TTTCATCCCT
1401 TCACAAAATT TTGTTTCACA TTCATGCAGC AAATATGGGC TGAGGTGCCA
1451 GACCTGTACC TGGGCTTGGT GCGTTTCAAA TTTCAGACCA GTTCTTTGGG
1501 CTGGGTCAAG GCAAAAGCTCA GTCGTCCCAG CAGCACCTCA GCCATCTGTA
1551 GAAGGTTCTA CCATTACCAC GGTTCAGCT TCCTCTAAAC TTCTACCCG
1601 CTTCTCCTGG CAATCTGTCA GAACGGTGTG ATCCTGGGGA AGAGAAGGAG
1651 CTTGGGTGCA TTTGCCCTCA TCCTGAGAAG GCCAGAATAC TGGAGACCAG
1701 CGTGAACCCT CACCCAGAGT CAGGGGAAGA TTTAGAAACA GTGACACCTG
1751 CATATAGAAT TTTGATTCCT TGAAGAGCCT ATTTAGTTCC ATAAAATTGG
1801 AGAACTGCTG AAGGTCAGTA ATTCGACTT TCTCAGCAGT GGTGTCTCTG
1851 AATTACTGCA AAGGGTAAAA AAAAAAATAA AAAAAACTTA TCGATACCGT
1901 CGACCTCGAT GATCATGATG ATGATGTCCA C
```

BLAST Results

Entry HS147M19 from database EMBL:

Homo sapiens DNA sequence from PAC 147M19 on chromosome 6p22.1-22.3.

Contains an unknown gene, ESTs and GSSs.

Score = 5540, P = 4.1e-275, identities = 1114/1120

3 exons 592-1884

Entry HS608E8 from database EMBL:

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 608E8

Score = 797, P = 1.2e-78, identities = 161/163

6 exons 1-592

Medline entries

90294724:

The involucrin gene of the gibbon: The middle region shared by the hominoids

Peptide information for frame 2

ORF from 107 bp to 1015 bp; peptide length: 303
 Category: similarity to known protein
 Classification: unset
 Prosite motifs: LEUCINE_ZIPPER (97-119)

```

1 MLETLRERLL SVQQDFTSGL KTLSDKSREA KVSKPRTVP FLPKYSAGLE
51 LLSRYEDTWA ALHRRRAKDCASAGELVDSEV VMLSAHWEKK KTSLEVELQEQ
101 LQQLPALIAD LESMTANLTH LEASFEEVEN NLLHLEDLCG QCELERCKHM
151 QSQLENYKK NKRKELETFK AELDAEHAQK VLEMEHTQQM KLKERQKFFE
201 EAFQDMEQY LSTGYLQIAE RREPIGSMSS MEVNVDMLEQ MVLMDISDQE
251 ALDVFLNSGG EENTVLSPAL GRVDKLALAE PGQYRCHSFP KVRRENHLPV
301 TYA

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2k19, frame 2

TREMBL:HSAB2376_1 gene: "KIAA0378"; Human mRNA for KIAA0378 gene, partial cds., N = 1, Score = 137, P = 4.8e-06

PIR:I37037 involucrin - common gibbon, N = 1, Score = 124, P = 7.4e-05

PIR:A57013 early endosome antigen 1 - human, N = 1, Score = 128, P = 9.5e-05

>TREMBL:HSAB2376_1 gene: "KIAA0378"; Human mRNA for KIAA0378 gene, partial cds.

Length = 808

HSPs:

Score = 137 (20.6 bits), Expect = 4.8e-06, P = 4.8e-06
 Identities = 59/222 (26%), Positives = 103/222 (46%)

```

Query:      2 LETLRERLLSVQQDFTSGLKTL---SDKSREAKVKS-KPRTVPFLPKYSAGLELLSRYED 57
            L T L E L S ++   LK      D+ R +++S +      K +A   L+   E
Sbjct:    434 LATLEEAL-SEKERIIERLKEQRRDDRERLEEIESFRKENKDLKEKVNALQAELETEKES 492

Query:      58 TWAALHRRRAKDCASAGELVDSEVVMLSAHWEKKKTSLEVELQEQQLPALIADLESMTAN 117
            +   L   A   ASAG   DS++   L   E+KK   +L+   QL++   I D   M
Sbjct:    493 SLIDLKEHASSLASAGLKRDSKLKSLEIAIEQKKEECSKLEAQLKKAHN-IEDDSRMNPE 551

Query:     118 LTHLEASFEEVENNLLHLEDLCG--QCELERCKHMQSQLENYKKNRK---ELETFAE 172
            +++++   +   D CG   Q E++R-   +   +++EN K +K+ K   ELE+
Sbjct:    552 FAD---QIKQLDKEASYRDECGKAQAEVDRLLLEIL-KEVENEKNDKDKKIAELESITLR 607

Query:     173 LDAEHAQKVLEMEHTQOMKLKERQKFFEEAFQDMEQYLLSTGYLQIAE 220
            +   KV   ++H   QQ++ K+   +   EE   +++   ++ +LQI E
Sbjct:    608 HMKDQNKKKVANLKHNNQLEKKKNAQLLEEVRREDMSADNSQHLQIEE 655

```

Score = 100 (15.0 bits), Expect = 6.2e-02, P = 6.0e-02
 Identities = 44/156 (28%), Positives = 76/156 (48%)

```

Query:      57 DTWAALHRRRAKDCASAGELVDSEVVMLSAHWEKKKTSLEVELQEQQLPAL-IALESMT 115
            D   A+ +R   +C   A   VD   ++L   E +K   +   +L+ L   + D
Sbjct:    560 DKEASYR--DECGKAQAEVDRLLLEILK-EVENEKNDKDKKIAELESITLRHMKDQNKKV 616

Query:     116 ANLTHLEASFEEVENNLLHLEDLCGQCE--LERCKHMQSQLENYKKNRKELETFKAEL 173

```

Sbjct: 617 ANL H + E+ +N L LE++ + + + +H+Q ++L N + R+EL+ KA L
 617 ANLKHNQ-QLEKKKNAQL-LEEVRREDSDMADNSQHLQIEELMNALEKTRQELDATKARL 674

Query: 174 DAEHAQKVLEME-HTQQMKLKERQKFFEEAFQDMEQYLS 212
 A Q + E E H +++ ER+K EE + E L+

Sbjct: 675 -ASTQQSLAEKEAHLANLRI-ERRKQLEEILEMKQEALLA 712

Pedant information for DKFZphfbr2_2k19, frame 2

Report for DKFZphfbr2_2k19.2

[LENGTH] 303
 [MW] 34814.78
 [pI] 5.23
 [PROSITE] LEUCINE_ZIPPER 1
 [KW] All_Alpha
 [KW] LOW_COMPLEXITY 3.63 %
 [KW] COILED_COIL 14.52 %

SEQ MLETLRERLLSVQQDFTSGLKTLSDKSREAKVSKPRTVPFLPKYSAGLELLSRYEDTWA
 SEG
 PRD ccc
 COILS

SEQ ALHRRAKDCASAGELVDSEVVMLSAHWEKKKTSLEVELQEQQLPALIADLESMTANLTH
 SEGxxxxxxxxxxxxx.....
 PRD hhh
 COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ LEASFEEVENLLHLEDLCGQCELERCKHMQSQLENYKKNRKELETFAELDAEHAQK
 SEG
 PRD hhh
 COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ VLEMEHTQQMKLKERQKFFEEAFQDMEQYLSSTGYLQIAERREPIGSMSSMEVNVDMLEQ
 SEG
 PRD hhh
 COILS

SEQ MVLMDISDQEALDVFLNSGGEENTVLSPALGRVDKLALAEPPGQYRCHSPPKVRRENHLPV
 SEG
 PRD hhhhhhchhh
 COILS

SEQ TYA
 SEG ...
 PRD CCC
 COILS ...

Prosite for DKFZphfbr2_2k19.2

PS00029 97->119 LEUCINE_ZIPPER PDOC00029

(No Pfam data available for DKFZphfbr2_2k19.2)

DKFZphfbr2_2k14

group: cell cycle

DKFZphfbr2_2k14 encodes a novel 335 amino acid protein with strong similarity to rattus rattus IAG2 "implantation-associated protein" and the human N33 tumour-suppressor gene.

Tumour-suppressor genes are known to be involved in the control of cell growth and division, interacting with proteins which control the cell cycle. The N33 gene is significantly methylated in tumour cells, a mechanism by which tumor-suppressor genes are inactivated in cancer. In addition, the novel protein contains a RGD cell attachment site. Therefore the novel protein is a new putative tumour-suppressor gene.

The new protein can find application in modulating/blocking the cell cycle and in the therapy of tumours.

strong similarity to human N33 tumor suppressor gene

complete cDNA, complete cds, EST hits,
potential start at Bp 30 matches kozak consensus ANCatgG
potential transmembran protein (4 TM)
similarity to yeast OST3p (oligosaccharyltransferase gamma chain)

Sequenced by Qiagen

Locus: unknown

Insert length: 2241 bp
Poly A stretch at pos. 2221, no polyadenylation signal found

```
1 TGGGACTTAT AGAAGGGAGA GGAGCGAACA TGCGAGCGCG TTGGCGGTTT
51 TGGTGTGTCT CTGTGACCAT GGTGGTGGCG CTGCTCATCG TTTGCGACGT
101 TCCCTCAGCC TCTGCCCAA GAAAGAAGGA GATGGTGTTA TCAGAAAAGG
151 TTAGTCAGCT GATGGAATGG ACTAACAAAA GACCTGTAAT AAGAATGAAT
201 GGAGACAAGT TCCGTCGCCT TGTCAAAGCC CCACCGAGAA ATTACTCCGT
251 TATCGTCATG TCCACTGCTC TCCAACGTGA TAGACAGTGT GTCGTTTGCA
301 AGCAAGCTGA TGAAGAATTC CAGATCCTGG CAAACTCCTG GCGATACTCC
351 AGTGCATTCA CCAACAGGAT ATTTTGTGCC ATGGTGGATT TTGATGAAGG
401 CTCTGATGTA TTTAGATGC TAAACATGAA TTCAGCTCCA ACTTTCATCA
451 ACTTTCTGTC AAAAGGGAAA CCCAAACGGG GTGATACATA TGAGTTACAG
501 GTGCGGGGTT TTTAGCTGA GCAGATTGCC CGGTGGATCG CCGACAGAAC
551 TGATGTCAAT ATTAGAGTGA TTAGACCCCC AAATTATGCT GGTCCCTTAA
601 TGTTGGGATT GCTTTTGGCT GTTATTGGTG GACTTGTGTA TCTTCGAAGA
651 AGTAATATGG AATTTCTCTT TAATAAACT GGATGGGCTT TTGCAGCTTT
701 GTCTTTTGTG CTGCTATGA CATCTGGTCA AATGTGGAAC CATATAAGAG
751 GACCACCATA TGCCCATAG AATCCCCACA CGGGACATGT GAATTATATC
801 CATGGAAGCA GTCAGGCCCA GTTTGTAGCT GAAACACACA TTGTTCTTCT
851 GTTTAATGGT GGAGTTACCT TAGGAATGGT GCTTTTGTGT GAAGCTGCTA
901 CCTCTGACAT GGATATTGGA AAGCGAAAGA TAATGTGTGT GGCTGGTATT
951 GGACTTGTG TATTATCTT CAGTTGGATG CTCTCTATT TTAGATCTAA
1001 ATATCATGGC TACCCATACA GCTTTCTGAT GACTTAAAAA GGTCCCAGAG
1051 ATATATAGAC ACTGGAGTAC TGGAAATTGA AAAACGAAAA TCGTGTGTGT
1101 TTGAAAAGAA GAATGCAACT TGTATATTCT GTATTACCTC TTTTTCCTAA
1151 GTGATTTTAA TAGTTAATCA TTTAACCAAA GAAGATGTGT AGTGCCTTAA
1201 CAAGCAATCC TCTGTCAAAA TCTGAGGTAT TTGAAAATAA TTATCCTCTT
1251 AACCTTCTCT TCCCAGTGAA CTTTATGGAA CATTTAATTT AGTACAATTA
1301 AGTATATTAT AAAAATTGTA AAACCTACTAC TTGTTTTAG TTAGAACAAA
1351 GCTCAAAACT ACTTTAGTTA ACTTGGTCAT CTGATCTTAT ATTGCCTTAT
1401 CCAAGATGAG GGAAGTAAG TCCTGACCAG GTGTTCCAC ATATGCCTGT
1451 TACAGATAAC TACATTAGGA ATTCATCTT AGCTTCTTCA TCTTGTGTG
1501 GATGTGTATA CTTTACGCAT CTTTCTTTT GAGTAGAGAA ATTATGTGTG
1551 TCATGTGGTC TTCTGAAAAT GGAACACCAT TCTTCAGAGC ACACGTCTAG
1601 CCTCAGCAA GACAGTTGTT TCTCCTCCTC CTGTCATATT TCCTACTGCG
1651 CTCCAGCCTG AGTGATAGAG TGAGACTCTG TCTCAAAAAA AAAGTATCTC
1701 TAAATACAGG ATTATAATTT CTGCTTGAGT ATGGTGTTAA CTACCTTGTA
1751 TTTAGAAAGA TTTAGATTTC ATTCCATCTC CTTAGTTTTC TTTTAAAGGTG
1801 ACCCATCTGT GATAAAAAATA TAGCTTAGTG CTAAATCAG TGTAACCTAT
1851 ACATGGCCTA AAATGTTTCT ACAAATTAGA GTTTGTCACT TATTCCATTT
1901 GTACCTAAGA GAAAAATAGG CTCAGTTAGA AAAGGACTCC CTGGCCAGGC
1951 GCAGTGACTT ACGCCTGTAA TCTCAGCACT TTGGGAGGCC AAGGCAGGCA
2001 GATCACGAGG TCAGGAGTTC GAGACCATCC TGGCCAAACAT GGTGAAACCC
2051 CGTCTCTACT AAAAATATAA AAATTAGCTG GGTGTGGTGG CAGGAGCCTG
2101 TAATCCAGC TGCACAGGAG GCTGAGGCAC GAGAATCACT TGAACCTAGG
2151 AGATGGAGGT TTCAGTGAGC CGAGATCAGC CCACTGCACT CCAGCCTGGC
2201 AACAGAGCGA GACTCCATCT CAAAAAATAA AAAAAAATAA A
```

BLAST Results

No BLAST result

Medline entries

96299740:

Structure and methylation-associated silencing of a gene within a homozygously deleted region of human chromosome band 8p22.

97243398:

Tumour-suppressor genes in prostatic oncogenesis: a positional approach.

98334474:

Concordant methylation of the ER and N33 genes in glioblastoma multiforme.

Peptide information for frame 3

ORF from 30 bp to 1034 bp; peptide length: 335
Category: strong similarity to known protein

```

1 MAARWREWCV SVTMVVALLI VCDVPSASAO RKKEMVLSEK VSQLEWNTNK
51 RPVIRMNGDK FRRLVKAPPR NYSVIVMFTA LQLHRQCVVC KQADEEFQIL
101 ANSWRYSSAF TNRIFFAMVD FDEGSDVFQM LNMNSAPTFI NFPKGGKPKR
151 GDTYELQVRG FSAEQIARWI ADRTDVNIRV IRPPNYAGPL MLGLLLAIVIG
201 GLVYLRRSNM EFLFNKTGWA FAALCFVLAM TSGQMNWHRIR GPPYAHKNPH
251 TGHVNYIHGS SQAQFVAETH IVLLFNGGVT LGMVLLCEAA TSDMDIGKRR
301 IMCVAGIGLV VLFFSWMLSI FRSKYHGYPY SFLMS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2k14, frame 3

TREMBL:RNAF8554_1 gene: "IAG2"; product: "implantation-associated protein"; Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds., N = 1, Score = 1560, P = 3.4e-160

PIR:G02297 gene N33 protein - human, N = 1, Score = 1256, P = 5.6e-128

TREMBL:HSN33S11_1 gene: "N33"; product: "N33 protein form 2"; Human N33 protein form 2 (N33) gene, exon 11 and complete cds., N = 1, Score = 1252, P = 1.5e-127

>TREMBL:RNAF8554_1 gene: "IAG2"; product: "implantation-associated protein"; Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.
Length = 308

HSPs:

Score = 1560 (234.1 bits), Expect = 3.4e-160, P = 3.4e-160
Identities = 295/307 (96%), Positives = 299/307 (97%)

```

Query:      29 AQRKKEMLVSEKVSQLEWNTNKRVPVIRMNGDKFRRLVKAPPRNYSVIVMFTALQLHRQCV 88
             AQRKKE VL EKV QLEWNTN+RPVIRMNGDKFR LVKAPPRNYSVIVMFTALQLHRQCV
Sbjct:      2 AQRKKEKVLVEKVIQLMEWNTNQRVPVIRMNGDKFRPLVKAPPRNYSVIVMFTALQLHRQCV 61

Query:      89 VCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEGSDVFQMLNMNSAPTFINFPKGGK 148
             VCKQADEEFQILAN WRYSSAFTNRIFFAMVDFDEGSDVFQMLNMNSAPTFINFP KGKP
Sbjct:      62 VCKQADEEFQILANFWRYSSAFTNRIFFAMVDFDEGSDVFQMLNMNSAPTFINFPKGGK 121

Query:      149 KRGDYELQVRGFSAEQIARWIADRTDVNIRVIRPPNYAGPLMLGLLLAIVIGGLVYLRRS 208
             KR DTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNYAGPLMLGLLLAIVIGGLVYLRRS
Sbjct:      122 KRADTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNYAGPLMLGLLLAIVIGGLVYLRRS 181

Query:      209 NMEFLFNKTGWAFALCFVLAMTSGQMNWHRIRGPPYAHKNPHTGHVNYIHGSSQAQFVAE 268
             NMEFLFNKTGWAFALCFVLAMTSGQMNWHRIRGPPYAHKNPHTGHVNYIHGSSQAQFVAE

```


Sbjct: 182 NMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKNPHTGHVNYIHGSSQAQFVAE 241
Query: 269 THIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLVVLFSSWMLSIFRSKYHGY 328
THIVLLFNGGVTLGMVLLCEAA SDMDIGKR++MC+AGIGLVVLFSSWMLSIFRSKYHGY
Sbjct: 242 THIVLLFNGGVTLGMVLLCEAAASDMDIGKRMMCIAGIGLVVLFSSWMLSIFRSKYHGY 301
Query: 329 PYSFLMS 335
PYSFLMS
Sbjct: 302 PYSFLMS 308

Pedant information for DKFZphfbr2_2k14, frame 3

Report for DKFZphfbr2_2k14.3

[LENGTH] 335
[MW] 38036.83
[pI] 9.68
[HOMOL] TREMBL:RNAF8554_1 gene: "IAG2"; product: "implantation-associated protein";
Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds. 1e-161
[FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YOR085w] 4e-14
[FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YOR085w] 4e-14
[FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae, YOR085w] 4e-14
[EC] 2.4.1.119 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 1e-12
[PIRKW] glycosyltransferase 1e-12
[PIRKW] transmembrane protein 6e-69
[PIRKW] hexosyltransferase 1e-12
[PROSITE] RGD 1
[PROSITE] MYRISTYL 4
[PROSITE] AMIDATION 1
[PROSITE] CK2_PHOSPHO_SITE 2
[PROSITE] PKC_PHOSPHO_SITE 4
[PROSITE] ASN_GLYCOSYLATION 2
[KW] SIGNAL PEPTIDE 30
[KW] TRANSMEMBRANE 4
[KW] LOW_COMPLEXITY 5.97 %

SEQ MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMWNTNKRVPVIRMNGDK
SEG
PRD ccc
MEM
SEQ FRRLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVD
SEG
PRD ccc
MEM
SEQ FDEGSDVFMQNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRV
SEG
PRD ccc
MEMM
SEQ IRPPNYAGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIR
SEGxx
PRD ecc
MEM MMM...
SEQ GPPYAHKNPHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRK
SEG
PRD ccc
MEMMM
SEQ IMCVAGIGLVVLFSSWMLSIFRSKYHGYPSFLMS
SEG
PRD eeeeecc
MEM MMM

Prositc for DKFZphfbr2_2k14.3

PS00001	71->75	ASN_GLYCOSYLATION	PDOC00001
PS00001	215->219	ASN_GLYCOSYLATION	PDOC00001
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00005	48->51	PKC_PHOSPHO_SITE	PDOC00005

PS00005	103->106	PKC_PHOSPHO_SITE	PDOC00005
PS00005	111->114	PKC_PHOSPHO_SITE	PDOC00005
PS00006	208->212	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
PS00008	193->199	MYRISTYL	PDOC00008
PS00008	233->239	MYRISTYL	PDOC00008
PS00008	259->265	MYRISTYL	PDOC00008
PS00008	278->284	MYRISTYL	PDOC00008
PS00009	296->300	AMIDATION	PDOC00009
PS00016	150->153	RGD	PDOC00016

(No Pfam data available for DKFZphfbr2_2k14.3)

DKFZphfbr2_3c18

group: nucleic acid management

DKFZphfbr2_3c18 encodes a novel 448 amino acid protein with strong similarity to mus musculus RNA helicase and several RNA-dependent ATPases from the DEAD box family.

RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. The novel protein contains a DEAD-box and is a new member of this subgroup.

The new protein can find application in modulating RNA metabolism and gene expression.

strong similarity to RNA helicase and RNA-dependent ATPase
from the DEAD box family
group helicases

Summary DKFZphfbr2_3c18 encodes a novel 448 amino acid protein with
similarity to DEAD-box subfamily ATP-dependent RNA helicases.
Deletion of the yeast homologue DBP5 is lethal.

strong similarity to RNA helicase and RNA-dependent ATPase from the
DEAD box family

complete cDNA, EST hits
complete cds ATG at Bp 109

Sequenced by AGOWA

Locus: /map="87.50 cR from top of Chr16 linkage group"

Insert length: 1713 bp
Poly A stretch at pos. 1696, no polyadenylation signal found

```
1 TGGGGTAGTG GGGCTGGAGC AGAGCCTGCC GCGAACCCCG GGAGCCCACG
51 ATCCCTCGTG CCATCCCTCG AATCCACCAG CACGAGCGTC CCACCCGCGC
101 CTGGGACCAT GGCCACTGAC TCATGGGCCC TGGCGGTGGA CGAGCAGGAA
151 GCTGGGGCTG AGTCGTTGAG CAACTTGCAT CTTAAGGAAG AGAAAAATCAA
201 ACCAGATACC AATGGTGCTG TTGTCAAGAC CAATGCCAAT GCAGAGAAGA
251 CAGATGAAGA AGAGAAAAGAG GACAGAGCTG CCCAGTCCTT ACTCAACAAG
301 CTGATCAGAA GCAACCTTGT TGATAACACA AACCAAGTGG AAGTCCTGCA
351 GCGGGATCCA AACTCCCCTC TGTAATCGGT GAAGTCTTTT GAAGAGCTTC
401 GGCTCCCAACA GAACTTAATT GCCCAATCTC AGTCTGGTAC TGGTAAAAACA
451 GCTGCCTTCG TGCTGGCCAT GCTTAGCCAA GTAGAACCTG CAAACAAATA
501 CCCCCAGTGT CTATGTCTCT CCCCACGTA TGAGCTCGCC CTCCAAACAG
551 GAAAAGTGAT TGAACAAATG GGCAAATTTT ACCCTGAACCT GAAGCTAGCT
601 TATGCTGTTT GAGGCAATAA ATTGGAAGA GGCAGAGA TCAGTGAGCA
651 GATTGTCATT GGCACCCCTG GGAAGTGTCT GGACTGGTGC TCCAAGCTCA
701 AGTTTCATTG TCCCAAGAAA ATCAAGGTGT TTGTTCTGGA TGAGGCTGAT
751 GTCATGATAG CCACTCAGGG CCACCAAGAT CAGAGCATCC GCATCCAGAG
801 GATGCTGCCC AGGAAGTCCC AGATGCTGCT TTTCTCGCC ACCTTTGAAG
851 ACTCTGTGTG GAAGTTTGCC CAGAAAGTGG TCCCAGACCC AAACGTTATC
901 AAAGTGAAGC GTGAGGAAGA GACCCTGGAC ACCATCAAGC AGTACTATGT
951 CCTGTGCAGC AGCAGAGACG AGAAGTTCCA GGCCTTGTGT AACCTCTACG
1001 GGGCCATCAC CATTGCTCAA GCCATGATCT TCTGCCATAC TCGCAAAACA
1051 GCTAGTTGGC TGGCAGCAGA GCTCTCAAAA GAAGGCCACC AGGTGGCTCT
1101 GCTGAGTGGG GAGATGATGG TGGAAACAGAG GGCTGCAGTG ATTGAGCGCT
1151 TCCGAGAGGG CAAAGAGAAG GTTTTGGTGA CCACCAACGT GTGTGCCCGC
1201 GGCATTGATG TTGAACAAGT GTCTGTCGTC ATGAACCTTG ATCTTCCCGT
1251 GGACAAGGAC GGGAACTCTG ACAATGAGAC CTACCTGCAC CGGATCGGGC
1301 GCACGGGGCCG CTTTGGCAAG AGGGGCTGAG CAGTGAACAT GGTGGACAGC
1351 AAGCACAGCA TGAACATCCT GAACAGAATC CAGGAGCATT TTAATAAGAA
1401 GATAGAAAGA TTGGACACAG ATGATTGGA CGAGATTGAG AAAATAGCCA
1451 ACTGAGAAGC TCCACAGGCC ACTGATGCCA GCCCTGGCAC TGCCCCTGCA
1501 CAGGAGACAA GTGCGTTCAG GGCACAGGCC CCGACATCAC CCAAGGACA
1551 ACGGCACAAG TAGAGAGAAA CTACCTACCT CACTTCAAAT TATGTTTGA
1601 CTTGACAAAA ATGTATGCAA ATGATGGGGG ATGGTAGAAA AAAATTATTT
1651 ACACAACCTT GGAAGATTAG GCATGAATAC ACAGAGATT ACCTTTAAAA
1701 AAAAAAAAAA AAA
```

BLAST Results

Entry G36496 from database EMBL:
SHGC-53094 Human Homo sapiens STS cDNA.
Length = 459

Minus Strand HSPs:
Score = 1693 (254.0 bits), Expect = 2.8e-70, P = 2.8e-70
Identities = 369/387 (95%), Positives = 369/387 (95%)

Entry G44014 from database EMBLNEW:
WIAF-3643-STH Human THudson SANGER Homo sapiens STS genomic, sequence
tagged site.
Score = 901, P = 2.3e-35, identities = 183/185

Medline entries

94192995:
Gene 1994 Mar 25;140(2):171-177
Mouse erythroid cells express multiple putative RNA helicase genes
exhibiting
high sequence conservation from yeast to mammals.

Peptide information for frame 1

ORF from 109 bp to 1452 bp; peptide length: 448
Category: strong similarity to known protein

```

1 MATDSWALAV DEQEAAAESL SNLHLKEEKI KPDTNGAVVK TNANAEKTDE
51 EEKEDRAAQS LLNKLIRSNL VDNTNQVEVL QRDPNSEPLYS VKSFEELRLP
101 QNLIAQSQSG TGKTAAFVLA MLSQVEPANK YPQCLCLSPT YELALQTGKV
151 IEQMGKFYFE LKLAYAVRGN KLERGQKISE QIVIGTPGTV LDWCSKLFKI
201 DPKKIKVFVL DEADVMIATQ GHQDQSIRIQ RMLPRNCQML LFSATFEDSV
251 WKFAQKVVPD PNVIKLKREE ETLDTIKQYY VLCSSRDEKF QALCNLYGAI
301 TIAQAMIFCH TRKTASWLA ELKEGHQVA LLSGEMMVEQ RAAVIERFRE
351 GKEKVLVTTN VCARGIDVEQ VSVVINFDLP VDKDGNPDNE TYLHRIGRTG
401 RFGKRGLAVN MVDSKHSNMI LNRIQEHFNK KIERLDTDDL DEIEKIAN

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_3c18, frame 1

PIR:I49731 RNA helicase - mouse, N = 2, Score = 1758, P = 3.8e-223

TREMBL:AF005239_1 gene: "Dbp80"; product: "DEAD-box helicase";
Drosophila melanogaster DEAD-box helicase (Dbp80) mRNA, complete cds.,
N = 2, Score = 1142, P = 1.8e-125

SWISSPROT:YB66_SCHPO PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06., N =
2, Score = 911, P = 5.5e-103

PIR:S66920 probable RNA helicase CA5/6 - yeast (Saccharomyces
cerevisiae), N = 2, Score = 887, P = 1.9e-98

>PIR:I49731 RNA helicase - mouse
Length = 478

HSPs:

Score = 1758 (263.8 bits), Expect = 3.8e-223, Sum P(2) = 3.8e-223
Identities = 338/349 (96%), Positives = 349/349 (100%)

```

Query:   100 PQNLIAQSQSGTGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQMGKFYP 159
          PQNLIAQSQSGTGKTAAFVLAMLS+VEPA++YPQCLCLSPTYELALQTGKVIEQMGKF+P
Sbjct:   130 PQNLIAQSQSGTGKTAAFVLAMLSRVEPADRYPQCLCLSPTYELALQTGKVIEQMGKFHP 189

Query:   160 ELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLFIDPKKIKVFVLDEADVMIAT 219
          ELKLAYAVRGNKLERGQK+SEQIVIGTPGTVLDWCSKLFIDPKKIKVFVLDEADVMIAT
Sbjct:   190 ELKLAYAVRGNKLERGQKVSEQIVIGTPGTVLDWCSKLFIDPKKIKVFVLDEADVMIAT 249

Query:   220 QGHQDQSIRIQRMLPRNCQMLLFSATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQY 279

```

Sbjct: 250 QGHQDQSIRIQR++PRNCQMLLFSATFEDSVWKFAQKVVPDPN+IKLKREEETLDTIKQY 309
 Query: 280 YVLCSSRDEKFQALCNLYGAITIAQAMIFCHTRKTASWLAELSKEGHQVALLSGEMMVE 339
 YVLC++R+EKFQALCNLYGAITIAQAMIFCHTRKTASWLAELSKEGHQVALLSGEMMVE
 Sbjct: 310 YVLCNNREEKFQALCNLYGAITIAQAMIFCHTRKTASWLAELSKEGHQVALLSGEMMVE 369
 Query: 340 QRAAVIERFREGKEKVLVTTNVCARGIDVEQSVVINFDPVOKDGNPDNETYLHRIGRT 399
 QRAAVIERFREGKEKVLVTTNVCARGIDVEQSVVINFDPVOKDGNPDNETYLHRIGRT
 Sbjct: 370 QRAAVIERFREGKEKVLVTTNVCARGIDVEQSVVINFDPVOKDGNPDNETYLHRIGRT 429
 Query: 400 GRFGKRGGLAVNMVDSKHSNMILNRIQEHFNKKIERLDTDDLDEIEKIAN 448
 GRFGKRGGLAVNMVDSKHSNMILNRIQEHFNKKIERLDTDDLDEIEKIAN
 Sbjct: 430 GRFGKRGGLAVNMVDSKHSNMILNRIQEHFNKKIERLDTDDLDEIEKIAN 478
 Score = 419 (62.9 bits), Expect = 3.8e-223, Sum P(2) = 3.8e-223
 Identities = 94/136 (69%), Positives = 104/136 (76%)
 Query: 1 MATDSWALAVDEQEAAESLSNLHLKEEKIKPDTNGAVVKTANANAECTDEEEKEDRAAQS 60
 MATDSWALAVDEQEAA +S+S+L +KEEK K DTNG V+KT+ AEKT+EEEEKEDRAAQS
 Sbjct: 1 MATDSWALAVDEQEAAVKSMSSSLQIKEEKAKSDTNG-VIKTSTTAEKTEEEEEKEDRAAQS 59
 Query: 61 LLNKLIRSNLVDNTNQVEVLQRDPSPLYSVKSFEELRL-PQNL---IAQSQSGTGKTAA 116
 LLNKLIRSNLVDNTNQVEVLQRDPSPLYSVKSFEELRL PQ L A + K
 Sbjct: 60 LLNKLIRSNLVDNTNQVEVLQRDPSPLYSVKSFEELRLKPQLLQGVYAMGFNRPSKIQE 119
 Query: 117 FVLAMLSQVEPANKYPQ 133
 L M+ P N Q
 Sbjct: 120 NALPMMLAEPQNLIAQ 136

Pedant information for DKFZphfbr2_3c18, frame 1

Report for DKFZphfbr2_3c18.1

[LENGTH] 448
 [MW] 50490.07
 [pI] 5.83
 [HMOL] PIR:I49731 RNA helicase - mouse 0.0
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YOR046c] 1e-102
 [FUNCAT] 04.01.04 rRNA processing [S. cerevisiae, YDR021w] 2e-65
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YDR021w] 2e-65
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YJL138c] 1e-63
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YJL138c] 1e-63
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YDL160c] 2e-49
 [FUNCAT] j mRNA translation and ribosome biogenesis [H. influenzae, HI0231 RNA] 9e-48
 [FUNCAT] 04.05.03 mRNA processing (splicing) [S. cerevisiae, YDL084w] 1e-43
 [FUNCAT] 1 genome replication, transcription, recombination and repair [H. influenzae, HI0892] 3e-39
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YLL008w] 1e-35
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YJL033w] 9e-27
 [FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YMR290c] 8e-26
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YDR194c] 1e-23
 [FUNCAT] r general function prediction [M. jannaschii, MJ1401] 9e-08
 [FUNCAT] 11.10 cell death [S. cerevisiae, YMR190c] 1e-05
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YMR190c] 1e-05
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YIR002c] 7e-04
 [BLOCKS] BL00039D DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039C DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039B DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039A DEAD-box subfamily ATP-dependent helicases proteins
 [PIRKW] nucleus 4e-64
 [PIRKW] RNA binding 1e-64
 [PIRKW] DEAD box 4e-64
 [PIRKW] transmembrane protein 3e-22
 [PIRKW] DNA binding 2e-32
 [PIRKW] ATP 1e-101
 [PIRKW] purine nucleotide binding 4e-64
 [PIRKW] P-loop 1e-101
 [PIRKW] hydrolase 4e-43
 [PIRKW] protein biosynthesis 1e-64
 [PIRKW] ATP binding 2e-35
 [SUPFAM] WW repeat homology 3e-29
 [SUPFAM] translation initiation factor eIF-4A 1e-64
 [SUPFAM] DEAD/H box helicase homology 1e-101
 [SUPFAM] DNA helicase recG 2e-06
 [SUPFAM] unassigned DEAD/H box helicases 1e-101
 [SUPFAM] ATP-dependent RNA helicase DBP1 9e-33

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[SUPFAM]      ATP-dependent RNA helicase DHH1 4e-48
[SUPFAM]      tobacco ATP-dependent RNA helicase DB10 3e-29
[PROSITE]     MYRISTYL 5
[PROSITE]     AMIDATION 1
[PROSITE]     CK2_PHOSPHO_SITE 6
[PROSITE]     GLYCOSAMINOGLYCAN 1
[PROSITE]     PKC_PHOSPHO_SITE 8
[PROSITE]     ASN_GLYCOSYLATION 1
[PFAM]        Helicases conserved C-terminal domain
[PFAM]        DEAD and DEAH box helicases
[KW]          Alpha_Beta

SEQ      MATDSWALAVDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANA EKTDEEEKEDRAAQS
PRD      ccchhhhhhhhhhhhhhhhhhhccchhhhhhhccccceeeeeehhhhhhhhhhhhhhhhhhh

SEQ      LLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEELRLPQNLIASQS SGTGKTA AFVLA
PRD      hhhhhhhhhhhccccceeeeeecccccceehhhhhhhhhccceeeeeecccccchhhhhhh

SEQ      MLSQVEPANKYPQCLCLSPITYELALQTGKVIEQMGKFYPELKLAYAVRGNKLERGQKISE
PRD      hhhhhhhhhhhccccceeeeeccchhhhhhhhhhhhhhhhhhhccccccccceeccccchhhhhhhhe

SEQ      QIVIGTPTGTVLDWC SKLKFIDPKKIKVFLDEADVM IATQGHQDQSIRIQ RMLPRNCQML
PRD      eeeccccccchhhhhhhhhhhhhhhhhccccceeeeeccchhhhhhhhhccchhhhhhhhhhhhhhhccccceee

SEQ      LFSATFEDSVWKFAQKVVPDPNVIKLKREETLDTIKQYYVLCSSRDEK FQALCNLYGAI
PRD      eeccccccchhhhhhhhhhhhhhhhhccccceeeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhch

SEQ      TIAQAMIFCHTRKTASWLAAELSKEGHQVALLSGEMMVEQRAAVIERFREGKEKVLVTTN
PRD      hhhhhhheecchhhhhhhhhhhhhhhhhccccceeeecchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ      VCARGIDVEQSVVINFDFLPVDKDG NPDNETYLHRI GRTGRFGKRG LAVNMVDSKHS MNII
PRD      cccccceeeeeeeeeccccccccccccccccceeeeeecccccccccceeeeeeeccchhhhh

SEQ      LNRIQE HFNKKIERLDTDDLDEIEKIAN
PRD      hhhhhhhhhhhhhccccccccccchhhhhhhcc

```

Prosites for DKFZphfbr2 3c18.1

PS000001	389->393	ASN_GLYCOSYLATION	PDOC000001
PS000002	109->113	GLYCOSAMINOGLYCAN	PDOC000002
PS000005	90->93	PKC_PHOSPHO_SITE	PDOC000005
PS000005	111->114	PKC_PHOSPHO_SITE	PDOC000005
PS000005	147->150	PKC_PHOSPHO_SITE	PDOC000005
PS000005	226->229	PKC_PHOSPHO_SITE	PDOC000005
PS000005	275->278	PKC_PHOSPHO_SITE	PDOC000005
PS000005	284->287	PKC_PHOSPHO_SITE	PDOC000005
PS000005	311->314	PKC_PHOSPHO_SITE	PDOC000005
PS000005	399->402	PKC_PHOSPHO_SITE	PDOC000005
PS000006	48->52	CK2_PHOSPHO_SITE	PDOC000006
PS000006	93->97	CK2_PHOSPHO_SITE	PDOC000006
PS000006	123->127	CK2_PHOSPHO_SITE	PDOC000006
PS000006	189->193	CK2_PHOSPHO_SITE	PDOC000006
PS000006	245->249	CK2_PHOSPHO_SITE	PDOC000006
PS000006	284->288	CK2_PHOSPHO_SITE	PDOC000006
PS000008	110->116	MYRISTYL	PDOC000008
PS000008	175->181	MYRISTYL	PDOC000008
PS000008	185->191	MYRISTYL	PDOC000008
PS000008	385->391	MYRISTYL	PDOC000008
PS000008	406->412	MYRISTYL	PDOC000008
PS000009	402->406	AMIDATION	PDOC000009

Pfam for DKFZphfbr2 3c18.1

HMM_NAME	DEAD and DEAH box helicases					
HMM	*gLpFWILRNiYeMGFEkPTPIQQqAIPiILEG...RDVMACAQTSGSK ++ ++ +N ++ P E+ +++A+++Q+G+GK					
Query	65	LIRSNLV DNTNQVEVLQRDPNSPLYSVKS FEEELRLPQNLI AQSQSGTGK	113			
HMM	TAAFLIPLMLQHIDwdPWppqpPdPrALILAPTRELAMQIEECrKfgkHM TAAF++ ML+++ + PQ +L L+PT ELA+Q+ ++++++GK++					
Query	114	TAAFVLA MLSQVEPAN--KY PQ--CLCLSPTYELAL QTKGVIEQM GKfY	158			
HMM	ngIRImcIYGgtmMRdQMRmLeRGpPHIVIA TPGRLLDHIHER.gtldLD r + + + + + + + + + + + + + + + I V I + T P G + D + + + + + D + +					

Query 159 PELKLAYAVR----GNKLERGQKISEQIVIGTPGTVLDWCSKLFIDPKK 204
HMM IeMLVMDEADRMLD.MGFIDQIRrIMrqIPMpwnRQTMMSATMPdeIQE
I+++V+DEAD M+ +G +DQ RI R++P +N Q ++FSAT+ D++ +
Query 205 IKVFLVLEADVMIATQGHQDQSIRIQRMPL--RNCQMLLFSAFEDSVWK 252
HMM LARrFMRNPIRInIdMdElTtnEnIkQwYiyVerEMWKfdclcrLIe*
+A ++ +P I ++++E T++ +IKQ+Y+ + + ++KF +LC+L++
Query 253 FAQKVVPDPNVIKLKREEETLD-TIKQYYVLCSSRDEKFQALCNLYG 298

HMM_NAME Helicases conserved C-terminal domain
HMM *EilleeWLknlGIrvmYIHGdMpQeERdeIMddFNnGEynVLicTDVggr
+L+ +L+++G +V+ + G M+ E+R +++++F++G+ +VL++T+V +R
Query 316 SWLAAELSKEGHQVALLSGEMMVEQRAAVIERFREGKEKVLVTTNVCAR 364
HMM GIDIPdVNVHVINYDM....PWNPEq..YIQRIGRTgRIG*
GID+++V++VIN+D+ + NP++ Y++RIGRTGR+G
Query 365 GIDVEQVSVVINFDLFVDKDGNDNETYLHRRIGRTGRFG 403

Medline
PMID: 10322435
"Unwinding RNA in : DEAD-box proteins and related families." de la Cruz J, Kressler D, Linder
P

DKFZphfbr2_3f16

group: brain derived

DKFZphfbr2_3f16 encodes a novel 127 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 1514 bp

Poly A stretch at pos. 1454, polyadenylation signal at pos. 1434

```
1 GGGGGGACTG GAGAAGGGAG GCGGCGGGCG AAGCGCACGT CGAGCGGGGG
51 AGCGGGCGCTG CCTGTGGAGA TCCGCGGAGG CCGACAGGAT TCGTTGGCTG
101 CCGTCCCCGC TGCTGTGCAT TGGGTTAAAA ACGACAACCA ACATCAGCCA
151 TGAAAGATCC AAGTCGCAGC AGTACTAGCC CAAGCATCAT CAATGAAGAT
201 GTGATTATTA ACGGTCATTC TCATGAAGAT GACAATCCAT TTGCAGAGTA
251 CATGTGGATG GAAAATGAAG AAGAATTCAA CAGACAAATA GAAGAGGAGT
301 TATGGGAAGA AGAATTTATT GAACGCTGTT TCCAAGAAAT GCTGGAAGAG
351 GAAGAAGAGC ATGAATGGTT TATTCAGCT CGAGATCTCC CACAAACTAT
401 GGACCAAATC CAAGACCAGT TTAATGACCT TGTATCAGT GAAGGCTCTT
451 CTCTGGAAGA TCTTGTGTC AAGAGCAATC TGAATCCAAA TGCAAAGGAG
501 TTTGTTCTTG GGGTGAAGTA CGGAAATATT TGAGTAGACG GGGCCCTCTT
551 TTGGTGGATG TAGCACAATT TCCACACTGT GAAGGCAGTA TTAGAAGACT
601 TAATTGTAAG AGCACTCTTG TCACTGTGTT ACACTTATGC ATTGCCAAAG
651 TTTTGTGTTAG TCTTGCAATG TTAATAAAAG TGCTGAGACT GTTACTAAGT
701 AAAAAAGCTGT CAAACATTTA CTGAAAATAG AATTGGCCCC ATGCCTTGAT
751 GTGAAGACAG CAAGGAAAGA AGCACCAGTC AAGTTGTGAA CAAGCACCAA
801 ATTAAGAGAC CTAACCTTA CCAAAATGTC TTTTGTGAG GCTAATCTAT
851 CACTTGTATA TGTCTAACT TTAATAATCAG TACATTTAAT TTGAGTTCCA
901 ACTGTTAAGC ATATTTCTCA GACTTAAAT TGATTATGTC CCCATCAAAA
951 ACAATCTCCA TTTTCTGAAG GTCTGTTAGT TAATTGAGA TAATTTGTTA
1001 AAGGCAAGTA TGTATATTA CTGAGGCTAC AAGTTAGTCA GCAGATGAGT
1051 GCCAGTCCAG CCTTTTCCGG TATGTTATTG TTAGAAATAT TGAGTTCTAA
1101 TGTTACATCT GAGGAAGTAT GTAATTTGAG AATTGTAAC TCTAAGGGAT
1151 TCACTGCATC ATAGCTATGC CTGTATGGAG TCTAACATAT GACCAATACC
1201 AACCCATAAT CCAGCTGAAC AAAGATACTG TAACATTATG ATTTGAGTGG
1251 TGCTTTTCTT TGCTTTGTTA ACCATCACGA GAGTCTGCAG CACAACTTT
1301 AACAAAGCTA GAACAGTTT GGCTTCTTAA ACTTCATATT TGGGTAGGTT
1351 AAGCTGCCAT ACGTGTTCAG TGTGAATAGT GTTTAAGTTG AAAATATTGT
1401 AAAAAAATTA TATTTTTC AATAATTTA AAAAAATAA TAATAGTAGA
1451 ACTGAAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAAAGAAAAA
1501 AAAAAAATA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 150 bp to 530 bp; peptide length: 127
Category: putative protein

1 MKDPSRSSTS PSIINEDVII NGHSHEDDNP FAEYMWME EEFNRQIEEE

51 LWEEEFIERC FQEMLEEEEE HEWFIPARDL PQTMDQIQDQ FNDLVISEGS
101 SLEDLVVKS NLPNAKEFVP GVKYGNI

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_3f16, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_3f16, frame 3

Report for DKFZphfbr2_3f16.3

[LENGTH] 127
[MW] 14998.41
[pI] 4.04
[BLOCKS] BL01269D
[PROSITE] MYRISTYL 1
[PROSITE] CK2_PHOSPHO_SITE 2
[KW] Alpha_Beta
[KW] LOW_COMPLEXITY 27.56 %

SEQ MKDPSRSSTSPSIINEDVIINGSHEDDNPFAYMWMENEEFNQIEEELWEEEFIERC
SEGxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD ccc

SEQ FQEMLEEEEEHEWFIPARDLPQTMDQIQDQFNDLVISEGSSLEDLVVKS NLPNAKEFVP
SEG xxx
PRD hhhhhhhhhhhhhccccccccchhhhhhhhhcccccccccccccccccccccccc

SEQ GVKYGNI
SEG
PRD ccccccc

Prosite for DKFZphfbr2_3f16.3

PS00006	24->28	CK2_PHOSPHO_SITE	PDOC00006
PS00006	100->104	CK2_PHOSPHO_SITE	PDOC00006
PS00008	121->127	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_3f16.3)

DKFZphfbr2_3g8

group: metabolism

DKFZphfbr2_3g8.1 encodes a novel 178 amino acid protein with similarity to yeast ARD1 protein.

In yeast, ARD1 and NAT1, are required for the expression of an N-terminal protein acetyltransferase 1. NAT1 controls full repression of the silent mating type locus HML, sporulation and entry into G0. ARD1 is involved in the assembly of the NAT 1-complex. The new protein could be part of this or an other NAT complex.

The new protein can find application modulating NAT assembly and action and therefore be important in metabolism of drugs and environmental mutagens.

strong similarity to N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 homolog

complete cDNA, complete cds? start at Bp 40, EST hits

Sequenced by AGOWA

Locus: /map="20"

Insert length: 1030 bp

Poly A stretch at pos. 1013, no polyadenylation signal found

```

1 TGGGCTTGGC GAACGGTCTT CGGAAGCGGC GGCGGCGCGA TGACCACGCT
51 ACGGGCCTTT ACCTGCGACG ACCTGTTCCG CTTCAACAAC ATTAACCTGG
101 ATCCACTTAC AGAAACTTAT GGGATTCCCT TCTACCTACA ATACCTCGCC
151 CACTGGCCAG AGTATTTTCAT TGTGTCAGTG GCACCTGGTG GAGAATTAAT
201 GGGTTATATT ATGGGTAAAG CAGAAGGCTC AGTAGCTAGG GAAGAATGGC
251 ACGGGCACGT CACAGCTCTG TCTGTTGCCC CAGAATTTTCG ACGCCTTGGT
301 TTGGCTGCTA AACTTATGGA GTTACTAGAG GAGATTTTCAG AAAGAAAGGG
351 TGGGTTTTTT GTGGATCTCT TTGTAAGAGT ATCTAACCAA GTTGCACTTA
401 ACATGTACAA GCAGTTGGGC TACAGTGTAT ATAGGACGGT CATAGAGTAC
451 TATTCGGCCA GCAACGGGGA GCCTGATGAG GACGCTTATG ATATGAGGAA
501 AGCACTTTCC AGGGATACTG AGAAGAAATC CATCATACCA TTACCTCATC
551 CTGTGAGGCC TGAAGACATT GAATAACCCT GGGCAGTGGT TCTTAGGCAG
601 ATACTCTACA TGCTTTATCG ACAATATTAT TTTCATTGGA TGATTCTGGA
651 GCTCTATTAG GAGAAAAGTA ATCATTTTAG GTCTTAAAGA CTTCAAGAAA
701 ATACAGGTTA TCAATTTATT TTAAATCTCA TTGTTTCCAG TTAGCAATAT
751 CATACCTATT AAAGCTGTTC ATTGTAACAA AATTCAATCA AAAAGGCAGC
801 TAGGTCAGAA GGAAACATAC CACTCTCATG GTTCATAGTA TTTACTGTAT
851 GTATGCTAGG GAAAAGACTT GCTCCAGTCT CCTCCTCAGT TCTGTGCCTG
901 AGAACCCTG CTGCATATAT TTGTTTTTAA ATTTTGTATT GAACTGTATA
951 TTGAAGCTTT AAAAGCATAT ATGAAATGTA TAAATCTAAG ATGTATAATA
1001 CATTATTGAC TCCAAAAAAA AAAAAAAAAA

```

BLAST Results

Entry HSG0101 from database EMBL:
human STS SHGC-35956.
Length = 401
Minus Strand HSPs:
Score = 1417 (212.6 bits), Expect = 9.3e-58, P = 9.3e-58
Identities = 301/311 (96%)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 40 bp to 573 bp; peptide length: 178
Category: strong similarity to known protein

```

1 MTTLRAFTCD DLFRFNNINL DPLTETYGIP FYLQYLAHWP EYFIVAVAPG
51 GELMGYIMGK AEGSVAREEW HGHVTAHSV PEFRRGLGLAA KLMELLEIS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_3g8, frame 1

PIR:S69021 hypothetical protein YPR131c - yeast (*Saccharomyces cerevisiae*), N = 1, Score = 382, P = 2.3e-35

HSPs:

Query: 119 AVNMYKQLGYSVYRTVIEYYASANGPEDEDAYDMRKALSRDTEKSI 165
A++ YK LGYSYR VI YYS +G+ DED++DMRK LSRD ++SI
Sbjct: 119 AIDFYKGLGYSVYRRVIGYYSNPHGK-DEDSFDMRKPLSRDVRRESI 164

Pedant information for DKFZphfbr2_3g8, frame 1

Report for DKFZphfbr2_3g8.1

```

[LENGTH]      178
[MW]           20338.24
[pI]           5.06
[HOMOL]        TREMBL:SPCC16C4_12 gene: "SPCC16C4.12"; product: "putative n-terminal
acetyltransferase complex subunit"; S.pombe chromosome III cosmid cl6C4. 7e-47
[FUNCAT]       06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YPR131c] 6e-37
[FUNCAT]       01.06.07 lipid, fatty-acid and sterol utilization [S. cerevisiae, YHR013c]
4e-14
[FUNCAT]       30.03 organization of cytoplasm [S. cerevisiae, YHR013c] 4e-14
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YHR013c] 4e-14
[FUNCAT]       r general function prediction [M. jannaschii, MJ1530] 6e-09
[PIRKW]        acyltransferase 1e-12
[SUPFAM]        arrest-defective protein 1 1e-12
[SUPFAM]        Escherichia coli peptide N-acetyltransferase rimI 1e-07
[PROSITE]       CK2_PHOSPHO_SITE 3
[PROSITE]       PKC_PHOSPHO_SITE 3
[KW]            Alpha Beta

```

SEQ	MTTLRAFTCDLFRFNINLDPLTETYGI PFYLQYLAHWPEYFIVAVAPGGELMGYIMGK
PRD	ccccccccccchhhhhhhccccccccccchhhhhhhccccceeeeeccccceeeehhhh
SEQ	AEGSVAREEWHGHVTSVAPEFRRLGLAAKLMELLEESI SERKGGFFVDLFVRVSNQVAV
PRD	hccccccccccccceeeehhhhhhhhcchhhhhhhhhhhhhhhccceeeeeeeecchhhh
SEQ	NMYKQLGFSVYRTVIEYSSASNGPEDDAYDMRKALS RDT EKKS I I PLHPVRPEDIE
PRD	hhhhhhccccchhhhhhhccccccccccccchhhhhhhhhhhhhhhhhhhcccccccccc

Prosites for DKFZphfbr2_3g8.1

PS00005	3->6	PKC_PHOSPHO_SITE	PDOC00005
PS00005	100->103	PKC_PHOSPHO_SITE	PDOC00005
PS00005	160->163	PKC_PHOSPHO_SITE	PDOC00005
PS00006	8->12	CK2_PHOSPHO_SITE	PDOC00006
PS00006	133->137	CK2_PHOSPHO_SITE	PDOC00006
PS00006	141->145	CK2_PHOSPHO_SITE	PDOC00006

(No Pfam data available for DKFZphfbr2_3g8.1)

DKFZphfbr2_312

group: brain derived

DKFZphfbr2_312 encodes a novel 589 amino acid protein with weak similarity to *S. cerevisiae* ubiquitin-like protein DSK2.

Pfam predicts for this protein similarity to the ubiquitin family; No informative BLAST results; No predictive prosite or SCOP motive

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to ubiquitin-like protein DSK2 yeast

complete cDNA, complete cds, EST hits
Dsk2p is involved in spindle pole body SPB duplication, SPB = centomer
strong similarity to HRIHFB2157 human mRNA

Sequenced by AGOWA

Locus: unknown

Insert length: 2978 bp
Poly A stretch at pos. 2958, polyadenylation signal at pos. 2924

```
1 GGGGGGAGGA AGCGGTGGCT GCTGCGGATG TCGGTGTGAG CGAGCGGCGC
51 CTGAACACAC GSCGGCTGCC GAGCGCCTGA CCCGGGCGCTG CGCCAGAGGCC
101 TGCACCGAGC TCCGGGGGCC CACACCGCT ACGGTGCCCC TCGGCCCGTT
151 GCTACTGAGG CGGCGTGCTC TGCATTCTTC GCTGTCCAGG CCTGCCGGCT
201 CTGGTGTCTG CTGGCTCCTC CTTGTCTGCC TGCTCCCTCC TGCTTGCTTG
251 AGTCACCGCC GCCCGCGCCG CCACAGCCAT GGCCGAGAGT GGTGAAAGCG
301 GCGGTCTCTC GGGCTCCAG GATAGCGCCG CCGGAGCCGA AGGTGCTGGC
351 GCCCCCGCGG CCGCTGCCTC CGCGGAGCCC AAAATCATGA AAGTCACCGT
401 GAAGACCCCG AAGGAAAAGG AGGAATTCCG CGTGCCCGAG AATAGCTCCG
451 TCCAGCAGTT TAAGGAAGAA ATCTCTAAAC GTTTTAAATC ACATACTGAC
501 CAACTTGTGT TGATATTGTC TGGAAAAATT TTGAAAGATC AAGATACTCT
551 GAGTCAGCAT GGAATTCATG ATGGACTTAC TGTTACCTTT GTCATTAAAA
601 CACAAAACAG GCCTCAGGAT CATTGAGCTC AGCAAAACAA TACAGCTGGA
651 GGCAATGTGA CTACATCATC AACTCCTAAT AGTAACTCTA CATCTGGTTC
701 TGCTACTAGC AACCTTTTG GTTTAGTGG CTTGGGGGGA CTTGCAAGTC
751 TGAGTAGCTT GGGTTTGAAT ACTACCAACT TCTCTGAATC ACAGAGTCAG
801 ATGCAGCGAC AACTTTTGTC TAACCCTGAA ATGATGGTCC AGATCATGGA
851 AAATCCCTTT GTTCAGAGCA TGCTCTCAAA TCCTGACCTG ATGAGACAGT
901 TAATTATGGC CAATCCACAA ATGCAGCAGT TGATACAGAG AAATCCAGAA
951 ATTAGTCATA TGTTGAATAA TCCAGATATA ATGAGACAAA CGTTGGAATC
1001 TGCCAGGAAT CCAGCAATGA TGCAGSAGAT GATGAGGAAC CAGGACCGAG
1051 CTTTGAGCAA CCTAGAAAGC ATCCCAGGGG GATATAATGC TTTAAGGCGC
1101 ATGTACACAG ATATTCAGGA ACCAATGCTG AGTGCTGCAC AAGAGCAGTT
1151 TGGTGGTAAT CCATTGTGCT CTTGGTGAG CAATACATCC TCTGGTGAAG
1201 GTAGTCAACC TTCCCGTACA GAAAATAGAG ATCCACTACC CAATCCATGG
1251 GCTCCACAGA CTTCCAGAG TTCATCAGCT TCCAGCGGCA CTGCCAGCAC
1301 TGTGGGTGGC ACTACTGGTA GTACTGCCAG TGGCACTTCT GGGCAGAGTA
1351 CTACTGCGCC AAATTTGGTG CCTGGAGTAG GAGCTAGTAT GTTCAACACA
1401 CCAGGAATGC AGAGCTTGTT GCAACAAATA ACTGAAAACC CACAATGAT
1451 GCAAAACATG TTGTCTGCCC CCTACATGAG AAGCATGATG CAGTCACTAA
1501 GCCAGAAATC TGACCTTGCT GCACAGATGA TGCTGAATAA TCCCCTATTT
1551 GCTGGAAATC CTCAGCTTCA AGAACAATG AGACAACAGC TCCCACTTT
1601 CCTCCAACAA ATGCAGAATC CTGATACACT ATCAGCAATG TCAAACCTTA
1651 GAGCAATGCA GGCCTTGTTA CAGATTCAGC AGGGTTTACA GACATTAGCA
1701 ACGGAAGCCC CGGGCTCAT CCCAGGGTTT ACTCCTGGCT TGGGGGCATT
1751 AGGAAGCACT GGAGGCTCTT CGGGAATCAA TGGATCTAAC GCCACACCTA
1801 GTGAAAACAC AAGTECCAGA GCAGGAACCA CTGAACCTGG ACATCAGCAG
1851 TTTATTTCAG AGATGCTGCA GGCTCTTGCT GGAGTAAATC CTCACTACA
1901 GAATCCAGAA GTCAGATTTC AGCAACAATC GGAACAATC AGTGCAATGG
1951 GATTTTTGAA CCGTGAAGCA AACTTGCAAG CTCTAATAGC AACAGGAGGT
2001 GATATCAATG CAGCTATTGA AAGTTACTG GGCTCCAGC CATCATAGCA
2051 GCATTCTGTG ATCTTGAAAA AATGTAATTT ATTTTGTATA ACGGCTCTTA
2101 AACTTTAAAA TACCTGCTTT ATTTCAATTT GACTCTTGGA ATTCTGTGCT
2151 GTTATAAACA AACCCAATAT GATGCATTTT AAGGTGGAGT ACAGTAAGAT
2201 GTGTGGGTTT TTCTGTATTT TTCTTTCTG GAACAGTGGG AATTAAGGCT
2251 ACTGCATGCA TCACCTTCTG ATTTATTGTA ATTTTAAAA AACATCACCT
2301 TTTATAGTTG GGTGACCAGA TTTTGTCTG CATCTGTCCA GTTTATTGTC
2351 TTTTAAACA TTAGCCTATG GTAGTAATTT ATGTAGAATA AAAGCATTAA
2401 AAAGAAGCAA ATCATTTGCA CTCTATAATT TGTGGTACAG TATTGCTTAT
2451 TGTGACTTTG GCATCCATTT TTGCAACAAA TGCTGTAAGA TTTATACTAC
2501 TGATAATTTT GTTTTATTTG TATACAATAT AGAGTATGCA CATTGGGGAC
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2551 TGCATTTCTG GAAACATACT GCAATAGGCT CTCTGAGCAA AACACCTGTA
2601 ACTAAAAAAG TGAAGATAAG AAAATACTCT TAAAGCTGAG TATTTCCTAA
2651 TTGTATAGAA TCTTACAGCA TCTTTGACAA ACATCTCCCA GCAAAAGTGC
2701 CGGTTAGTCA GGTTTGTTGA AAATACAGTA GAAAAGCTGA TTCTGGTTAT
2751 CTCTTTAAGG ACAATTAATT GTACAGACAC ATAATGTAAC ATTGTCTCAA
2801 CATTCAITCA CAGATTGACT GTAAATTACC TTAATCTTTG TGCAGACTGA
2851 AGGAACACTG TAGTATACCC CAAAGTGCAT TTGCCTAGGA CTTCTCAGCT
2901 TCTCCCATAG GTAGTTTAAC AGGCATTAAA ATTTGTAATT GAAATGTTGC
2951 TTTCACTCAA AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 279 bp to 2045 bp; peptide length: 589
 Category: similarity to known protein

```

1 MAESGESGGP PGSODSAGA EGAGAPAAAA SAEPKIMKVT VKTPKEKEEF
51 AVPENSSVQQ FKEEISKRFK SHTDQLVLIF AGKILKDQDT LSQHGIDHGL
101 TVHLVIKTQN RPQDHSAAQT NTAGGNVTTS STPNSTSTSG SATSNPFGLG
151 GLGGLAGLSS LGLNTTNFSE LQSOMQRQLL SNPEMMVQIM ENPEVQSMLS
201 NPDLMRQLIM ANPQMQLLIQ RNPEISHMLN NPDIMRQTL LARNFAMMQE
251 MMRNQDRALS NLESIPGGYN ALRRMYTDIQ EPMLSAAQEQ FGGNFFASLV
301 SNTSSGEGSQ PSRTENRDPL PNPWAPQTSQ SSSASSGTAS TVGGTTGSTA
351 SGTSGQSTTA PNLVPGVGAS MFNTPGMQSL LQKITENPQL MQNMLSAPYM
401 RSMQSLSQN PDLAAQMMLN NPLFAGNPQL QEOMRQQLPT FLQQMQNPDT
451 LSAMSNPRAM QALLQIQQLL QTLATEAPGL IPGFTPLGLA LGSTGGSSGT
501 NGSNATPSEN TSPTAGTTEP GHQOFIQOQL QALAGVNPQL QNPEVRFOQQ
551 LEQLSAMGFL NREANLQALI ATGGDINAAI ERLLSQPS

```

BLASTP hits

Entry CE1_1 from database TREMBL:
 "F15C11.2"; Caenorhabditis elegans cosmid VF15C11L
 Length = 293
 Score = 454 (159.8 bits), Expect = 4.4e-43, P = 4.4e-43
 Identities = 81/162 (50%), Positives = 113/162 (69%)

Entry S54583 from database PIR:
 ubiquitin-like protein DSK2 - yeast (Saccharomyces cerevisiae)
 Length = 373
 Score = 278 (97.9 bits), Expect = 1.2e-23, P = 1.2e-23
 Identities = 100/307 (32%), Positives = 155/307 (50%)

Entry AB015344_1 from database TREMBLNEW:
 gene: "HRIHFB2157"; Homo sapiens HRIHFB2157 mRNA, partial cds.
 Score = 1135, P = 3.6e-115, identities = 227/301, positives = 253/301

Alert BLASTP hits for DKFZphfbr2_312, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_312, frame 3

Report for DKFZphfbr2_312.3

```

[LENGTH]      589
[MW]           62489.22
[pI]           5.02
[HOMOL]        TREMBL:AB015344_1 gene: "HRIHFB2157"; Homo sapiens HRIHFB2157 mRNA, partial
cds. 1e-121
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YMR276w] 2e-17

```

[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YMR276w] 2e-17
 [BLOCKS] BL00299 Ubiquitin family proteins
 [SUPFAM] unassigned ubiquitin-related proteins 5e-16
 [SUPFAM] ubiquitin homology 5e-16
 [PROSITE] MYRISTYL 24
 [PROSITE] CK2_PHOSPHO_SITE 9
 [PROSITE] GLYCOSAMINOGLYCAN 1
 [PROSITE] PKC_PHOSPHO_SITE 3
 [PROSITE] ASN_GLYCOSYLATION 7
 [PFAM] Ubiquitin family
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 23.43 %

SEQ MAESGESGGPPGSQDSAAGAEGAGAPAAAASAEPKIMKVTVKTPKEKEEFAVPENSSVQQ
 SEG ..xxxxxxxxxxxx..xxxxxxxxxxxxxxxxxxxxxx..xxxxxxxxxxxx
 laaraCEEEEEETTCEEEECTTTTBHHH

SEQ FKEEISKREKSHTDQLVLI FAGKILKDQDTLSQHGHDGLTVHLVIKTONRPQDHSAQQT
 SEG
 laara HHHHHHHHHCCCGGEEEEETTEECTTTTBGGGGCCTTTTEEEEBEBC.....

SEQ NTAGGNVTTSSTPNSNSTSGSATSNPFGGLGGLAGLSSLGNTTNFSELQSQMQRQLL
 SEG
 laara

SEQ SNPEMMVQIMENPFVQSMLSNPDLMRQLIMANPQMQLIQRNPEISHMLNPNPDIMRQLE
 SEG
 laara

SEQ LARNPAMMQEMMRNQDRALSNLESIPGGYNALRRMYTDIQEPMLSAAQEQFGGNPFASLV
 SEG
 laara

SEQ SNTSSGEGSQPSRTENRDLPLNPWPAPQTSQSSSASGTASTVGGTTGSTASGTSGQSTTA
 SEG
 laara

SEQ PNLVPGVGASMFNTPGMQSLLQQTENPQLMQNMLSAPYMRSMQSLSQNPDLAAQMMLN
 SEG
 laara

SEQ NPLFAGNPQLQEQMRQQLPTFLQQMQNPDTLSAMSNPRAMQALLQIQGLQTLATEAPGL
 SEG
 laara

SEQ IPGFTPLGALGSTGGSSGTNGSNATPSENTSPTAGTTEPGHQQFIQOMLQALAGVNPQL
 SEG
 laara

SEQ QNPEVRFOQQLEQLSAMGFLNREANLQALQIATGGDINAAIERLLGSQPS
 SEG
 laara

Prosites for DKFZphfbr2_312.3

PS00001	55->59	ASN_GLYCOSYLATION	PDOC00001
PS00001	126->130	ASN_GLYCOSYLATION	PDOC00001
PS00001	136->140	ASN_GLYCOSYLATION	PDOC00001
PS00001	164->168	ASN_GLYCOSYLATION	PDOC00001
PS00001	167->171	ASN_GLYCOSYLATION	PDOC00001
PS00001	302->306	ASN_GLYCOSYLATION	PDOC00001
PS00001	501->505	ASN_GLYCOSYLATION	PDOC00001
PS00002	305->309	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	40->43	PKC_PHOSPHO_SITE	PDOC00005
PS00005	43->46	PKC_PHOSPHO_SITE	PDOC00005
PS00005	66->69	PKC_PHOSPHO_SITE	PDOC00005
PS00006	43->47	CK2_PHOSPHO_SITE	PDOC00006
PS00006	71->75	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00006	200->204	CK2_PHOSPHO_SITE	PDOC00006
PS00006	260->264	CK2_PHOSPHO_SITE	PDOC00006
PS00006	304->308	CK2_PHOSPHO_SITE	PDOC00006
PS00006	312->316	CK2_PHOSPHO_SITE	PDOC00006
PS00006	506->510	CK2_PHOSPHO_SITE	PDOC00006
PS00006	572->576	CK2_PHOSPHO_SITE	PDOC00006
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	12->18	MYRISTYL	PDOC00008

PS00008	19->25	MYRISTYL	PDOC00008
PS00008	24->30	MYRISTYL	PDOC00008
PS00008	95->101	MYRISTYL	PDOC00008
PS00008	124->130	MYRISTYL	PDOC00008
PS00008	140->146	MYRISTYL	PDOC00008
PS00008	150->156	MYRISTYL	PDOC00008
PS00008	153->159	MYRISTYL	PDOC00008
PS00008	162->168	MYRISTYL	PDOC00008
PS00008	267->273	MYRISTYL	PDOC00008
PS00008	293->299	MYRISTYL	PDOC00008
PS00008	308->314	MYRISTYL	PDOC00008
PS00008	337->343	MYRISTYL	PDOC00008
PS00008	343->349	MYRISTYL	PDOC00008
PS00008	347->353	MYRISTYL	PDOC00008
PS00008	355->361	MYRISTYL	PDOC00008
PS00008	366->372	MYRISTYL	PDOC00008
PS00008	479->485	MYRISTYL	PDOC00008
PS00008	489->495	MYRISTYL	PDOC00008
PS00008	492->498	MYRISTYL	PDOC00008
PS00008	495->501	MYRISTYL	PDOC00008
PS00008	499->505	MYRISTYL	PDOC00008
PS00008	573->579	MYRISTYL	PDOC00008

Pfam for DKFZphfbr2_312.3

HMM_NAME	Ubiquitin family		
HMM	*MQIFVKTLtGRTcTFEVepQEetVeqIKQHieekEGIPPeQQRLIFaGRQ		
	M ++VKT + +F V+++ V Q+K+ I+ +Q +LIFAG+		
Query	37 MKVTVKTPK-EKEEFAVPENSSVQQFKEEISKRFKSHTDQLVLIFAGKI	84	
HMM	LEDeKTLsDYNiggeSTLHLVlR*		
	L D TLS+++I + T+HLV++		
Query	85 LKDQDTLSQHGIIHDGLTVHLVIK	107	

DKFZphfbr2_62b11

group: signal transduction

DKFZphfbr2_62b11 encodes a novel 655 amino acid putative GTPase-activating protein, related to human chimaerins.

The rac small GTPase is associated with type-I phosphatidylinositol 4-phosphate 5-kinase and regulating the production of phosphatidylinositol 4,5-bisphosphate. The new protein is expected to activate p21rac-related small GTPases.

The new protein can find clinical application in modulating/blocking the response to a cellular receptor.

similarity to CHIMAERIN

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="4"

Insert length: 4593 bp

Poly A stretch at pos. 4571, polyadenylation signal at pos. 4553

```
1 GGGGGAGTTT GAAGACAGAA AGGAAAGGGG AGAAACCTGC AGAGAGCATC
51 AAAGGATGGG GGGTGCTATA AAAGAAGCAG GGGGGTCCTT TGAAAGAAAT
101 CTATCATGCA CTGAAATGCT TTCTGGAGAA GGTGCCGTTA TTTTCCTCCC
151 CTCTTGCTCA GATGAAAGGA GCCAGCAAGG ACAGTCCTGA AATATTCCTC
201 AGGGGACTTT TTGTCATTGT TCCTCTTTCC TCTTGACAG AGCTATTTGC
251 TGACCTTTCC AGAGGAATCT CAGTCCAGCT GAGAAGACAG TTCTTAATAA
301 AAACAAAAAA ATGCAAAAAC CAATTCCTGC TGTTTGAATG GGAATGGTAG
351 CTTGCTTGCT GCAGTTCTTT TCCTGTGACA TTTTGGAATG TCTGCAGAAA
401 CTTAAAAAAA AGAAAAAAA AACCTTAAAA ACTCCCTGGA TTAGGCAAGA
451 GAAAAGGAAG TTTTTTTTTG CTAACAGGA GTAAATGAGA GGTGGTAACT
501 TATCCCTAAG CCAGGACCTG GATGATCAAA ACCTTCAAAT TCTAGGGATC
551 AGCACTTCAA AAATAACAAG TAAACAAGCA TGAGGAGTGG CTGTTGGGTT
601 TCGCTCAGAG GCAGGTTTTA AAGGAAGCCA AAACCGGGTT CAGAAGTTCA
651 GGCCTGTACG ATGCTGAAG ACCGGAATTC TGGGGGGTGC CCGGCTGGTG
701 CCTTAGCCTC AACTCCTTTC ATCCCTAAAA CTACATACAG AAGAATCAAA
751 CGGTCTTTTA GTTTTCGGAA AGGCATTTTT GGACAGAAAC TGGAGGATAC
801 TGTTCCGTAT GAGAAGAGAT ATGGGAACCG TCTGGCTCCG ATGTTGGTGG
851 AGCAGTGCCT GGACTTTATC CGACAAAGGG GGCTGAAAGA AGAGGGTCTC
901 TTTTCGACTG CAGGCCAGGC TAATCTGTGT AAGGAGCTCC AAGATGCCCT
951 TGACTGTGGG GAGAAGCCAT CATTTGACAG CAACACAGAT GTACACACGG
1001 TGGCATCACT TCTTAAGCTG TACCTCCGAG AACTTCCAGA ACCAGTTATT
1051 CCTTATGCGA AGTATGAAGA TTTTGTGTC TGTGCCAAAC TGCTCAGCAA
1101 GGAAGAGGAA GCAGGTGTTA AGGAATTAGC AAAGCAGGTG AAGAGTTTGC
1151 CAGTGGTAAA TTACAACCTC CTCAAGTATA TTTGCAGATT CTTGGATGAA
1201 GTACAGTCTC ACTCGGGAGT TAACAAAATG AGTGTGCAGA ACTTGGCAAC
1251 GGTCTTTGGT CCTAATATCC TGCGCCCCAA AGTGGAAAGT CCTTTGACTA
1301 TCATGGAGGG CACTGTGGTG GTCCAGCAGT TGATGTCAGT GATGATTAGC
1351 AAACATGATT GCCTCTTTCC CAAAGATGCA GAACTACAAA GCAAGCCCCA
1401 AGATGGAGTG AGCAACAACA ATGAAATTCA GAAGAAAGCC ACCATGGGGC
1451 TGTTACAGAA CAAGGAGAAC AATAACACCA AGGACAGCCC TAGTAGGCAG
1501 TGCTCCTGGG ACAAGTCTGA GTCACCCAG AGAAGCAGCA TGAACAATGG
1551 ATCCCCCACA GCTCTATCAG GCAGCAAAAC CAACAGCCCA AAGAACAGTG
1601 TTCACAAGCT AGATGTGTCT AGAAGCCCCC CTCTCATGGT CAAAAAGAAC
1651 CCAGCCTTTA ATAAGGGTAG TGGGATAGTT ACCAATGGGT CCTTCAGCAG
1701 CAGTAATGCA GAAGGTCTTG AGAAAACCCA AACCACCCCC AATGGGAGCC
1751 TACAGGCCAG AAGGAGCTCT TCACTGAAGG TATCTGGTAC CAAAATGGGC
1801 ACGCACAGTG TACAGAATGG AACGGTGCGC ATGGGCATTT TGAACAGCGA
1851 CACACTCGGG AACCCACAAA ATGTTTCAAAA CATGAGCTGG CTGCCAAATG
1901 GCTATGTGAC CCTGAGGGAT AACAAGCAGA AAGAACAAGC TGGAGAGTTA
1951 GGCCAGCACA ACAGACTGTC CACCTATGAT AATGTCCATC AACAGTTCTC
2001 CATGATGAAC CTTGATGACA AGCAGAGCAT TGACAGTGCT ACCTGGTCCA
2051 CTTCTCTCTG TGAAATCTCC CTCCTGAGA ACTCCAATC CTGTCGCTCT
2101 TCTACCAACA CCTGCCCAGA GCAAGACTTT TTTGGGGGGA ACTTTGAGGA
2151 CCCTGTTTTG GATGGGCCCC CGCAGGACGA CCTTTCCAC CCCAGGGACT
2201 ATGAAAGCAA AGGTGACCAC AGGAGTGTGG GAGGTCGAAG TAGTCTGTCC
2251 ACCAGTAGCA GTGACAACAG TGAGACATTT GTGGGCAACA GCAGCAGCAA
2301 CCACAGTGCA CTGCACAGTT TAGTTTCCAG CCTGAAACAG GAAATGACCA
2351 AACAGAAGAT AGAGTATGAG TCCAGGATAA AGAGCTTAGA ACAGCGAAAC
2401 TTGACTTTGG AAACAGAAAT GATGAGCCTC CATGATGAAC TGGATCAGGA
2451 GAGGAAAAAG TTCACATATG TAGAAATAAA AATGCGAAAT GCCGAGCGAG
2501 CAAAAGAAAG TGCCGAGAAA AGAAATGACA TGCTACAGAA AGAAATGGAG
2551 CAGTTTTTTT CCACGTTTGG AGAACTGACA GTGGAACCCA GGAGAACCGA
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2601 GAGAGGAAAC ACAATATGGA TTCAGTGAGC CTGCTTTCGC CTGCTGTCTC
2651 TGATGGCTCT GGCAAGGACT CCAGGGATTG TGGTGGGATA TGAAGGATA
2701 CCAGGTGGCT GGTACCTGG ATGTACAGAA GTCTAACTGG TGAAGGAATA
2751 TCATTACAG ACATTAAACA TCCATATCTG CAATGTGTAC CAAAGTATA
2801 TCATGCCCCA TAATGCTACT GTCAAGTGT ACAACTGGAT ATGTGTATAT
2851 AGAGTAGTTT TTCAAAAGTA AACTAAAAAT GAGAAGCATA TTTCAAGAAT
2901 TATTTTATTG CAAGTCTTGT ATTTAAATGT TAAATCAATA TGTGTGTGCA
2951 ATTTAGCTTG CTTTCAAGCT TCACCCCTTG CACTTAACAT AAGCTATTTT
3001 TGGCATTGTG TTATCATCGG CTTATTTTAT AGATCAATAT TTTTATTTC
3051 CTTTTTTGCT GAGGAAATGA AGATAAGCAA AAATATAAAT ATATATATAA
3101 ATATATGAGT TATTAACC AGAAGAATAC TTTGTGGCTG TGCTGTTTGT
3151 GGACCGAATC TCTTAACTG CCAAAAAGAG AAATGTAAAT AGTTTTATAA
3201 AATACAGTCG AATCACCAGG AACCTTTGAG CTGCTTTTAA AATTCTTCCC
3251 CTGGCACCAC TCAGTTTTCG TTTTGCAGG CGATTGACA TAGGAACCTT
3301 GAGACTCCAT GAGAAAGTCC CTTTCTGAGG CCCACTGTCT ACCTTGCCAG
3351 ATCCTCAGTG CGTATCGCCA ATGCAGGATG CTCCTTAGAA AAGAAAAAAT
3401 GGTAAAGGAT GGCATTTAAC GATTCAAGCT TTGAATTACT CTGCTCCCTC
3451 GGACCGAATC TCTTAACTG CTGGATAGTT TTAGAGGAAT TCTCTGCTA
3501 CTTAGGTACT GGGAAACAAT GCTTGCTAAA CCATGCCAC GTGAGCACCT
3551 GTCTCCCACT CAAACCTCTC CCATCTCCA ACAACTGCAC TTTAGAATAC
3601 CAGCAGTGAA ATGGTATTAC TGTTTCCCTC TGAGTGAAAC TGCTAGAGTA
3651 TATCTACAGT AGTGACATTT TTTTCTCACT CAGGCTATTG CCATCTGGGA
3701 TTCTCTCCCT ACTACAGCTG GCAAAGTTGG TTTGCAGCAA GAAGATAGTG
3751 GGAGGGGGCC AGGCTGCAGG AGAAGGAGAA AAGTTTAGAA GAAACAAACC
3801 ATTTTGCTTC TAATTTTGAC AGTATCACTT TCCTGTTAAA ACATACAATA
3851 ATTTTAAAG GTGAATGCCT AAAGTTCCAA TTTTAGCAA TATGGGAACC
3901 TCAGCAATGC TAATTTTCTA GAAAAACCCA GGGCTCTTTG GAGCTAGAGT
3951 TTTGGGAGAA CAGTCTTCA CAATAAGGCA ATGGTTTGA GAGGCCAGGC
4001 AAATAATCTT TCTACCGTA GAACAAAAG TTACAAAAGG CATAATCGGA
4051 AATAGAGACT ACATACTTGA GTTTATGGG TTTGTGTTGT TTGAAGGTC
4101 AATGCTTGCA TGTGTTTATT TATTTTCAAG AGGGAAAGTG GTCTGTACTG
4151 CTTTCATCCT TGCCACTGTC TTGCTTTTAT TTTTACTCT CCCACTGAGC
4201 AAGCGTCTGT GGTCTATGG TATCAACCAG TATCTTTATA GCAATAATTT
4251 CTTAATTTCC CTTTCTCTC TCTTTCCAAT TATTAACCA GTTACTTCCA
4301 CCTGGACATA CGATAGGAAA TTCAAACCTCA AAATATGAAA ATTGATCTTA
4351 ATAACCTCTC CTTTATATCT TTTACCTAT TTCCAGTCCT TATCATAGTT
4401 GATAAAACC TCAGACTCAT CCAGAAAGCT ATATGATGCA CTAGTAAAAA
4451 AAACAAAGAT ATTTAAACTG CTTGGGTTCA AATGGTATAC AATTTGCCAG
4501 CTGTTACTGA ACCTTCTATG CATAACTTTT TTTTCTCTCT GTGCAATTGG
4551 AATAATAAAA ATACTACTCC CATAAAAAA AAAAAAANA AAC

```

BLAST Results

Entry G38474 from database EMBLNEW:
 SHGC-58303 Human Homo sapiens STS genomic, sequence tagged site.
 Score = 2175, P = 1.2e-92, identities = 439/441

Medline entries

97476250:
 Beta2-chimaerin is a high affinity receptor for the phorbol ester tumor promoters.

Peptide information for frame 1

ORF from 661 bp to 2625 bp; peptide length: 655
 Category: similarity to known protein

```

1 MPEDRNSGGC PAGALASTPF IPKTTYRRIK RCFSFRKGIF GQKLEDTVRY
51 EKRYGNRLAP MLVEQCVDIF RQRGLKEEGL FRLPGQANLV KELQDAFDCG
101 EKPSFDSNTD VHTVASLLKL YLRELPEPVI FYAKYEDFLS CAKLLSKEEE
151 AGVKELAKQV KSLPVVNYNL LKYICRFLDE VQSYSGVNMK SVQNLATVFG
201 PNILRPKVED PLTIMEGTVV VQQLMSVMIS KHDCLFPKDA ELQSKPDQGV
251 SNNNEIQKKA TMGLLQNKEN NNTKDSPSRQ CSWDKSESPQ RSSMNNGSPT
301 ALSGSKTNSP KNSVHKLDVS RSPPLMVKKK PAFNKGSGIV TNGSFSSSNA
351 EGLEKTQTFP NGSLOARRSS SLKVSQTKMG THSVQNGTVR MGILNSDTLG
401 NPTNVRNMSW LPNGYVTLRD NKQKEQAGEL GQHNRLSTYD NVHQFQSMN
451 LDDKQSIDSA TWSTSSCEIS LPENSNSCRS STTTCPEQDF GGGNFEDPVL
501 DGPPQDDLSH PRDYESKSDH RSVGGRSSRA TSSSDNSETF VGNSSSNHSA
551 LHSLVSSLKQ EMTKQKIEYE SRIKSLEQRN LTLETEMMSL HDELDQERKK

```

601 FTMIEIKMRN AERAKEDAEK RNDMLQKEME QFFSTFGELT VEPRRTERGN
651 TIWIQ

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_62b11, frame 1

SWISSPROT:Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053., N = 3, Score = 661, P = 2.4e-89

TREMBL:HSU0908_1 product: "unknown"; Human clones 23549 and 23762 mRNA, complete cds., N = 1, Score = 348, P = 1.1e-29

PIR:S29128 N-chimerin - rat, N = 1, Score = 286, P = 2.8e-24

PIR:S29956 beta-chimerin - rat, N = 1, Score = 279, P = 1.6e-23

TREMBL:AB014572_1 gene: "KIAA0672"; product: "KIAA0672 protein"; Homo sapiens mRNA for KIAA0672 protein, complete cds., N = 1, Score = 314, P = 1e-24

>SWISSPROT:Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053.
Length = 638

HSPs:

Score = 661 (99.2 bits), Expect = 2.4e-89, Sum P(3) = 2.4e-89
Identities = 122/209 (58%), Positives = 160/209 (76%)

Query: 38 GIFGQKLEDTVRYEKRYGNRLAPMLVEQCVDIFRORGLKEEGLFRLPGQANLVKELQDAF 97
G+FGQ+L++TV YE+++C L P+LVE+C +FI + G EEG+FRLPGQ NLVK+L+DAF
Sbjct: 148 GVFGQRLDETVAEQKFGPHLVPILEKCAEFIEHGRNEEGIFRLPGQDNLVKQLRDAF 207

Query: 98 DCGEKPSFSDNTDVHTVASLLKLYLRLEPEPVIPYAKYEDFLSCAKLLSKEEEAGVKELA 157
D GE+PSFD +TDVHTVASLLKLYLR+LPEPV+P++YE FL C +L + +E +EL
Sbjct: 208 DAGERPSFDRDTHVHTVASLLKLYLRDLPEPVVPSQYEGFLLCGQLTNADEAKAQQLM 267

Query: 158 KQVKSPLVVVNYNLLKYICRFLDEVQSYSGVNMKMSVQNLATVFGPNILRPKVEDPLTIMEG 217
KQ+ LP NY+LL YICRFL E+Q VNMKMSV NLATV G N++R KVEDP IM G
Sbjct: 268 KQLSILPRDNYSLLSYICRFLHEIQLNCAVNMKMSVDNLATVIGVNLIRSKVEDPAVIMRG 327

Query: 218 TVVVQQLMSVMISKHDCFLPKDAELQSKP 246
T +Q++M++MI H+ LFPK ++ P
Sbjct: 328 TPQIQRVMTMMIRDHEVLFPKSKDIPLSP 356

Score = 210 (31.5 bits), Expect = 2.4e-89, Sum P(3) = 2.4e-89
Identities = 45/115 (39%), Positives = 73/115 (63%)

Query: 531 TSSSDNSETFVGNSSSNHSALHSL---VSSLKQEMTKQKIEYESRIKSLEQRNLTLTEM 587
T +S NSET G +S + SL V L++E+ QK YE +IK+LE+ N + ++
Sbjct: 523 TLASPNSETGPGKNSGEEIDSLQRMVQELRKEIETQKQMYEEQIKNLEKENYDVWAKV 582

Query: 588 MSLHDELQDERKKFTMIEIKMRNAERAKEDAEKRNNDMLQKEMEQQFFSTFGELTVE 642
+ L++EL++E+KK +EI +RN ER++ED EKRN L++E+++F + E E
Sbjct: 583 VRLNEELEKEKKKSAALEISLRNMERSREDVEKRNKALEEEVKEFVKSMKEPKTE 637

Score = 70 (10.5 bits), Expect = 1.2e-74, Sum P(3) = 1.2e-74
Identities = 28/121 (23%), Positives = 54/121 (44%)

Query: 528 SRATSSSDNSETFVGNSSSNHSALHSLVSSLKQE-MTKOKIEYESRIKSLEQRNL-TLET 585
S+ TS+ DN + G+ SAL S K + + E K+ + + +L+
Sbjct: 489 SQRSTSYDNVPSLPGSPGEEASALSSQACDSKGDTLASPNSETGPGKNSGEEIDSLQR 548

Query: 586 EMMSLHDELQDERKKFTMIEIKMRNAERAKEDAEKRNNDMLQKEMEQQFFSTFGELTVEPRR 645
+ L E++ +++ ME +++N E+ D + L +E+E+ L + R
Sbjct: 549 MVQELRKEIETQKQ---MYEEQIKNLEKENYDVWAKVVRLNEELEKEKKKSAALEISLRN 605

Query: 646 TER 648
ER
Sbjct: 606 MER 608

Score = 53 (8.0 bits), Expect = 2.4e-89, Sum P(3) = 2.4e-89
Identities = 31/111 (27%), Positives = 46/111 (41%)

Query: 344 SFSSSNAEGLEKTQTTPNGSLQARRSSSLKVSQKMGTHSVQNG----TV--RMGILNSD 397
SFSS ++ + T T A S KV K G +Q+ T+ R L S
Sbjct: 388 SFSSMTSDS-DTTSPTGOQPSDAFEDSSKVPREKPGDWKMSRKRTQTLNPKCFLTSA 446

Query: 398 TLG-NPTNV---RNMSWLPNGYVTLRDNKQKEQAGELGQ---HNRLSTYDNV 442
 G N + + +N W P+ + ++ + +L Q R STYDNV
 Sbjct: 447 FQGANSSKMEIFKNEFWSPSSEAKAGEGHRRTMSQDLRQLSDSQRTSTYDNV 498

Score = 53 (8.0 bits), Expect = 3.5e-14, Sum P(3) = 3.5e-14
 Identities = 32/125 (25%), Positives = 56/125 (44%)

Query: 242 LQSKPDG---VSNNEIQKKATMGLLQNKEN---NNTKD---SPSRQCSWDKSESPQRSS 293
 ++SK +D + +IQ+ TM ++++ E +KD SP Q + K RSS
 Sbjct: 314 IRSKVEDPAVIMRGTPQIQRVMTM-MIRDHEVLFPKSKDIPLSPPAQKNDPKKAPVARSS 372

Query: 294 MNNGSPTALSGSKTNSPKNSVHKLDVSRSPPLMVKKNPAPFNKSGIVTNGSFSSSSNAEGL 353
 + + L S+T+S + D + P ++ AF + S V +
 Sbjct: 373 VGWDATEDLRISRTDSFSSMTSDSDTTS--PTGQQPSDAFPEDSSKVPREKPGDWMQSR 430

Query: 354 EKTQTTPN 361
 ++TQT PN
 Sbjct: 431 KRTQTLPN 438

Pedant information for DKFZphfbr2_62b11, frame 1

Report for DKFZphfbr2_62b11.1

{LENGTH} 655
 {MW} 73394.60
 {pI} 8.13
 {HOMOL} SWISSPROT:Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053. 3e-71
 {FUNCAT} 03.07 pheromone response, mating-type determination, sex-specific proteins
 [S. cerevisiae, YPL115c] 1e-16
 {FUNCAT} 09.04 biogenesis of cytoskeleton [S. cerevisiae, YPL115c] 1e-16
 {FUNCAT} 03.04 budding, cell polarity and filament formation [S. cerevisiae, YPL115c] 1e-16
 {FUNCAT} 10.02.09 regulation of g-protein activity [S. cerevisiae, YPL115c] 1e-16
 {FUNCAT} 03.22 cell cycle control and mitosis [S. cerevisiae, YER155c] 2e-16
 {FUNCAT} 30.03 organization of cytoplasm [S. cerevisiae, YER155c] 2e-16
 {FUNCAT} 10.99 other signal-transduction activities [S. cerevisiae, YDR379w] 4e-16
 {FUNCAT} 03.10 sporulation and germination [S. cerevisiae, YDL240w] 3e-15
 {FUNCAT} 06.10 assembly of protein complexes [S. cerevisiae, YOR134w] 2e-13
 {FUNCAT} 30.04 organization of cytoskeleton [S. cerevisiae, YOR134w] 2e-13
 {SCOP} dlrgp_1.83.1.1.1 p50 RhoGAP domain [human (Homo sapiens)] 2e-46
 {SCOP} dlpbwa_1.83.1.1.2 p85 alpha subunit RhoGAP domain [human (Homo sapiens)] 6e-37
 {PIRKW} phosphotransferase 3e-13
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 {PIRKW} alternative splicing 2e-20
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 {PIRKW} cytoskeleton 1e-08
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 {SUPFAM} bcr protein 7e-21
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 {SUPFAM} pleckstrin repeat homology 2e-15
 {SUPFAM} LIM metal-binding repeat homology 9e-15
 {SUPFAM} protein kinase C zinc-binding repeat homology 5e-24
 {PROSITE} MYRISTYL 16
 {PROSITE} CAMP_PHOSPHO_SITE 3
 {PROSITE} CK2_PHOSPHO_SITE 15
 {PROSITE} TYR_PHOSPHO_SITE 2
 {PROSITE} PKC_PHOSPHO_SITE 11
 {PROSITE} ASN_GLYCOSYLATION 8
 {KW} Irregular
 {KW} 3D
 {KW} LOW_COMPLEXITY 6.87 %
 {KW} COILED_COIL 12.06 %

SEQ MPEDRNSGGCPAGALASTPFIPKTTYRRIKRCFSFRKGIFGQKLEDTVRYEKRYGNRLAP
 SEG
 COILS
 lrgp-

SEQ MLVEQCVDIFIRQGLKEEGLFRLPGQANLVKELQDAFDCGEKPSFDSNTDVHTVASLLKL
 SEG
 COILS
 lrgp- HHHHHHHHHHHHHHTTTTTTTTCCCHHHHHHHHHHHHHCCCCGGGGCCCCCHHHHHHHHH

SEQ YLRELPEPVIPIYAKYEDFLSCAKLLSKEEEAGVKELAKQVKSPLPVVNYNLLKYICRFLDE
 SEG

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COILS .....
lrgp- HHHHTTTTTTGGGHHHHH--TTTTCGGGHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHH
SEQ    VQSYSGVNKMSVQNLATVFGPNILRPKVEDPLT IMEGTVVVVQQLMSVMISKHDCLFPKDA
SEG    .....
COILS .....
lrgp- HHHHHHHHCCCHHHHHHHHGGGCC.....
SEQ    ELQSKPQDGVSNNEIQKKATMGLLQNKENNNTKQSPSRQCSWDKSESPQRSSMNNGSP
SEG    .....
COILS .....
lrgp- .....
SEQ    ALSGSKTNSPKNSVHKLDVSRSPPLMVKKNPAPFNKSGIVTNGSFSSSNAEGLEKTQTTP
SEG    .....
COILS .....
lrgp- .....
SEQ    NGSLOARRSSSLKVSQTKMGTHSVQNGTVRMGILNSDTLGNPTNVRNMSWLPNGYVTLRD
SEG    .....
COILS .....
lrgp- .....
SEQ    NKQKEQAGELGQHNLSTYDNVHQFQSMNLDDKQSIDSATWSTSSCEISLPENSNSCRS
SEG    .....
COILS .....
lrgp- .....
SEQ    STTTCPEQDFGGNFEDPVLDPQDDLSHPRDYESKSDHRSVGGRSSRATSSSDNSETF
SEG    .....
COILS .....
lrgp- .....
SEQ    VGNSSSNHSLVSSSLKQEMTKQKIEYESRIKSLEQRNLTLETMMSLHDELQDERKK
SEG    .....
COILS .....
lrgp- .....
SEQ    FTMIEIKMRNAERAKEDAERNDMLQKEMEQQFFSTFGELTVEPRRTERGNTIWIQ
SEG    .....
COILS .....
lrgp- .....

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Prosites for DKFZphfbr2_62b11.1

PS00001	271->275	ASN_GLYCOSYLATION	PDOC00001
PS00001	342->346	ASN_GLYCOSYLATION	PDOC00001
PS00001	361->365	ASN_GLYCOSYLATION	PDOC00001
PS00001	386->390	ASN_GLYCOSYLATION	PDOC00001
PS00001	407->411	ASN_GLYCOSYLATION	PDOC00001
PS00001	543->547	ASN_GLYCOSYLATION	PDOC00001
PS00001	547->551	ASN_GLYCOSYLATION	PDOC00001
PS00001	580->584	ASN_GLYCOSYLATION	PDOC00001
PS00004	258->262	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	367->371	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	599->603	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	25->28	PKC_PHOSPHO_SITE	PDOC00005
PS00005	34->37	PKC_PHOSPHO_SITE	PDOC00005
PS00005	47->50	PKC_PHOSPHO_SITE	PDOC00005
PS00005	309->312	PKC_PHOSPHO_SITE	PDOC00005
PS00005	371->374	PKC_PHOSPHO_SITE	PDOC00005
PS00005	388->391	PKC_PHOSPHO_SITE	PDOC00005
PS00005	417->420	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	527->530	PKC_PHOSPHO_SITE	PDOC00005
PS00005	557->560	PKC_PHOSPHO_SITE	PDOC00005
PS00005	646->649	PKC_PHOSPHO_SITE	PDOC00005
PS00006	107->111	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	213->217	CK2_PHOSPHO_SITE	PDOC00006
PS00006	230->234	CK2_PHOSPHO_SITE	PDOC00006
PS00006	348->352	CK2_PHOSPHO_SITE	PDOC00006
PS00006	417->421	CK2_PHOSPHO_SITE	PDOC00006
PS00006	437->441	CK2_PHOSPHO_SITE	PDOC00006
PS00006	465->469	CK2_PHOSPHO_SITE	PDOC00006
PS00006	470->474	CK2_PHOSPHO_SITE	PDOC00006
PS00006	484->488	CK2_PHOSPHO_SITE	PDOC00006
PS00006	516->520	CK2_PHOSPHO_SITE	PDOC00006
PS00006	532->536	CK2_PHOSPHO_SITE	PDOC00006

PS00006	589->593	CK2_PHOSPHO_SITE	PDOC00006
PS00006	602->606	CK2_PHOSPHO_SITE	PDOC00006
PS00006	635->639	CK2_PHOSPHO_SITE	PDOC00006
PS00007	43->51	TYR_PHOSPHO_SITE	PDOC00007
PS00007	176->185	TYR_PHOSPHO_SITE	PDOC00007
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	9->15	MYRISTYL	PDOC00008
PS00008	13->19	MYRISTYL	PDOC00008
PS00008	249->255	MYRISTYL	PDOC00008
PS00008	263->269	MYRISTYL	PDOC00008
PS00008	297->303	MYRISTYL	PDOC00008
PS00008	304->310	MYRISTYL	PDOC00008
PS00008	338->344	MYRISTYL	PDOC00008
PS00008	343->349	MYRISTYL	PDOC00008
PS00008	352->358	MYRISTYL	PDOC00008
PS00008	362->368	MYRISTYL	PDOC00008
PS00008	376->382	MYRISTYL	PDOC00008
PS00008	392->398	MYRISTYL	PDOC00008
PS00008	400->406	MYRISTYL	PDOC00008
PS00008	524->530	MYRISTYL	PDOC00008
PS00008	542->548	MYRISTYL	PDOC00008

(No Pfam data available for DKF2phfbr2_62b11.1)

DKFZphfbr2_62f10

group: intracellular transport and trafficking

DKFZphfbr2_62f10 encodes a novel 320 amino acid protein with strong similarity to mammalian zinc transporter proteins.

The novel proteins is a membrane protein, which should be involved in the transport of Zinc across the cell membrane.

The Zn-T-transporters are membrane proteins that facilitates sequestration of zinc in endosomal vesicles. In the brain, ZnT-3 mRNA seems to be involved in the accumulation of zinc in synaptic vesicles. Zinc (Zn) is an essential element in normal development and metabolism. Recent studies show that in Alzheimer's disease, Zn functions as a double-edged sword, affording protection against Alzheimer's amyloid beta peptide (the major component of senile plaques) at low concentrations and enhancing toxicity at high concentrations by accelerated aggregation of the amyloid beta peptide.

The new protein can find application in modulation of Zinc transport in neuronal cells, thus providing means for a modulation of Alzheimer's amyloid beta peptide plaque formation.

strong similarity to zinc transporter proteins ;

membrane regions: 5

Summary DKFZphfbr2_62f10 encodes a novel 320 amino acid protein with similarity to zinc transporter protein.

The new protein can find clinical application in modulating Zn²⁺ uptake.

strong similarity to zinc transporter proteins

complete cDNA, complete cds, few EST hits

Sequenced by LMU

Locus: unknown

Insert length: 5422 bp

Poly A stretch at pos. 5397, polyadenylation signal at pos. 5381

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1  GTCTAACTTT  GGAAATATCA  CCTCATGCT  GTCTTCCCAG  GATGTCTCTC
51  TCCCTAAGTA  AGGGATGTTA  CTCCTGGAG  GGAATGCAGT  GTTGGGAATC
101 TGAAGACCCA  GCTTTGAGCT  GAATTTGCTT  TGTGATACCT  GGAGAGAAGA
151 CGTGTTTCT  TGACAACAGC  ACAGTACCTA  GTGAGTTCAA  CAACAACGAC
201 AACAACAGCC  GCAGCTCATC  CTGGCCGTCA  TGGAGTTTCT  TGAAAGAGCG
251 TATCTTGTA  ATGATAAAGC  TGCCAAGATG  TATGCTTTCA  CACTAGAAAG
301 AAGGAGCTGC  AAATGAACAC  TTCATAGCAA  TGTGGAATC  CAACAGAAAC
351 CGGTGAATAA  AGATCAGTGT  CCCAGAGAGA  GACCAGAGGA  GCTGGAGTCA
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451 GAATGAGTAC  GCCTATGCCA  AGTGGAACT  CTGTTCTGCT  TCAGCAATAT
501 GCTTCATTT  CATGATTGCA  GAGGTCGTGG  GTGGGCACAT  TGCTGGGAGT
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1101 GCCTGAATTA  CAGTGGTGTG  AAAGAGCTTA  TTTTAGCAGT  CGACGGGGTG
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1251 GGAGAGAAAT  TGCTAAAGCC  CTTAGCAAAA  GCTTTACGAT  GCACTCACTC
1301 ACCATTGAGA  TGGAACTTCC  AGTTGACCAG  GACCCCGACT  GCCTTTTCTG
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1401 CAGGCCACCT  TCAAACATGC  TGCTATGCAA  TTTCTGCATC  ATAGAAAATA
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1601 ATATAGATTA  TTCCTGAGTG  GAGCCGAAGT  AACAGCTGTT  TGTAACATATC
1651 GGCAATACCA  AATTCATCTC  CCTCCAATA  ATGCATCTTG  AGAACACATA
1701 GGTAATTTTG  AACTCAGGAA  AGTCTTACTA  GAAATCAGTG  GAAGGGACAA
1751 ATAGTCACAA  AATTTTACCA  AAACATTAGA  AACAAAAAAT  AAGGAGAGCC
1801 AAGTCAGGAA  TAAAAGTGAC  TCTGTATGCT  AACGCCACAT  TAGAACTTGG
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1851 TTCTCTCACC AAGCTGTAAT GTGATTTTTT TTTCTACTCT GAATTGGAAA
1901 TATGTATGAA TATACAGAGA AGTGCTTACA ACTAATTTTT ATTTACTTGT
1951 CACATTTTGG CAATAAATCC CTCTTATTTT TAAATTTCTAA CTTGTTTATT
2001 TCAAAAACCTT ATATAATCAC TGTTCAAAAG GAAATATTTT CACCTACCAG
2051 AGTGCTTAAA CACTGGCACC AGCCAAAGAA TGTGGTTGTA GAGACCCAGA
2101 AGTCTTCAAG AACAGCCGAC AAAAACATTC GAGTTGACCC CACCAAGTTG
2151 TTGCCACAGA TAATTTAGAT ATTTACCTGC AAGAAGGAAT AAAGCAGATG
2201 CAACCAATTC ATTCAGTCCA CGAGCATGAT GTGAGCACTG CTTTGTGCTA
2251 GACATTTGGG TTAGCACTGA AACTATAAAG AGGAATCAGA CGCAGCAAGT
2301 GCTTCTGTGT TCTGGTAGCA ACTCAACACT ATCTGTGGAG AGTAAACTGA
2351 AGATGTGCAG GCCAACATTC TGGAAATCCT ATGTCAGTGG GTTTGGTTTG
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2501 AGCTAGACAC ATACATTGGC AGTTACAATA GTATCATGAA TTGCAATGAT
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2651 ATATGGAGGC TCTCCAGGAA GACGAAGAAG AGAAGGACAT TCTAGGCAAA
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2851 GGAGATAGGT CTTAGATGAT TTTTATGTTG TTGTCAGACT CTAGCAAGGT
2901 ACTAGAAACC TAGCAGGCAT TAATAATTGT TGAGGCAATG ACTCTGAGGC
2951 TATATCTGGG CCTTGTCAAT ATTTATCATT TATATTTGTA TTTTCTCTG
3001 AAATTTGAGG GCCAAGAAAA CATTGACTTT GACTGAGGAG GTCACATCTG
3051 TGCCATCTCT GCAATCAAT CAGCACCAC GAAATAACTA CTTAGCATT
3101 TGTGTAGCTT TCCCTGCTCA GTAGAGACAA ATATACTCAT CCCCCACCTC
3151 AGTGAGCTTG TTTAGGCAAC CAGGATTAGA GCTGCTCAGG TTCCCAACGT
3201 CTCTGCCAC ATCGGGTCT CAAAATGGAA AGAATGGTTT ATGCCAAATC
3251 ACTTTTCCCT TCTGAAGGAC CACTGAATGG TTTTGTTTTT CCATATTTTG
3301 CATAGGACGC CCTAAAGACT AGGTGACTTG GCAAACACAC AAGTGTTAGT
3351 ATAATTCTTT GCTTCTGCTT CTTTGTGAAA ATCATGTTTA GATTTGATTT
3401 TAAGTCAGAA ATTCAGTGA TGTCAGGTAA TCATTATGGA GGGAGATTTG
3451 TGTGTCAACC AAAGTAATTG TCCCATGGCC CCAGGGTATT TCTGTTGTTT
3501 CCTGTAAATT CTGCTTTTTT AGTCAGCTAG ATTGAAAAC CTGAACAGTA
3551 GATGTTTATA TGGCAAAATG CAAGACAATC TATAAGGGAG ATTTTAAGGA
3601 TTTTGAATG AAAAAACAGA TGCTACTCAG GGGCTTTATG GACCATCCAT
3651 CAATTCTGAA GTTCTGACTC TCCCATTACC CTTTCCCTGG TGTGGTCAGA
3701 ACTCCAGGTC ACTGGAAGTT AGTGAATCA TGTAGTTGAA TTCTTTACTT
3751 CAAGACATTG TATTCTCTCC AGCTATCAAA ACATTAATGA TCTTTTATGT
3801 CTTTTTTTTT TTATTGTTAT ACTTTAAGTT CTGGGGTACA TGTGCGGAAC
3851 ATTAGGTTT GTTACATAGG TATACATGTG CCATGGTGGT TTGCTGCACT
3901 CATCAACCTG TCATCTACAT TCTTTTATGT CTGCTTTTCA AAGCAACACT
3951 CTGTTCTTCT GAGTAGTGAA ATCAGGTCAA CTTTACCACC AGCCTCCATT
4001 TTTAATATGT TTCACCATCA TCCAGCACCT ACTTAAGATT TATCTAGGGC
4051 TCTGTGGTGA TGTTAGGACC CATAAAGAA ATTTATGCCT TCCATATGTT
4101 TGGTTACAGA TGGGAAATGG GAATGTTGAA GGACATGAAA GAAAGGATGT
4151 TTACACATTA AGCATCAGTT CTGAAGCTAG ATTGTCTGAG TTTGAATCTT
4201 AGCTCTTCCC TTTATTAGCT CTGTGACCTC GAGCTAGTTA CTTAAATGCT
4251 CTGATCCTCT ATTTCTCTGAT CAGTGAAACC TCCCTATTCA AATGTGTGAG
4301 AGTTTAATAA ATTAGGACAC TTAAAAATGT TGGAGCAGTG CATAGCATGT
4351 AGTGTTCACT ACATGTTAAA TGTTGTTTTT TATTATGTAC AAACATGTGT
4401 GGGCACAGAA TTTTAAATCA TCTCAACTTT TGAGAAATTT TGAGTTATCA
4451 ACACCGTTCC CACAAGACAG TGGCAAAATT ATTGGTGAGA ATTAACAGC
4501 TGTTCTCAG AGGAAGCAAT GGAGGCTTGC TGGGATAAAG GCATTTACTG
4551 AGAGGCTGTT ACCTAGTGAG AGTGATGAAT TAATTAAAT AGTCGAATCC
4601 CTTTCTGACT GTCTCTGAAA GCTTCCGCTT TTATCTTTGA AGAGCAGAA
4651 TGTCAACCCA AGGACATTTA TTAATAAAAA GAACAACCTG CCAGTGCAAT
4701 GAAGGCAAG TCATAGGTCT CCCAAGTCTT ACUCCATTCC TGTGAAATAT
4751 CAAGTTCTTG GCTTTCTCT GTCATGTAGC CTCAACTTTC TCCGACCGGG
4801 TGCATTTCTT TCTCTGGTTT CTAAATTGCC AGTGGCAAAT TTGGATCACT
4851 TACTTAATAT CTGTTAAATT TTGTGACCCA ACAAAGTCTT TTAGCACTGT
4901 GGTGTCAAAA AGAAAAACAC CTCCCAGGCA TATACATTTT ATAGATTCTT
4951 GGAGAATGTT GCTCTCCAGC TCCATCCCCA CCCAATGAAA TATGATCCAG
5001 AGAGTCTTGC AAAGAGACAA GCCTCATTTT CCACAATTAG CTCTAAAGTG
5051 CCTCCAGGAA ATGATTTTCT CAGCTCATCT CTCTGTATTC CTTGTTTGG
5101 ATACAGGGGC AATCTGTTTA AATGACTAAT TACAGAAATC ATTAAGGCA
5151 CCAAGCAAAAT GTCATCTCTG AATACACACA TCCCAGCTT TACAAATCCT
5201 GCCTGGCTTG ACAGTGATGA GGCCACTTAA CAGTCCAGCG CAGGCGGATG
5251 TTAATAAAAA TAAAAAGGTG ACCATCTGCG GTTTAGTTTT TTAACTTTCT
5301 GATTTACAC TTAACGTCTG TCATTCTGTT ACTGGGCACC TGTTTAAAT
5351 CTATTTTAAA ATGTTAATGA GTGTTGTTTA AAATAAAATC AGGAAAGAGA
5401 GAAAAAATAA AAAAAAATAA AC

```

BLAST Results

No BLAST result

Medline entries

97121493:
ZnT-3, a putative transporter of zinc into synaptic vesicles.

96203098:
ZnT-2, a mammalian protein that confers resistance to zinc by facilitating vesicular sequestration.

Peptide information for frame 2

ORF from 407 bp to 1366 bp; peptide length: 320
Category: strong similarity to known protein

```

1 MYHCHSGSKP TEKGANEYAY AKWKLCSASA ICFIFMIAEV VGGHIAGSLA
51 VVTDAAHLLI DLTSFLLSLF SLWLSSKPPS KRLTFGWHRA EILGALLSIL
101 CIWVVTGVLV YLACERLLYP DYQIQATVMI IVSSCAVAAN IVLTVVLHQR
151 CLGHNHKEVQ ANASVRAAFV HAPGDLFQSI SVLISALIIY FKPEYKIADP
201 ICTFIFSIIV LASTITILKD FSILLMEGVP KSLNYSVGVE LILAVDGVLS
251 VHCLHIWILT MNQVILSAHV ATAASRDSQV VRREIAKALS KSFTMHSITI
301 QMESPVDDQP DCLFCEDPCD

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_62f10, frame 2

PIR:S70632 zinc transporter ZnT-2 - rat, N = 1, Score = 884, P = 1.5e-88

TREMBL:MMU76007_1 gene: "ZnT-3"; product: "ZnT-3"; Mus musculus zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds., N = 1, Score = 772, P = 1.1e-76

TREMBL:HSU76010_1 gene: "ZnT-3"; product: "ZnT-3"; Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds., N = 1, Score = 742, P = 1.6e-73

TREMBL:MMUZNT02_1 gene: "ZnT-3"; product: "zinc transporter"; Mus musculus zinc transporter (ZnT-3) gene, complete cds., N = 1, Score = 715, P = 1.2e-70

TREMBL:CET18D3_3 gene: "T18D3.3"; Caenorhabditis elegans cosmid T18D3, N = 1, Score = 699, P = 5.9e-69

>PIR:S70632 zinc transporter ZnT-2 - rat
Length = 359

HSPs:

Score = 884 (132.6 bits), Expect = 1.5e-88, P = 1.5e-88
Identities = 171/326 (52%), Positives = 230/326 (70%)

```

Query:      2 YHCHSGSKPTEKGANEYAYAKWKLCSASAICFIFMIAEVVGGHIAGSLAVVTDAAHLLID 61
              ++CH+          +E   A+ KL  ASAIC +FMI E++GG++A SLA++TDAHLL D
Sbjct:     34 HYCHAQKDSGSHPNSEKQRRARKLYVASAICLVFMIGEIIIGGYLAQSLAIMTDAHLLTD 93

Query:     62 LTSFLLSLFSLWLSSKPPSKRLTFGWHRAEILGALLSILCIWVVTGVLVYLACERLLYPD 121
              S L+SLFSLW+SS+P +K + FGW RAEILGALLS+L IWVVTGVLVYLA +RL+  D
Sbjct:     94 FASMLISLFLWSSRPATKTMNFGWQRAEILGALLSVLSIWVVTGVLVYLAVQRLISGD 153

Query:    122 YQIQATVMIIVSSCAVAANIVLTVVLHQRCLGHNH-----KEVQANASVRAAFVHAPG 174
              Y+I+   M+I S CAVA NI++ + LHQ  GH+H          + Q N SVRAAF+H  G
Sbjct:    154 YEIKGDTMLITSGCAVAVNIIMGLALHQSGHGHSHGHSHEDSSQQQNPSVRAAFIHVVG 213

Query:    175 DLFQSIISVLISALIIYFKPEYKIADPICTFIFSIIVLASTITILKDFSILLMEGVPKSLN 234
              DL QS+ VL++A IIYFKPEYK  DICTF+FSILVL +T+TIL+D  ++LMEG PK ++
Sbjct:    214 DLLQSVGVLVAAYIIYFKPEYKYVDICTFLFSILVLGTTTLILRDVILVLMEGTPKGV 273

Query:    235 YSGVKELILAVDGVLSVHCLHIWILTMNQVILSAHVATAASRDSQVVRREIAKALSKSFT 294
              ++ VK L+L+VDGV ++H LHIW+LT+ O +LS H+A A + D+Q V +   L   F
Sbjct:    274 FTTVKNLLLSVDGVEALHSLHIWALTVAQPVLVSHIAIAQNVDAAVLKVARDRLQGKFN 333

```

Pedant information for DKFZphfbr2 62f10, frame 2

Report for DKF2phfbr2 62f10.2

Prosites for DKFZphfbr2 62f10.2

267

PS00005	80->83	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00006	304->308	CK2_PHOSPHO_SITE	PDOC00006
PS00007	13->21	TYR_PHOSPHO_SITE	PDOC00007
PS00008	7->13	MYRISTYL	PDOC00008
PS00008	42->48	MYRISTYL	PDOC00008
PS00008	94->100	MYRISTYL	PDOC00008
PS00008	228->234	MYRISTYL	PDOC00008
PS00013	125->136	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKF2phfbr2_62f10.2)

DKFZphfbr2_62n10

group: brain derived

DKFZphfbr2_62n10 encodes a novel 541 amino acid protein with similarity to Plasmodium vivax reticulocyte-binding protein 1.

The novel protein contains one Leucine Zipper, involved in protein-protein-interaction. No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to reticulocyte-binding protein

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="13"

Insert length: 3522 bp

Poly A stretch at pos. 3503, polyadenylation signal at pos. 3479

```
1 GGGGCGTGTT GCGGGGATTC TGAACGCTGC CATGGCTCAG ACCGTGTAGA
51 ATGTTACATT GTCGCTCACT CTGCCCATCA CGTGCCACAT TTGCTTGGGG
101 AAGGTACGTC AGCCTGTCAT ATGCATCAAC AACCATGTAT TTTGTTTCGAT
151 TTGTATTGAT TTGTGGTTGA AGAATAATAG CCAGTGTCCTA GCTTGCAGAG
201 TCCCCATCAC TCCTGAAAAT CCTTGCAAAG AAATTATAGG AGGAACAAGT
251 GAAAGTGAAC CTATGCTAAG CCATACGGTC AGGAAGCATC TTCGGAAGAAC
301 TAGACTTGAA TTAATACACA AAGAATATGA GGACGAAATA GATTGTTTAC
351 AGAAAGAAAGT AGAAGAGCTT AAGAGTAAAA ATCTCAGCTT GGAGTCACAG
401 ATCAAAGCTA TTCTGGATCC TTTAACCTTG GTGCAGGGCA ACCAAAATGA
451 AGACAAACAT CTAGTCACAG ATAATCCAAG TATAATTAAC CCAGAAACTG
501 TAGCAGAGTG GAAGAAAAAA CTCAGAACAG CTAATGAAAT CTATGAAAAA
551 GTGAAAGATG ATGTGGATAA GCTAAAGGAG GCAAATAAAA AATTGAAATT
601 GGAAAATGGT GGTCTGGTGA GGGAGAATT ACCACTGAAG GCTGAAGTTG
651 ATAACAGATC ACCTCAAAAG TTTGGAAGGT TTGCAGTTGC TGCTCTTCAG
701 TCCAAAGTAG AACAGTATGA GCGTGAAACC AATCGCCTCA AGAAAGCCCT
751 GGAACGAAAGT GATAAGTATA TAGAGGAACT AGAATCTCAA GTTGACACAGC
801 TAAAAAATTC AAGTGAAGAG AAAGAGGCTA TGAATTCAT TTGCCAGACA
851 GCACTTTCTG CAGATGGCAA AGGGAGCAAA GGCAGTGAGG AGGATGTGGT
901 GTCAAAGAAGT CAAGGCGATA GTGCCAGAAA GCAGCCTGGC TCATCCACCT
951 CCAGTTCTTC TCACCTAGCG AAGCCTTCCA GCAGCAGACT GTGTGACACC
1001 ACTTCTGCAA GGCAGGAAAG TACCAGCAAA GCAGACCTTA ACTGTTCTAA
1051 GAACAAAGAGC CTATATCAAG AACAGGTAGA AGTAATGTTA GATGTGACAG
1101 ATACAAGTAT GGATACTTAT TTGGAAGAG AATGGGGGAA TAAACCAAGT
1151 GACTGTGTAC CCTACAAAGA TGAAGAACTT TATGATTTTC CAGCTCCTTG
1201 TACTCCTTTG TCCCTTAGTT GCCTTCAGCT CAGTACTCCA GAAAATAGAG
1251 AGAGCTCTGT GGTCCAAGCA GGAGGTTCCTA AAAAGCACTC AAACCATCTC
1301 AGAAATTGGT TGTGTGATGA TTTTGTGAT TCTTCAAATG TTTCTAATAA
1351 AGATTCTTCA GAAGATGATA TAAGTAGAAG TGAAATGAG AAGAAATCAG
1401 AATGTTTTTC TTCCACAAAG ACAGGATTTT GGGACTGTTG TTCCACAAGC
1451 TATGCCCAAA ACTTAGATTT TGAAAGTTCA GAGGGGAACA CGATAGCAAA
1501 TTCTGTTGGA GAAATATCTT CAAAATTGAG TGAGAAATCA GGCTTATGTT
1551 TATCCAAAAG GTTGAATTCT ATTCGCTCTT TTGAAATGAA CCGGACAAGA
1601 ACATCCAGAT AAGCATCGAT GGATGCTGCT TACCTTGACA AAATCTCTGA
1651 GTTGGATTCA ATGATGTCAG AGTCAGACAA CAGCAAGAGC CCTTGTATA
1701 ACGGTTTTAA GTCCTGGAT TTGGATGGGT TATCAAAGTC ATCTCAAGGC
1751 AGTGAATTTT TTAGGAACCT TGATAAGTTG GAAGAAAAAA CTGAGCTAAA
1801 CCTTTCCAAA GGTCTCTTAA CTAATGATCA GTTAGAAAAT GGAAGTGAAT
1851 GGAACCCAC TCTTTTTTTT TCTCCTCTCT CCATCTGACC AAGAAATGAA
1901 TGAAGATTTT TCACTCCATT CCAGTTCTTG TCCAGTAACT AATGAAATCA
1951 AACCCECAAG CTGCTGTGTT CAGACAGAGT TTTCCAGGG CATTTGTGTA
2001 AGCAGTTCAC ATCAGCTATT GGAAGATCAA AGATTTGGGT CATCTTTGTT
2051 TAAGATGTCC TCAGAGATGC ACAGTCTTCA TAACCACCTT CAGTCTCCTT
2101 GGTCTACTTC CTTTGTGCCT GAAAAGAGGA ATAAAAATGT GAATCAATCA
2151 ACAAAAAGAA AAATCCAGAG CAGCCTTTCC AGTGCCAGCC CATCAAAAGC
2201 AACTAAAAGT TGACTCATT GAAAGGTGTC ATTTGTGGTT TTGCTCTGAG
2251 AGAAATAGAA AAGTTGTTAA AGTTACCTTT TTTCTCATA AAAGTTCTAT
2301 ACAAATTGGA ATTGATAATC TTTAGTCAAG TATCAAGTCA GGATGGTGGA
2351 TTAACTGTGA CTCAGAATAC TTATTGTTCA TTTTGAAAAG ACTTTGTTCT
2401 TTTCAATTTT ATTTGGGAGT CTTTGTGACC AGAGAAGTTA GGGAGGAGGT
2451 TATTTTTGTT TTTTGGGTTT GGTGGTTGGT TTGGTTTGT TTTTGGTTT
2501 GTTTTTTTAC TGAATTTGAT ATGTATCTCG GTTGGATATA CATTGTTTTT
2551 TTAAAAAATG TTATTTAACT GTTAGATACA GTGGCCTGTT GATAAGCCCC
2601 ACTTGCTTTC AGAAGTTGGA TTTCTTAAAT AAAACTTTTA GTGTTGTCTA
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2651 TACACTGCTC AATAAGACAC TTGAGTTTAA GCTTTTCCCA GGGTGGAAAT
2701 TATTTTACCT GTCCCTTTTT ATTTATGTTT AGTGATGGCC TAGTTTTTCT
2751 GCAGGGCCAT GATGGAGAAA TAGCACTCTA GCCTTAGTCC AATATTGATT
2801 TACTTTCTTT TTTTAGGTTT TATGTATATG TTTGCATTTT TTAGCATTGT
2851 GTTTTGTCCA GTTTTGTGAA AATGTTCTGC TAGTATGAAA GAAAACATTT
2901 TCTATATGAA GACATTGTGT TTATGTTAGG TAGCTTACAT TTCTCCTCT
2951 GCGTGTGTGT GTATGTGTGT AAAATCAGAA ATTTAGCATA CTATGGAAAG
3001 AAGGCATGGA GCACTTGGGT TTAGAGGAAC CTAAAACATC ATAGCTTCAT
3051 TGTTCAGAT GTAACAGGTT TGAAAGAGCT CATCGCCAAG TTCTTGATCC
3101 ACTTGCAATC CAGGGGAGTT CTCTTTTGAG TAGTATGTTT CTTGTTTGCA
3151 TGTTCCTGTT CTTTGTGGAA ACTATGCATG GTAGCATTTT TGCTTGCTGT
3201 GTTTTCCATA CTTAAGAAAA AGAGGTTTCA GTTGCTGAT AGAATATCTT
3251 TTATGTAGGA CAAAACTTT CTGTGAAGAG TGTGAGGGG GTGAAGATAG
3301 GTAAGAGGTA AGCACAATTT TTAATTAGG CTCTGAAAAA GTGTATTGTT
3351 CTAACGTAT TTGGTATGCC TATATAGGTC TTTAAAAATG GGTTTGATG
3401 CTGTTTAATG TGCACGAAC ATTTTACATT AATATTGTAC TGTTTTACAT
3451 TAATACTGCA TGCTTTTCTA TGTGAATTGA ATAAAGAATG TCATAAGCAC
3501 TGGAAAAAAA AAAAAAAA AA

```

BLAST Results

Entry HS658254 from database EMBL:
human STS SHGC-11774.
Score = 1643, P = 8.0e-67, identities = 345/355

Entry HS513217 from database EMBL:
human STS SHGC-14656.
Score = 1193, P = 5.8e-46, identities = 241/244

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 263 bp to 1885 bp; peptide length: 541
Category: similarity to known protein

```

1  MLSHTVRKHL RKTRLELLHK EYEDEIDCLQ KEVEELKSKN LSLESQIKAI
51  LDPLTLVQGN QNEDKHLVTD NPSIINPETV AEWKKKLRTA NEIYEKVKDD
101 VDKLKEANKK LKLENGGLVR ENLRLKAEVD NRSPQKFRGF AVAALQSKVE
151 QYERETNRLK KALERSDKYI EELESQVAQL KNSSEEKAM NSICQTALSA
201 DGKSGSGSEE DVVSKNQGDS ARKQPGSSTS SSSHLAKPSS SRLCDTSSAR
251 QUESTSKADLN CSKNKDLYQE QVEVMDVTD TSMDTYLERE WGNKPSDCVP
301 YKDEELYDFP APCTPLSLSC LQLSTPENRE SSVVQAGGSK KHSNHLRKLKLV
351 FDDFCDSNNV SNKDSSEDDI SRSENEKKSE CFSSTKTGFW DCCSTSYAQN
401 LDFESSEGNT IANSVGEISS KLSEKSLCL SKRLNSIRSF EMNRTRTSSE
451 ASMDAAYLDK ISELDMMSE SDNSKSPCNN GFKSLDLDGL SKSSQGSEFL
501 EEPDKLEEK ETLNLSKGLT NDQLENGSEW KPTSFFSPLS I

```

BLASTP hits

Entry A42771 from database PIR:
reticulocyte-binding protein 1 - Plasmodium vivax
Score = 127, P = 3.7e-08, identities = 68/300, positives = 145/300

Entry RBP1_PLAVB from database SWISSPROT:
RETICULOCYTE BINDING PROTEIN 1 PRECURSOR.
Score = 127, P = 3.9e-08, identities = 68/300, positives = 145/300

Entry MMDSPPG_1 from database TREMBL:
gene: "DSPP"; product: "dentin sialophosphoprotein"; Mus musculus DSPP
gene
Score = 160, P = 5.2e-08, identities = 87/373, positives = 146/373

Alert BLASTP hits for DKFZphfbr2_62n10, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_62n10, frame 2

Report for DKFZphfbr2_62n10.2

```

[LENGTH]      541
[MW]           60533.06
[pI]           5.10
[FUNCAT]      04.99 other transcription activities [S. cerevisiae, YKR092c] 3e-05
[FUNCAT]      30.10 nuclear organization [S. cerevisiae, YKR092c] 3e-05
[PROSITE]     LEUCINE ZIPPER 1
[PROSITE]     MYRISTYL 7
[PROSITE]     CAMP_PHOSPHO_SITE 1
[PROSITE]     CK2_PHOSPHO_SITE 18
[PROSITE]     PROKAR_LIPOPROTEIN 1
[PROSITE]     TYR_PHOSPHO_SITE 1
[PROSITE]     PKC_PHOSPHO_SITE 14
[PROSITE]     ASN_GLYCOSYLATION 7
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY 9.24 %
[KW]           COILED_COIL 22.55 %

```

```

SEQ      MLSHTVRKHLRKRTRLELLHKEYEDEIDCLQKEVEELKSKNLSLESQIKAILDPLTLVQGN
SEG
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      QNEDKHLVTDNPSIINPETVAEWKKLRTANEIYEKVKDDVDKLKEANKKLKLENGGLVR
SEG      .XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX.
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      ENLRLKAEDVNRSPQKFRFAVAALQSKVEQYERETNRLKKALERSDKYIEELESQVAQL
SEG
PRD      ehhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      KNSSEEKAMNSICQTALSADGKSGKSGSEEDVVSKNQGDARKQPGSSTSSSSHLAKPSS
SEG      .XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX.
PRD      hcchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    CCCCCC.CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      SRLCDTSSARQESTSKADLNCSKNKDLYQEVEVMLDVTDTSDTYLEREWGNKPSDCVP
SEG      X.
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      YKDEELYDFPAPCTPLSLCLQLSTPENRESSVQAGGSKKHSNHLRKLVDFFDCDSSNV
SEG
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      SNKDSSEDDISRENEKKSECFSTKTGFWDCCSTSYAQNLDSESSEGTIANSVGEISS
SEG
PRD      cccccccchhhhhcccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      KLSEKSGCLCLSKRLNSIRS FEMNRTRTSSEASMDAAYLDKISELDSMMSES DNSKSPCNN
SEG
PRD      cccccccchhhhhcccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      GFKSLDLGLSKSSQGSEFLEEPDKLEEKTELNLKSGSLTNDQLENGSEWKPTSFFSPLS
SEG      .XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX.
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.

```

```

SEQ      I
SEG
PRD      C
COILS    .

```

Prosites for DKFZphfbr2_62n10.2

```

PS00001      40->44      ASN_GLYCOSYLATION      PDOC00001
PS00001      182->186     ASN_GLYCOSYLATION      PDOC00001
PS00001      260->264     ASN_GLYCOSYLATION      PDOC00001

```

PS00001	359->363	ASN_GLYCOSYLATION	PDOC00001
PS00001	443->447	ASN_GLYCOSYLATION	PDOC00001
PS00001	513->517	ASN_GLYCOSYLATION	PDOC00001
PS00001	526->530	ASN_GLYCOSYLATION	PDOC00001
PS00004	340->344	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	5->8	PKC_PHOSPHO_SITE	PDOC00005
PS00005	156->159	PKC_PHOSPHO_SITE	PDOC00005
PS00005	166->169	PKC_PHOSPHO_SITE	PDOC00005
PS00005	220->223	PKC_PHOSPHO_SITE	PDOC00005
PS00005	240->243	PKC_PHOSPHO_SITE	PDOC00005
PS00005	248->251	PKC_PHOSPHO_SITE	PDOC00005
PS00005	254->257	PKC_PHOSPHO_SITE	PDOC00005
PS00005	339->342	PKC_PHOSPHO_SITE	PDOC00005
PS00005	361->364	PKC_PHOSPHO_SITE	PDOC00005
PS00005	384->387	PKC_PHOSPHO_SITE	PDOC00005
PS00005	419->422	PKC_PHOSPHO_SITE	PDOC00005
PS00005	423->426	PKC_PHOSPHO_SITE	PDOC00005
PS00005	431->434	PKC_PHOSPHO_SITE	PDOC00005
PS00005	436->439	PKC_PHOSPHO_SITE	PDOC00005
PS00006	13->17	CK2_PHOSPHO_SITE	PDOC00006
PS00006	79->83	CK2_PHOSPHO_SITE	PDOC00006
PS00006	89->93	CK2_PHOSPHO_SITE	PDOC00006
PS00006	147->151	CK2_PHOSPHO_SITE	PDOC00006
PS00006	183->187	CK2_PHOSPHO_SITE	PDOC00006
PS00006	208->212	CK2_PHOSPHO_SITE	PDOC00006
PS00006	255->259	CK2_PHOSPHO_SITE	PDOC00006
PS00006	281->285	CK2_PHOSPHO_SITE	PDOC00006
PS00006	285->289	CK2_PHOSPHO_SITE	PDOC00006
PS00006	324->328	CK2_PHOSPHO_SITE	PDOC00006
PS00006	361->365	CK2_PHOSPHO_SITE	PDOC00006
PS00006	365->369	CK2_PHOSPHO_SITE	PDOC00006
PS00006	371->375	CK2_PHOSPHO_SITE	PDOC00006
PS00006	373->377	CK2_PHOSPHO_SITE	PDOC00006
PS00006	414->418	CK2_PHOSPHO_SITE	PDOC00006
PS00006	447->451	CK2_PHOSPHO_SITE	PDOC00006
PS00006	462->466	CK2_PHOSPHO_SITE	PDOC00006
PS00006	469->473	CK2_PHOSPHO_SITE	PDOC00006
PS00007	294->302	TYR_PHOSPHO_SITE	PDOC00007
PS00008	204->210	MYRISTYL	PDOC00008
PS00008	226->232	MYRISTYL	PDOC00008
PS00008	292->298	MYRISTYL	PDOC00008
PS00008	408->414	MYRISTYL	PDOC00008
PS00008	427->433	MYRISTYL	PDOC00008
PS00008	489->495	MYRISTYL	PDOC00008
PS00008	517->523	MYRISTYL	PDOC00008
PS00013	310->321	PROKAR_LIPOPROTEIN	PDOC00013
PS00029	104->126	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphfbr2_62n10.2)

DKFZphfbr2_62o17

group: metabolism

DKFZphfbr2_62o17.2 encodes a novel 282 amino acid protein with weak similarity to the apolipoprotein E receptor.

The new protein contains a leucine zipper for protein-protein interaction, and three LDL-receptor class A domain (LDLRA_1) patterns. In LDL-receptors the class A domains form the binding site for LDL and calcium. The acidic residues between the fourth and sixth cysteines are important for high-affinity binding of positively charged sequences in LDLR's ligands.

The new protein can find application in modulation of cholesterol binding and transport by LDL-receptors and LDL-binding proteins

similarity to apolipoprotein E receptor

complete cDNA, complete cds, start at Bp 56 matches kozak consensus
ANCatg EST hits

Sequenced by LMU

Locus: unknown

Insert length: 1260 bp

Poly A stretch at pos. 1240, polyadenylation signal at pos. 1218

```
1 GGGGGATAAG AGAGCGGTCT GGACAGCGCG TGGCCGGCGC CGCTGTGGGG
51 ACAGCATGAG CGGCGGTTGG ATGGCGCAGG TTGGAGCGTG GCGAACAGGG
101 GCTCTGGGCC TGGCGCTGCT GCTGCTGCTC GGCCTCGGAC TAGGCCTGGA
151 GGCCGCCGCG AGCCCGCTTT CCACCCCGAC CTCTGCCAG GCCGCAGGCC
201 CCAGCTCAGG CTCGTGCCCA CCCACCAAGT TCCAGTGCCG CACCAGTGGC
251 TTATGCGTGC CCCTCACCTG GCGCTGCGAC AGGGAATTGG ACTGCAGCGA
301 TGCCAGCGAT GAGGAGGAGT GCAGGATTGA GCCATGTACC CAGAAAGGGC
351 AATGCCCCACC GCCCCCTGGC CTCCCCTGCC CCTGCACCGG CGTCAGTGAC
401 TGCTCTGGGG GAACTGACAA GAAACTGCGC AACTGCAGCC GCCTGGCCTG
451 CCTAGCAGGC GAGCTCCGTT GCACGCTGAG CGATGACTGC ATTCCACTCA
501 CGTGGCGCTG CGACGGCCAC CCAGACTGTC CCGACTCCAG CGACGAGCTC
551 GGCTGTGGAA CCAATGAGAT CCTCCCGGAA GGGGATGCCA CAACCATGGG
601 GCCCCCTGTG ACCCTGGAGA GCGTCACCTC TCTCAGGAAT GCCACAACCA
651 TGGGGCCCCC TGTGACCCTG GAGAGTGTCC CCTCTGTCGG GAATGCCACA
701 TCCTCCTCTG CCGGAGACCA GTCTGGAAGC CCAACTGCCT ATGGGGTTAT
751 TGCAGCTGCT GCGGTGCTCA GTGCAAGCCT GGTACCGGCC ACCCTCCTCC
801 TTTTGTCTTG GCTCCGAGCC CAGGAGCGCC TCCGCCCACT GGGGTTACTG
851 GTGGCCATGA AGGAGTCCCT GCTGCTGTCA GAACAGAAGA CCTCGCTGCC
901 CTGAGGACAA GCACTTGCCA CCACCGTCAC TCAGCCCTGG GCGTAGCCCG
951 ACAGGAGCAG AGCAGTGATG CCGATGGGTA CCCGGGCACA CCAGCCCTCA
1001 GAGACCTGAG CTCTTCTGGC CACGTGGAAC CTCGAACCCG AGTCCTGCA
1051 GAACTGGCCC TGGAGATTGA GGGTCCCTGG ACACTCCCTA TGGAGATCCG
1101 GGGAGCTAGG ATGGGGAACC TGCCACAGCC AGAACCAGAG GGCTGGCCCC
1151 AGGCAGCTCC CAGGGGGTAG GACGGCCCTG TGCTTAAGAC ACTCCTGCTG
1201 CCCCGTCTGA GGGTGGCGAT TAAAGTTGCT TCACATCCTC AAAAAAAAAA
1251 AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 56 bp to 901 bp; peptide length: 282
Category: similarity to known protein
Classification: unset
Prosites motifs: LDLRA_1 (67-90)
LDLRA_1 (67-90)
LDLRA_1 (145-168)

LEUCINE_ZIPPER (17-39)

```

1 MSGGWMAQVG AWRTGALGLA LLLLLGLGLG LEAAASPLST PTSQAAGPS
51 SGSCPPTKFQ CRTSGLCVPL TWRCRDRLDC SDGSDEEECR IEPCTQKGQC
101 PPPPGLPCPC TGVSDCSGGT DKKLRNCSRL ACLAGELRCT LSDDCIPLTW
151 RCDGHPDCPD SSDELGCGTN EILPEGDATT MGPPVTLESV TSLRNATTMG
201 PPVTLESVPS VGNATSSSAG DQSGSPTAYG VIAAAVLSA SLVTATLLLL
251 SWLRAQERLR PLGLLVAMKE SLLSEQKTS LP

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_62o17, frame 2

TREMBL:AF110520_6 product: "NG29"; Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial cds; and unknown gene., N = 1, Score = 733, P = 1.5e-72

PIR:JE0237 apolipoprotein E receptor 2 precursor - mouse, N = 2, Score = 290, P = 1.1e-26

TREMBL:HSZ75190_1 product: "apolipoprotein E receptor 2 906"; H.sapiens mRNA for apolipoprotein E receptor 2, N = 1, Score = 279, P = 1.8e-23

>TREMBL:AF110520_6 product: "NG29"; Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial cds; and unknown gene.
Length = 260

HSPs:

Score = 733 (110.0 bits), Expect = 1.5e-72, P = 1.5e-72
Identities = 157/276 (56%), Positives = 178/276 (64%)

```

Query:      6 MAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKFQCRTSG 65
             MA+ GA R ALGL L LL GL GLEAA +P T   Q +G + SCP   FQC TSG
Sbjct:      1 MARGGAGRAVALGLVLRLLFGLRTGLEAAPAPAHT--RVQVSGSRADSCPTDTFQCLTSG 58

Query:     66 LCVPLTWRCRDRLDCSDGSDEEECRIEPCQKGCPPPPGLPCPCTGVSDCSGGTDDKKLR 125
             CVPL+WRCD D DCSQGSDEE+CRIE C Q GQC P   LPC C +S CS +DK L
Sbjct:     59 YCVPLSWRCDDGQDCSDGSDEEDCRIESCAQNGQCQPQSALPCSCDNISGCSDDVSDKNL- 117

Query:    126 NCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPV 185
             NCSR C   EL C L D CIP TWRCDGHPDC DSSDEL C T+
Sbjct:    118 NCSRPPCQESLHCILDDVCIPHTWRCDGHPDCLDSSDELSCDTD-----T 163

Query:    186 TLESVTSRLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTA 245
             ++ +   NATT   T+E+ S N T +SAGD S +P+AYGVIAAA VLSA LV+A
Sbjct:    164 EIDKIFQEENATTTRISTMTENETSFERNVTFTSAGDSSRNPSAYGVIAAAGVLSAILVSA 223

Query:    246 TLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSL 281
             TLL+L LR Q L P GLLVA+KESLLLSE+KTSL
Sbjct:    224 TLLILLRLRGQGYLPPPGLLVAVKESLLLSEKTSL 259

```

Pedant information for DKFZphfbr2_62o17, frame 2

Report for DKFZphfbr2_62o17.2

```

[LENGTH]      282
[MW]           28991.19
[pI]           4.61
[HOMOL]        TREMBL:AF110520_6 product: "NG29"; Mus musculus major histocompatibility
                complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein,
                BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes,
                complete cds; Sacm21 gene, partial cds; and unknown gene. 5e-55
[BLOCKS]        BL01209 LDL-receptor class A (LDLRA) domain proteins
[SCOP]          d1ajj_ 7.11.1.1.1 Ligand-binding domain of low-density lipoprotei 2e-10

```

[illegible]

Prosites for DKFZphfbr2 62o17.2

PS01209	67->90	LDLRA_1	PDOC00929
PS01209	67->90	LDLRA_1	PDOC00929
PS01209	145->168	LDLRA_1	PDOC00929
PS00029	17->39	LEUCINE ZIPPER	PDOC00029

Pfam for DKFZphfbr2 62017.2

HMM_NAME	TNFR/NGFR cysteine-rich region		
HMM	*CpeGtYtD.WNHvpqClpC.trCePEMGQYMvqPCTwTQNT.VC*		
	CP+	++ +	+ C+P RC+ ++ +C + ++ +C
Query	54	CPPTKFCRTS--GLCVPLTWRCR--DL----	DCSDGSDEEEC 89

HMM_NAME Low-density lipoprotein receptor domain class A

HMM *tTCeGPDEFQCgSGeMRCIPMsWvCDGDpDCeDWSDEWPENChp*
C P +FQC+++ C+P+ W+CD D DC D+SDE E+C+

Query 52 GSCP-PTKFCRTSG-LCVPLTWRCRDRLDCSDGSDE--EECRI 91

54.99 (bits) f: 130 t: 169 Target: dkfzphfbr2_62o17.2 similarity to apolipoprotein E receptor

Alignment to HMM consensus:
Query *tTCeGPDEFQCgSGeMRCIPMsWvCDGDpDCeDWSDEWPENChp*
C + E +C + CIP+ W+CDG PDC D SDE ++C+
dkfzphfbr2 130 LACL-AGELRCTLSD-DCIPLTWRCDGHPDCPDSSDE--LGCGT 169

DKFZphfbr2_64a15

group: nucleic acid management

DKFZphfbr2_64a15 encodes a novel 255 amino acid protein with strong similarity to inorganic pyrophosphatases

Inorganic pyrophosphatase (EC 3.6.1.1) (PPase) is the enzyme responsible for the hydrolysis of pyrophosphate (PPi) which is formed as the product of the many biosynthetic reactions that utilize ATP. All known PPases require the presence of divalent metal cations, with magnesium conferring the highest activity.

The new protein can find application as a new enzyme for biotechnologic processes.

strong similarity to inorganic pyrophosphatases

unspliced Intron 212-256 see EST HS1190948

Sequenced by Qiagen

Locus: unknown

Insert length: 1188 bp

Poly A stretch at pos. 1170, polyadenylation signal at pos. 1151

```

1 GGGGGTTGGG GACCAGTGCA GGGACCGGGT CGCGCCGTGC TATGGCCCTG
51 TACCACACTG AGGAGCGCGG CCAGCCCTGC TCGCAGAATT ACCGCCTCTT
101 CTTTAAGAAAT GTAAC TGGTC ACTACATTTT CCCCTTTCAT GATATTCTCT
151 TGAAGGTGAA CTCTAAAGAG GACACTGAGG CTCAGGCAT TTTTATAGAC
201 TTGTCTAAGA TCTGGAAAAT GGCATTCTTA TGAAGAAAGC ACGAAATGAT
251 GAATATGAGA ATCTGTTTAA TATGATTGTA GAAATACCTC GGTGGACAAA
301 GGCCTAAAATG GAGATTGCCA CCAAGGAGCC AATGAATCCC ATTAACAAT
351 ATGTAAAGGA TGGAAAGCTA CGCTATGTGG CGAATATCTT CCCTTACAAG
401 GGTATATAT GGAATTATGG TACCCTCCCT CAGACTTGGG AAGATCCCCA
451 TGAAAAAGAT AAGAGCACGA ACTGCTTTGG AGATAATGAT CCTATTGATG
501 TTTGCGAAAT AGGCTCAAAG ATTCTTTCTT GTGGAGAAGT TATTCATGTG
551 AAGATCCTTG GAATTTTGGC TCTTATTGAT GAAGGTGAAA CAGATTGGAA
601 ATTAATTGCT ATCAATGCGA ATGATCCTGA AGCCTCAAAG TTTCATGATA
651 TTGATGATGT TAAGAAGTTC AAACCGGGTT ACCTGGAAGC TACTCTTAAT
701 TGCTTTAGAT TATGTAAGGT ACCAGATGGA AAACCAAGAA ACCAGTTTGC
751 TTTTAATGGA GAATTCAAAA ACAAGGCTTT TGCTCTTGAA GTTATTAAAT
801 CCACTCATCA ATGTTGGAAA GCATTGCTTA TGAAGAACTG TAATGGAGGA
851 GCTACAAATT GCACAAACGT GCAGATATCT GATAGCCCTT TCCGTTGCAC
901 TCAAGAGGAA GCAAGATCAT TAGTTGAATC GGTATCATCT TCACCAATAA
951 AAGAAAGTAA TGAGAAGAG CAAGTGTGGC ACTTCCTTGG CAAGTGATTG
1001 AAACATCTGA AATTCTGCTG TCAAGATTCC CATCTCTAAG GACTCCAAGA
1051 CTCTTTTCC CCAAGTGCTA GAGACAAGGG GGTCTATGAG CATTACTGA
1101 CTTCTGTGTA AAACCTTCAAT TTTTCAAACT TTTTGAGCTA TGCAATATAT
1151 AAATAAACAG TAAGAATTTT AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

Entry HSPPASEMR from database EMBL:
H.sapiens partial mRNA for pyrophosphatase.
Score = 1706, P = 1.6e-70, identities = 342/343

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 230 bp to 994 bp; peptide length: 255
Category: strong similarity to known protein
Classification: unset
Prosites motifs: PPASE (85-92)

```

1 MKKARNDEYE NLFNMIVEIP RWTAKMEIA TKEPMNPIQ YVKDGKLRVY
51 ANIFPYKGYI WNYGTLPTW EDPHEKDKST NCFGDNPDID VCEIGSKILS
101 CGEVIHVKIL GILALIDEGE TDWKLIANA NDPEASKFHD IDDVKKFKPG
151 YLEATLNWFR LCKVPDGKPE NQFAFNGEFK NKAFALVVIK STHQCWKALL
201 MKNCNGGATN CTNVQISDSP FRCTQEEARS LVESVSSSPN KESNEEEQVW
251 HFLGK

```

BLASTP hits

Entry IPYR_KLULA from database SWISSPROT:
INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
HYDROLASE) (PPASE).
Score = 689, P = 6.0e-68, identities = 128/248, positives = 170/248

Entry A45153 from database PIR:
inorganic pyrophosphatase (EC 3.6.1.1) - bovine
Score = 862, P = 2.8e-86, identities = 146/226, positives = 190/226

Entry AF085600.1 from database TREMBLNEW:
gene: "Nurf-38"; product: "inorganic pyrophosphatase NURF-38";
Drosophila melanogaster inorganic pyrophosphatase NURF-38 (Nurf-38)
gene, complete cds.
Score = 731, P = 2.1e-72, identities = 134/248, positives = 177/248

Entry PWBY from database PIR:
inorganic pyrophosphatase (EC 3.6.1.1) - yeast (Saccharomyces
cerevisiae)
Score = 688, P = 7.7e-68, identities = 133/251, positives = 174/251

Alert BLASTP hits for DKFZphfbr2_64a15, frame 2

SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
(PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE)., N = 1, Score = 731, P =
2.4e-72

>SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
PHOSPHO- HYDROLASE) (PPASE).
Length = 290

HSPs:

Score = 731 (109.7 bits), Expect = 2.4e-72, P = 2.4e-72
Identities = 134/248 (54%), Positives = 177/248 (71%)

```

Query:      7 DEYENLFNMIVEIPRWTAKMEIATKEPMNPIQYVKDGKLRVYVANIFPYKGYIWNNGTL 66
             +E + ++NM+VE+PRWT AKMEI+ K PMNPIQ +K CKLR+VAN FP+KCYIWNNG L
Sbjct:     40 NEEKTIYNMVVEVPRWTNAKMEISLKTMPNPIQDIKKGKLRVANCFFPHKGYIWNNGAL 99

Query:     67 PQTWEDPHEKDKSTNCFGDNPDIDVCEIGSKILSCGEVIHVKILGILALIDEGETDWKLI 126
             POTWE+P + ST C GDNDPIDV EIG ++ G+V+ VK+LG ALIDEGETDWK+I
Sbjct:    100 PQTWENPDHIEPSTGCKGDNDPIDVIEIGYRVAKRGDVLKVKVLGGQFALIDEGETDWKII 159

Query:    127 AINANDPEASKFHDIDDVKKFKPGYLEATLNWFR LCKVPDGKPKENQFAFNGEFKNKAFAL 186
             AI+ NDP ASK +DI DV ++ PG L AT+ WF++ K+PDGKPKENQFAFNG+ KN FA
Sbjct:    160 AIDVNDPLASKVNDIADVQYFPGLLRATVEWFKIYKIPDGKPKENQFAFNGDAKNADFAN 219

Query:    187 EVIKSTHQCWKALLMKNCNGGATNCTNVQISDSPFRCTQEEARS-LVESVSSSPNKESNE 245
             +I TH+ W+ L+ ++ G+ + TN+ +S +EEA L E+ +E ++
Sbjct:    220 TIIAETHKFWQNLVHQSPASGSISTTNITNRNSEHVIPKEEA EKILAEAPDGGQVEEVSD 279

Query:    246 EEQVWHFL 253
             WHF+
Sbjct:    280 TVDTWHFI 287

```

Peptide information for frame 3

ORF from 42 bp to 230 bp; peptide length: 63
Category: strong similarity to known protein
Classification: unset

```

1 MALYHTEERG QPCSQNYRLF FKNVTGHIYS PFHDIPLKVN SKEDTEAQGI
51 FIDLSKIWKM AFL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64a15, frame 3

SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
(PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE)., N = 1, Score = 118, P = 8.8e-07

PIR:A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine, N = 1,
Score = 113, P = 3.1e-06

TREMBLNEW:AF108211_1 product: "cytosolic inorganic pyrophosphatase";
Homo sapiens cytosolic inorganic pyrophosphatase mRNA, partial cds., N
= 1, Score = 106, P = 1.8e-05

>SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
PHOSPHO- HYDROLASE) (PPASE).
Length = 290

HSPs:

Score = 118 (17.7 bits), Expect = 8.8e-07, P = 8.8e-07
Identities = 23/43 (53%), Positives = 29/43 (67%)

Query: 1 MALYHTEERGQPCSONYRLFFKNVTGHIYISPFHDIPLKVNKE 43
MALY T E+G S +Y L+FKN G+ ISP HDIPL N ++
Sbjct: 1 MALYETVEKGAKNSPSYSLYFKNKCGNVISPMHDIPLYANEK 43

Pedant information for DKFZphfbr2_64a15, frame 2

Report for DKFZphfbr2_64a15.2

[LENGTH] 255
[MW] 29177.34
[pI] 5.67
[HOMOL] TREMBLNEW:AF108211_1 product: "cytosolic inorganic pyrophosphatase"; Homo
sapiens cytosolic inorganic pyrophosphatase mRNA, partial cds. 2e-93
[FUNCAT] 01.04.01 phosphate utilization [S. cerevisiae, YBR011c] 9e-73
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YBR011c] 9e-73
[FUNCAT] 02.99 other energy generation activities [S. cerevisiae, YMR267w] 1e-58
[FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YMR267w] 1e-58
[FUNCAT] 1 genome replication, transcription, recombination and repair [M.
genitalium, MG351] 1e-06
[FUNCAT] g carbohydrate metabolism and transport [H. influenzae, HI0124] 2e-06
[BLOCKS] BL00387D
[BLOCKS] BL00387C
[BLOCKS] BL00387B
[BLOCKS] BL00387A
[SCOP] dlwgja_2.29.5.1.1 Inorganic pyrophosphatase [baker's yeas 1e-113
[EC] 3.6.1.1 inorganic pyrophosphatase 7e-92
[PIRKW] mitochondrion 3e-57
[PIRKW] hydrolase 7e-92
[PIRKW] homodimer 2e-71
[SUPFAM] inorganic pyrophosphatase 7e-92
[PROSITE] PPASE 1
[KW] Alpha_Beta
[KW] 3D
[KW] LOW_COMPLEXITY 6.27 %

SEQ MKKARNDEYENLFNMIVEIPRWTKAKMEIATKEPMNPIKQYVKDGKLRVANIFPYKGYI
SEG
lhukBEGGGCEEEEEETTTbCBCEETTTTTTCEEECEETTEECBCCBTTBTbTbT

SEQ WNYGTLPQTWEDPHEKDKSTNCFGDNDPIDVCEIGSKILSCGEVIHVILGILALIDEGE
SEG
lhukB CEEETTTTbCBTTTTEETTTTECCCBCEEEECCECCCTTTTEEEEEEEEEETTTTbT

SEQ TDWKLIANANDPEASKFHDIIDDVKKFKPGYLEATLNWFRLLCKVPDGKPFENQFAFNGEFK
SEG
lhukB CEEEEETTTTGGGCCCHHHHHHHTTTTHHHHHHHHHHHHCGGGCCCCCBGGGCCB

SEQ NKAFALEVIKSTHCQWKALLMKNCGGATNCTNVQISDSPFRCTQEEARSLVESVSSSPN
SEGxxxxxxx
lhukB CHHHHHHHHHHHHHHHHHHHCTTTTTTCCCBTTTTTTT.....

DKFZphfbr2_64c16

group: brain derived

DKFZphfbr2_64a16.2 encodes a novel 101 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: /map="745_A_2; 756_F_2; 842_C_2"

Insert length: 1866 bp

Poly A stretch at pos. 1848, polyadenylation signal at pos. 1829

```
1 GGGCGCGGCG CCGGAGGAGG AAGTGGTGAG GTTGTGCTC CTTAGCGGCC
51 TATCGCTGGC TCTTGGGGCG CAGAGAGGGG CCGCAGTCTC CGCGGCTGCG
101 TCGAGCTCCC TTGCACTCCC CTCCATGTTC CCCGGCGCCA CTACTCCCTT
151 TCCTAAGGCC GCGCTTACC CCGGGTCTA TGAAGTAAT GGAAGGACCC
201 CTCACCTTGG CTCATCAACA GAGCAGACGA GCAGACCGTT TATTAGCTGC
251 AGGCAAATAC GAAGAGGCTA TTTCTTGTCA CAAAAGGCT GCAGCATATC
301 TTTCTGAAGC CATGAAGCTG ACACAGTCAG AGCAGGCTCA TCTTCACTG
351 GAATTGCAAA GGGATAGCCA TATGAAACAG CTCCTCTCA TCCAAGAGAG
401 ATGGAAAAGC GCCCAGCGTG AAGAAAGATT GAAAGCCAG CAGAACACAG
451 ACAAGGATGC AGCTGCCCCAT CTTAGACAT CTCACAAACC CTCTGCAGAG
501 GATGCAGAGG GCCAGAGTCC CCTTCTCAG AAGTACAGCC CTCCACAGA
551 GAAATGCCTG CTTGAGATTC AGGGGATCTT TGACAGGGAT CCAGACACAC
601 TACTTTATTT ACTTCAGCAA AAGAGTGAGC CAGCAGAGCC ATGTATTGGA
651 AGCAAAGCCC CAAAAGATGA TAAACAATT ATAGAGGAGC AGGCAACCAA
701 AATTGCAGAT TTGAAGAGGC ATGTGGAATT CCTTGTGGCT GAGAATGAAA
751 GATTAAGGAA AGAAAATAAA CAACTAAAGG CTGAAAAGGC CAGACTTCTA
801 AAAGGTCCAA TAGAAAAGGA GCTGGATGTA GATGCTGATT TTGTAGAAAC
851 GTCAGAGTTA TGGAGCTTGC CACCACATGC AGAACTGCT ACAGCCTCCT
901 CAACCTGGCA GAAGTTCGCA GCAAACTAGT GGAAGCCAA GGACATTCCA
951 ATCCCCAATC TTCCTCCCTT GGATTTTCCA TCTCCAGAAC TTCTCTTAT
1001 GGAGCTCTCT GAGGATATTC TGAAGGACT TATGAATAAT TAAATGGAA
1051 GGCCACAGAA AAGGGGAAAA GAGGAAATAA TACAGTAATC GTTAATCCAG
1101 CAAAAAGAAA TGAAGAGGGA AAACACATA GAAGGGTAAT CCCGGAATG
1151 CTTATCTTGG TGGACTGTGG GAGCAGAGGC ATTGCCAGGA CTTGGGAAAC
1201 AGTCACTGTG AAATGCGCTG CGTATCTCAT TCACTCACTT CAGCTAATGA
1251 CTCCGACTTG GCAGACGCTA AACTCATGGA GGTTCCGTTT CTCCTGATAC
1301 AAACCAATAG GCTACCTGGA AGAATTTCTT TCAAGCAACA GTTATTTTTC
1351 TTATCTTTCG GGTAAAAATG TATAAAAGTT ATGTGTAATT AATCTATAAT
1401 GCCATAAATG ATAATGCAAA ACCTAAATAA TATGGTGGCC GGAGGGGCTG
1451 CCTTATATTT GAAACATGCT TTCTATCATG CATGACTGTG ATGCATTTTG
1501 TTAATGCACA TTCTGTTTGT TTAAGGTGTG TGAGATACAC ACCTTTCTAG
1551 ATGAAACTAT ATGTGCCACA CTTTGCCTA CTCATAATGA TAACCTCAAG
1601 ACTATCAGAA GAAATATTTA AATTTCCATT TTATGAAGAA AGGAACCAA
1651 TTATTATGCT TTTTAAAAACA AATTACCAGT TTACATAATT AATCAGGGTG
1701 CATTTTAAGT TCTAACTTCG TTTATTGTAT AATGCATCAT TTGAAAATAC
1751 CAAGGAGGAA ATACCCCTTG TTTTAAATGA TGCAAGAGTG GACGTAATGC
1801 TAGTTGGCAG TATTTTATTG TAAGAAATCA ATAAAGTAAT TGTGTTTTAA
1851 AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HS286143 from database EMBL:

human STS WI-6844.

Score = 1460, P = 3.4e-61, identities = 292/292

Medline entries

No Medline entry

1000 2000 3000 4000 5000 6000 7000 8000 9000 10000 11000 12000 13000 14000 15000 16000 17000 18000 19000 20000 21000 22000 23000 24000 25000 26000 27000 28000 29000 30000 31000 32000 33000 34000 35000 36000 37000 38000 39000 40000 41000 42000 43000 44000 45000 46000 47000 48000 49000 50000 51000 52000 53000 54000 55000 56000 57000 58000 59000 60000 61000 62000 63000 64000 65000 66000 67000 68000 69000 70000 71000 72000 73000 74000 75000 76000 77000 78000 79000 80000 81000 82000 83000 84000 85000 86000 87000 88000 89000 90000 91000 92000 93000 94000 95000 96000 97000 98000 99000 100000

.....

.....

Report for DKFZphfbr2_64c16.3

```

[LENGTH]      287
[MW]           32343.79
[PI]           5.61
[PROSITE]      LEUCINE_ZIPPER 2
[KW]           All_Alpha
[KW]           COILED_COIL      14.98 %

SEQ    MEVMEGPLNLAHQQSRRADRLLAAGKYEEAISCHKKAAAYLSEAMKLTQSEQAHLSELEQ
PRD    cccccchhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....

SEQ    RDSHMKQLLLIQRWKRAQREERLKAQQNTDKDAAHLQTSBKPSAEDAEGQSPLSQKYS
PRD    hhcchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....

SEQ    PSTEKCLPEIQGIFDRDPDTLLYLLQKSEPAEPCIGSKAPKDDKTIIEEQATKIADLKR
PRD    cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....CCCCCCCCCCCCCCCC

SEQ    HVEFLVAENERLRKENKQLKAEKARLLKGPIEKELDVDADFVETSELWSLPPHAETATAS
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ    STWQKFAANTGKAKDIPNLPPLDFPSPPELPLMELSEDILKGLMNN
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....

```

Prosites for DKFZphfbr2_64c16.3

```

PS00029    178->200    LEUCINE_ZIPPER    PDOC00029
PS00029    185->207    LEUCINE_ZIPPER    PDOC00029

```

(No Pfam data available for DKFZphfbr2_64c16.3)

DKFZphfbr2_64c4

group: brain derived

DKFZphfbr2_64c4 encodes a novel 467 amino acid protein with similarity to A. thaliana T08I13.5

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to A. thaliana T08I13.5

complete cDNA, complete cds, EST hits
on genomic level encoded by AC005043 11 exons

Sequenced by Qiagen

Locus: unknown

Insert length: 1559 bp

Poly A stretch at pos. 1540, no polyadenylation signal found

```
1 TGGGACCGCC GGAAGTTTCT GCCGCGGCTT TCGGGGACG GGGGAGTGGT
51 AGTGGGGGCT GCAGCTGCCG GACCCAGGCG CGATGGCTAC GGGCGCGGAT
101 GTACGGGACA TTCTAGAAGT CCGGGGTCCA GAAGGGGATG CAGCCTCTGG
151 GACCATCAGC AAGAAGGACA TTATCAACCC GGACAAGAAA AAATCCAAGA
201 AGTCCTCTGA GACACTGACT TTCAAGAGGC CCGAGGGCAT GCACCGGGAA
251 GTCTATGCCT TGCTCTACTC TGACAAGAAG GATGCACCCC CACTGCTACC
301 CAGTGACACT GGCCAGGGAT ACCGTACAGT GAAGGCCAAG TTGGGCTCCA
351 AGAAGGTGCG GCCTTGGAAG TGGATGCCAT TCACCAACCC GGCCCGCAAG
401 GACGGAGCAA TGTTCTTCCA CTGGCGACGT GCAGCGGAGG AGGGCAAGGA
451 CTACCCCTTT GCCAGGTTCA ATAAGACTGT GCAGGAGCCT GTGTACTCGG
501 AGCAGGAGTA CCAGCTTTAT CTCCACGATA ATGCTTGGAC TAAGGCAGAA
551 ACTGACCACC TCTTTGACCT CAGCCGCCG TTTGACCTGC GTTTTGTGT
601 TATCCATGAC CGGTATGACC ACCAGCAGTT CAAGAAGCGT TCTGTGGAAG
651 ACCTGAAGGA GCGGTACTAC CACATCTGTG CTAAGCTTGC CAACGTGCGG
701 GCTGTGCCAG GCACAGACCT TAAGATACCA GTATTGTATG CTGGGCACGA
751 ACGACGGCGG AAGGAACAGC TTGAGCGTCT CTACAACCGG ACCCCAGAGC
801 AGGTGGCAGA GGAGGAGTAC CTGTACAGG AGCTGCGCAA GATTGAGGCC
851 CGGAAGAAGG AGCGGGAGAA ACGCAGCCAG GACCTGCAGA AGCTGATCAC
901 ACCGGCAGAC ACCACTGCAG ACGACCGGCG CACGGAACCG AAGGCCCCCA
951 AAAAGAAGCT ACCCCAGAAA AAGGAGGCTG AGAAGCCGGC TGTTCTGAG
1001 ACTGCAGGCA TCAAGTTTCC AGACTTCAAG TCTGCAGGTG TCACGCTGCG
1051 GAGCCAACGG ATGAAGCTGC CAAGCTCTGT GGGACAGAAG AAGATCAAGG
1101 CCTTGGAACA GATGCTGCTG GAGCTTGGTG TGGAGCTGAG CCCGACACCT
1151 ACGGAGGAGC TGGTGCACAT GTTCAATGAG CTGCGAAGCG ACCTGGTGCT
1201 GCTCTACGAG CTCAAGCAGG CCTGTGCCAA CTGCGAGTAT GAGCTGCAGA
1251 TGCTGCGGCA CCGTCATGAG GCACTGGCCC GGGCTGGTGT GCTAGGGGGC
1301 CCTGCCACAC CAGCATCAGG CCCAGGCCCG GCCTCTGCTG AGCCGGCAGT
1351 GTCTGAACCC GGACTTGGTC CTGACCCCAA GGACACCATC ATTGATGTGG
1401 TGGGCGCACC CCTCAGCCCC AATTGAGAAA AGCGACGGGA GTCGGCCTCC
1451 AGTCTATCTT CCGTGAAGAA AGCCAAGAAG CCGTGAGAGG CCCCACGGGG
1501 TGTGGGCGAC GCTGTTATGT AAATAGAGCT GCTGAGTTGG AAAAAAAAAA
1551 AAAAAAAAAA
```

BLAST Results

Entry AC005043 from database EMBL:
Homo sapiens clone NH0576N21; HTGS phase 1, 5 unordered pieces.
Score = 1506, P = 4.6e-244, identities = 316/330

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 83 bp to 1483 bp; peptide length: 467

Category: similarity to unknown protein

```

1 MATGADVVDI LELGGPEGDA ASGTISKKDI INPDKKKSKK SSETLTFRKP
51 EGMHREYVAL LYSDDKDAPP LLPSDTGQGY RTVKAKLGSK KVRPWKWMPPF
101 TNPARKDGAM FFHWRRAAEE GKDYPFARFN KTVQEPVYSE QEYQLYLHDN
151 AWTKAETDHL FDLRRRFDLR FVVIHNDYDH QQFKKRSVED LKERYYYHICA
201 KLANVRVAVG TDLKIPVFDA GHERRRKEQL ERLYNRTPEQ VAEEEYLLQE
251 LRKIEARKKE REKRSQDLQK LITAAATTAE QRRTERKAPK KKLPOKKEAE
301 KPAVPETAGI KFPDFKSAGV TLRSQRMKLP SSVGQKKIKA LEQMLLELGV
351 ELSPPTTEEL VHMFNELRSD LVLLEYLQKA CANCEYELQM LRHRHEALAR
401 AGVLGGPATP ASGPGPASAE PAVSEPLGFP DPKDTIIDVY GAPLTPNSRK
451 RRESASSSSS VKKAKKP

```

BLASTP hits

Entry ATAC2337_5 from database TREMBLNEW:
 gene: "T08I13.5"; Arabidopsis thaliana chromosome II BAC T08I13
 genomic sequence, complete sequence.
 Score = 340, P = 2.6e-30, identities = 115/374, positives = 176/374

Entry YE8D_SCHPO from database SWISSPROT:
 HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.
 Score = 221, P = 1.9e-20, identities = 67/192, positives = 97/192

Entry S64291 from database PIR:
 hypothetical protein YGR002c - yeast (Saccharomyces cerevisiae)
 Score = 202, P = 2.8e-13, identities = 71/260, positives = 124/260

Alert BLASTP hits for DKFZphfbr2_64c4, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_64c4, frame 2

Report for DKFZphfbr2_64c4.2

```

[LENGTH]      467
[MW]           53007.60
[pI]           9.51
[HOMOL]        TREMBL:ATAC2337_5 gene: "T08I13.5"; Arabidopsis thaliana chromosome II BAC
T08I13 genomic sequence, complete sequence. 4e-29
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YGR002c] 1e-19
[PROSITE]      MYRISTYL 1
[PROSITE]      CAMP_PHOSPHO_SITE 4
[PROSITE]      CK2_PHOSPHO_SITE 10
[PROSITE]      TYR_PHOSPHO_SITE 3
[PROSITE]      GLYCOSAMINOGLYCAN 1
[PROSITE]      PKC_PHOSPHO_SITE 12
[PROSITE]      ASN_GLYCOSYLATION 1
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY 20.13 %

```

```

SEQ  MATGADVVDILELGGPEGDAASGTISKKDIINPDKKKSKKSSETLTFRKP EGMHREYVAL
SEG  .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhh

SEQ  LYSDDKDAPPLPSDTGQGYRTVKAKLGSKKVRPWKWMPPFTNPARKDGAMFFHWRRAAEE
SEG  .....
PRD  hhhheccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhe

SEQ  GKDYPFARFNKTVQEPVYSEQEYQLYLHDNAWTKAETDHLFDLRRRFDLRFVVIHNDYDH
SEG  .....
PRD  cccccccccccccccccchhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhhhccceeeeeecccccc

SEQ  QQFKKRSVEDLKERYYYHICAKLANVRVAVPGTDLKIPVFDAGHERRRKEQLERLYNRTPEQ
SEG  .....
PRD  chhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhchhhh

SEQ  VAEEEYLLQELRKIEARKKEREKRSQDLQKLITAAATTAEQRRTERKAPKKKLPOKKEAE
SEG  .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  KPAVPETAGIKFPDFKSAGVTLRSQRMKLPSSVGQKKIKALEQMLLELGV ELSPTTEEL
SEG  xxx.....

```

```
PRD      hccccccccccccccccceehhhhhhhccccccchhhhhhhhhhhhhhhccccchhh
SEQ      VHMENELRSDLVLLYELKQACANCEYELQMLRHRHEALARAGVLGGPATPASGPGPASAE
SEG      .....
PRD      hhhhhhccchhhhhhhhhhhccccchhhhhhhhhhhhhhhccccccccccccccccccccc

SEQ      PAVSEPLGLPDPKDTIIDVVGAPLTPNSRKRRESASSSSSVKKAKKP
SEG      xxxxxxxx.....
PRD      cccccccccccccceeeccccccccccccccccccccccccceeecccc
```

Prosites for DKFZphfbr2_64c4.2

PS00001	130->134	ASN_GLYCOSYLATION	PDOC00001
PS00002	412->416	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	35->39	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	39->43	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	184->188	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	451->455	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00005	46->49	PKC_PHOSPHO_SITE	PDOC00005
PS00005	63->66	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00005	284->287	PKC_PHOSPHO_SITE	PDOC00005
PS00005	321->324	PKC_PHOSPHO_SITE	PDOC00005
PS00005	324->327	PKC_PHOSPHO_SITE	PDOC00005
PS00005	448->451	PKC_PHOSPHO_SITE	PDOC00005
PS00005	460->463	PKC_PHOSPHO_SITE	PDOC00005
PS00006	3->7	CK2_PHOSPHO_SITE	PDOC00006
PS00006	26->30	CK2_PHOSPHO_SITE	PDOC00006
PS00006	132->136	CK2_PHOSPHO_SITE	PDOC00006
PS00006	139->143	CK2_PHOSPHO_SITE	PDOC00006
PS00006	153->157	CK2_PHOSPHO_SITE	PDOC00006
PS00006	187->191	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	355->359	CK2_PHOSPHO_SITE	PDOC00006
PS00006	435->439	CK2_PHOSPHO_SITE	PDOC00006
PS00007	131->139	TYR_PHOSPHO_SITE	PDOC00007
PS00007	227->235	TYR_PHOSPHO_SITE	PDOC00007
PS00007	116->125	TYR_PHOSPHO_SITE	PDOC00007
PS00008	14->20	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_64c4.2)

DKFZphfbr2_64h6

group: brain derived

DKFZphfbr2_64h6 encodes a novel 176 amino acid protein with similarity to predicted yeast proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to *S.pombe* SPBC337.09 and *S.cerevisiae* YER044c

complete cDNA, complete cds accoring to YER044c/SPBC337.09,
start at Bp 111, EST hits

Sequenced by Qiagen

Locus: /map="14"

Insert length: 1212 bp

Poly A stretch at pos. 1192, polyadenylation signal at pos. 1168

```

1 GGGCTGGAGC TGTCCTGGGG GAGCTTGTTT GCGGCAGCGG CTGCTGCTGC
51 CACTGCTGTG CTGGGGGCCC GGTCGCCAGG CAAAAAGCCC TCCCACGTTT
101 GAGGGGAGTC ATGAGCCGTT TCCTGAATGT GTTAAGAAGT TGGCTGGTTA
151 TGGTGTCCAT CATAGCCATG GGAACACGC TGCAGAGCTT CCGAGACCAC
201 ACTTTTCTCT ATGAAAAGCT CTACACTGGC AAGCCAAACC TTGTGAATGG
251 CCTCCAAGCT CGGACCTTTG GGATCTGGAC GCTGCTCTCA TCAGTGATCC
301 GCTGCCCTCT TGCCATTGAC ATTCACAACA AGACGCTCTA TCACATCACA
351 CTCTGGACCT TCCTCCTTGC CCTGGGGCAT TTCCTCTCTG AGTTGTTTGT
401 CTATGGAAC TGCAGCTCCCA CGATTGGCGT CCTGGCACCC CTGATGGTGG
451 CAAGTTTCTC CATCCTGGGT ATGCTGGTCG GGCTCCGGTA TCTAGAAAGTA
501 GAACCAAGTAT CCAGACAGAA GAAGAGAAAC TGAGGCCAGC ATTATCACCT
551 CCAGGACTTT CTCGTTTTCC ACCTTGGCCA TCTTCTTCTC TCGTCGTCTC
601 TCCCCTTTAA TTTCTTTTCT ATTCCATCAT CTGCCCTTTT ACTCACTTTT
651 AGCCTCTTTT TTTAATTTT AAAATTTAAA GATATGCATA CTGAAAAGTA
701 TATAACATGT ACGTACAATT TAAAGAATAA TTTTAAAGTG AATACTACGT
751 AACTCCATCC AAGTCAAGAA ATTGCCAGCT TCTCGGAAGC CCACTGTGTC
801 TCC'TTCCCCT ACCTGCAACC TCTTCCAGGC TCCCTTTTCC AGCCTTCCCC
851 TTTTTCCTT TTATTTTCAT GCCTTGATTG GACTTGTGTG GTGGGAACAT
901 GTGAACTATG AAACCTTAAAC CTGCTGCCCA CCCAGAGCAG CTGTGACCAA
951 GGGCTGCCTC AAGGGGTGTG CCACGCAGGT TGGGCTCCTC TCTGCTGCTG
1001 GACCCAAGAC TCTCAACCTT CCAAGGCACA GGCAGTTCTT CTGAGAAGGG
1051 CTCCCCTGTG TGTGAGCAAG ACCACAGCTC TCCTTCTATC TACAGATGCA
1101 TGAGGGTTGG AAGAGTCTGG GCTGTTTTTA GACCTTCTGG TCAGCTGTAT
1151 TTGTGTAACA ACTTTGTAA TAAATAGAAA AACCTCTGCT TCAAAAAAAA
1201 AAAAAAAAAA AA

```

BLAST Results

Entry G38566 from database EMBL:
SHGC-64295 Human Homo sapiens STS genomic, sequence tagged site.
Score = 1398, P = 1.4e-56, identities = 284/288

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 0 bp to 530 bp; peptide length: 177
Category: similarity to unknown protein
Classification: unclassified

```

1 AGAVLGELVC GSGCCCHCCA GGPVARQKAL PRLRGVMSRF LNVLRSLVLM
51 VSIAMGNLT QSFDRHTFLY EKLYTGKPNL VNGLQARTFG IWTLLSSVIR
101 CLCAIDITHNK TLYHITLWTF LLALGHFLSE LFVYGTAAPT IGVLAPLMVA

```

151 SFSILGMLVG LRYLEVEPVSRQKKRN

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64h6, frame 3

TREMBL:SPBC337_9 gene: "SPBC337.09"; product: "conserved hypothetical protein"; S.pombe chromosome II cosmid c337., N = 1, Score = 224, P = 1.4e-18

PIR:S50547 hypothetical protein YER044c - yeast (Saccharomyces cerevisiae), N = 1, Score = 192, P = 3.4e-15

>TREMBL:SPBC337_9 gene: "SPBC337.09"; product: "conserved hypothetical protein"; S.pombe chromosome II cosmid c337.
Length = 136

HSPs:

Score = 224 (33.6 bits), Expect = 1.4e-18, P = 1.4e-18
Identities = 49/113 (43%), Positives = 74/113 (65%)

Query: 42 NVLRSWLVMVSIAMGNTLQSFDRHTFLYEKLYTGKPNLVNGLQARTFGIWTLLSSVIRC 101
+++ W V+VS+ A+ NT+QSF L +++Y+ N VNGLO RTFGIWTLLS+++R
Sbjct: 11 SLVAKWNVVVSVAALFNTVQSFLTPK-LTKRVYSNT-NEVNGLOGRFTFGIWTLLSAIVRF 68

Query: 102 LCAIDIHNKTLYHITLWTFLLALGHFLSELFVYGTAAPTIGVLAPLMVASFSI 154
CA I N +Y + T+ LA HFLSE ++ T G+L+P++V++ SI
Sbjct: 69 YCAYHITNPDVYFLCQCTYYLACFHFLSEWLLFRTTNLGPGLLSPIVVSTVSI 121

Pedant information for DKFZphfbr2_64h6, frame 3

Report for DKFZphfbr2_64h6.3

[LENGTH] 176
[MW] 19359.31
[pI] 9.53
[HOMOL] TREMBL:SPBC337_9 gene: "SPBC337.09"; product: "conserved hypothetical protein";
S.pombe chromosome II cosmid c337. 2e-17
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YER044c] 7e-16
[KW] TRANSMEMBRANE 2
[KW] LOW_COMPLEXITY 7.39 %

SEQ AGAVLGELVCGSGCCCHCCAGGPVARQKALPRLRGVMSRFLNVLRSLVMVSIAMGNTL
SEGXXXXXXXXXXXXXXXXX.....
PRD ccc
MEMMMMMMMMMMMMMMMMMMM.....

SEQ QSFDRHTFLYEKLYTGKPNLVNGLQARTFGIWTLLSSVIRCLCAIDIHNKTLYHITLWTF
SEG
PRD ccc
MEM
.....

SEQ LLALGHFLSELFVYGTAAPTIGVLAPLMVASFSILGMLVGLRYLEVEPVSRQKKRN
SEG
PRD hhh
MEMMMMMMMMMMMMMMMMMMM.....

(No Prosite data available for DKFZphfbr2_64h6.3)

(No Pfam data available for DKFZphfbr2_64h6.3)

DKF2phfbr2_64j18

group: Intracellular transport and trafficking

DKF2phfbr2_64j18.1 encodes a novel 180 amino acid protein nearly identical to the microsomal signal peptidase 23 kd subunit of *canis familiaris*, *gallus gallus* and *C. elegans*.

The new protein is identical to canine and chicken microsomal signal peptidase 23 kd subunit. The canine microsomal signal peptidase is a protein complex comprised of five subunits (25, 22/23, 21, 18, and 12 kDa). The 23kDa subunit is tightly associated with the 18- and 21-kDa subunits, that are integral membrane proteins.

The new protein can find application in modulation of protein transport into microsomal compartments and as a tool for proteomic analysis.

strong similarity to dog signal peptidase (EC 3.4.99.-)

complete cDNA, complete cds, potential start at Bp 109, EST hits,

Sequenced by Qiagen

Locus: unknown

Insert length: 690 bp

Poly A stretch at pos. 666, polyadenylation signal at pos. 646

```
1 GCCGGAACGC GCGCACCGCA GACGGCGCGG ATCGCAGGGA GCCGGTCCGC
51 CGCCGGAACG GGAGCCTGGG TGTGCGTGTG GAGTCCGGAC TCGTGGGAGA
101 CGATCGCGAT GAACACGGTG CTGTCGCGGG CGAACTCACT GTTCGCCTTC
151 TCGCTGAGCG TGATGGCGGC GCTCACCTTC GGCTGCTTCA TCACCACCGC
201 CTTCAAAGAC AGGAGCGTCC CGGTGCGGCT GCACGTCTCG CGGATCATGC
251 TAAAAAATGT AGAAGATTTC ACTGGACCTA GAGAAAGAAG TCATCTGGGA
301 TTTATCACAT CTGATATAAC TGCTGATCTA GAGAAATATAT TTGATTGGAA
351 TGTTAAGCAG TTGTTTCTTT ATTTATCAGC AGAATATTCA ACAAAAAATA
401 ATGCTCTGAA CCAAGTTGTC CTATGGGACA AGATTGTTT GAGAGGTGAT
451 AATCCGAAGC TGCTGCTGAA AGATATGAAA ACAAATATT TTTTCTTTGA
501 CGATGGAAT GGTCTCAAGG GAAACAGGAA TGTCACCTTG ACCCTGTCTT
551 GGAACGTCGT ACCAAATGCT GGAATTCTAC CTCTGTGAC AGGATCAGGA
601 CACGTATCTG TCCCATTTCC AGATACATAT GAAATAACGA AGAGTTATTA
651 AATTATTCTG AATTTGAAAC AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

89034208:

cDNA-derived primary structure of the glycoprotein component of canine microsomal signal peptidase complex.

Peptide information for frame 1

ORF from 109 bp to 648 bp; peptide length: 180

Category: strong similarity to known protein

Prosite motifs: TONB_DEPENDENT_REC_1 (1-58)

RGD (148-151)

```
1 MNTVLSRANS LFAFSLSVMA ALTFGCFITT AFKDRSVPVR LHSRIMLKN
51 VEDFTGPRER SDLGFIITSDI TADLENIFDW NVKQLFLYLS AEYSTKNNAL
101 NQVVLWDKIV LRGNPKLLL KDMKTKYFFF DDGNLKGNR NVTLTLSWNV
151 VPNAGILPLV TSGHVSVPF PDTYEITKSY
```

BLASTP hits

Report for DKFZphfbr2_64j18.1

```

[LENGTH]      180
[MW]           20253.39
[pI]           8.66
[HOMOL]        PIR:A31788 signal peptidase (EC 3.4.99.-) (SPC 22/23) - dog 1e-100
[FUNCAT]       30.07 organization of endoplasmatic reticulum [S. cerevisiae, YLR066w]
6e-15
[FUNCAT]       06.07 protein modification (glycosylation, acylation, myristylation,
palmitylation, farnesylation and processing) [S. cerevisiae, YLR066w] 6e-15
[PIRKW]        transmembrane protein 2e-92
[PIRKW]        glycoprotein 2e-92
[PIRKW]        hydrolase 2e-92
[PROSITE]      RGD 1
[PROSITE]      MYRISTYL 2
[PROSITE]      PROKAR_LIPOPROTEIN 1
[PROSITE]      TONB_DEPENDENT_REC_1 1
[PROSITE]      PKC_PHOSPHO_SITE 1
[PROSITE]      ASN_GLYCOSYLATION 1
[KW]           Alpha_Beta
[KW]           SIGNAL PEPTIDE 32

```

SEQ. MNTVLSRANSLFAFSLSVMAALTFGCFITTAFKDRSVPVRLHVSRIMLKNVEDFTGPRER
PRD cccccccchhhhhhhhhhhhhhhhhhhhhheeeccccccceehhhhhhhhhhhhhccccccc

SEQ SDLGFITSDITADLENI FDNVVKQLFLYLSAEYSTKNNALNQVVLWDKIVLRGDNPKLLL
PRD cccccchhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhccccceeeeeeeceeecccccchhhhh

SEQ KDMKTKYFFFDGNGLGKGNRVTLTLSWNVVPNAGILPLVTGSGHVSVPFPDYEITKSY
PRD hhccccceeeccccccccceeeccccceeeccccceeecccccccccc

Prosites for DKFZphfbr2_64j18.1

PS000001	141->145	ASN_GLYCOSYLATION	PDOC000001
PS000005	94->97	PKC_PHOSPHO_SITE	PDOC000005
PS000008	25->31	MYRISTYL	PDOC000008
PS000008	135->141	MYRISTYL	PDOC000008
PS000113	16->27	PROKAR_LIPOPROTEIN	PDOC000113
PS000116	112->115	RGD	PDOC000116
PS00430	1->22	TONB_DEPENDENT_REC_1	PDOC00354

(No Pfam data available for DKFZphfbr2_64j18.1)

DKFZphfbr2_64k24

group: transmembrane proteins

DKFZphfbr2_64k24 encodes a novel 412 amino acid protein with weak similarity to several known proteins.

The novel protein contains 5 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to AMAC1 "testicular condensing enzyme" ;
membrane regions: 5
Summary DKFZphfbr2_64k24 encodes a novel 412 amino acid protein, with
similarity to AMAC1"; product: "testicular condensing enzyme"

similarity to AMAC1 "testicular condensing enzyme"

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 1958 bp

Poly A stretch at pos. 1939, polyadenylation signal at pos. 1918

```
1 GGGCCCGCCT CGATTTTCCC AGGCGAGGGC ACGCCCGCGT CAGTCGCCTC
51 CCGGGCACCT TCCTCGCCAC GACACGCAGG TAACCGGGCC CCGGGAGCCG
101 GTCGGCGGCG GCGGACTGGG ACCTTGATCC TGCTGCCCCG GCCGCCCCGAC
151 AAGGGAATGA GAGCGGACCC CGAACTCCAC ACACCCGCGT TTAGCCGCCA
201 CACCTAAGGG GCAGAACAGT CTTTTGGGT AAGGGCCGGG CTGGGGGCGA
251 CGCGCCCCGC CGCTTTGCA GACTTCGGGG TGCTCTGCAC GACGCCTGAA
301 AGGCCGCGGG GCCCGCATTT CTCTGTGCTG CCCTCCTGGA GAACCGGGAC
351 ACGGGGACGG GAGGGCCAGC ATCGGCTACG GCCCGGTTTC CCGTTTCTTT
401 CCTCTGTGCG GTCTGGGCCC TCCTGCAGCG TCCATGATGA AGGCCAGGGG
451 CTGTTGCTTT CCTCTGCCCC AGTAGCCAAC CCAAGCAAGG GAATTAATTA
501 TCTGAAGAAA TGATACTTC TCCTCCAGA AAATATCCAG TTAACAAACG
551 GGTGAAAATA CATCCCAACA CAGTGATGGT GAAATATACT TCTCATTATC
601 CCCAGCCTCG CGATGATGGA TATGAAGAAA TCAATGAAGC CTATGGGAAT
651 TTTATGGAGG AAAATCCAAA GAAAGGTCTG CTGAGTGAAA TGAAAAAATA
701 AGGGAGAGGT TTCTTTGGAA CCATGGATAC CCTACCTCCA CCAACAGAAG
751 ACCCAATGAT CAATGAGATT GGACAATTCC AGAGCTTTGC AGAAAAAAC
801 ATTTTTCAT CCCGAAAAAT GTGGATAGTG CTGTTTGGAT CTGCTTTGGC
851 TCATGGATGT GTAGCTCTTA TCACTAGGCT TGTTCCTGAT CGGTCTAAG
901 TTCCATCTCT AGAACTGATT TTTATCCGTT CTGTTTTTCA GGTCTTATCT
951 GTGTTAGTTG TGTGTTACTA TCAGGAGGCC CCCTTTGGAC CCAGTGGATA
1001 CAGATTACGA CTCCTCTTTT ATGGTGTATG CAATGTCATT TCTATCACTT
1051 GTGCTTATAC ATCATTTCAT ATAGTTCCTC CCAGCAATGG GACCACTATG
1101 TGGAGAGCCA CAACTACAGT CTTCAAGTCC ATTTTGGCTT TTTTACTCGT
1151 AGATGAGAAA ATGGCTTATG TTGACATGGC TACAGTTGTT TGCAGCATCT
1201 TAGGTGTTTG TCTGTCTATG ATCCCAACA TTGTTGATGA AGACAATTCT
1251 TTGTTAAATG CCTGGAAAGA AGCCTTTGGG TACACCATGA CTGTGATGGC
1301 TGGACTGACC ACTGCTCTCT CAATGATAGT ATACAGATCC ATCAAGGAGA
1351 AGATCAGCAT GTGGACTGCG CTGTTTACTT TTGGTTGGAC TGGGACAATT
1401 TGGGGAATAT CTAATATGTT TATTCTTCAA GAACCATCA TCCCATTAGA
1451 TGGAGAAACC TGGAGTTATC TCATTGCTAT ATGTGCTGTT TCTACTGCAG
1501 CATTCTTAGG AGTTTATTAT GCCTTGGACA AATTCCATCC AGCTTTGGTT
1551 AGCACAGTAC AACATTTGGA GATTGTGTA GCTATGGTCT TGCAGCTTCT
1601 CGTGCTGCAC ATATTTCTTA GCATCTATGA TGTTTTTGGA GGGGTAATCA
1651 TTATGATTAG TGTTTTTGTC CTGCTGGCT ATAACTTTA CTGGAGGAAT
1701 TTAAGAAGGC AGGACTACCA GAAATACTA GACTCTCCCA TTAATGAAT
1751 ACCTGATTAT TATTGTCTCA TTAATGTTCA GTTATTAATA TGTATACTGC
1801 CATTTTAATG TTTACCTATG AATGTCTTTT GTGTTATATA ACTGACAGAG
1851 TCGTATAAAA TATATAATAT ATACAAATGC AGAAAATTTA TTCTAGTCTA
1901 ATATATTTCAA ATACAAATAT TAAATATATG AAATACGTTA AAAAAAATA
1951 AAAAAAATA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 510 bp to 1745 bp; peptide length: 412
 Category: similarity to known protein

```

1 MDTSPSRKYP VKKRVKIHPN TVMVKYTSHY PQPGDDGYEE INEGYGNFME
51 ENPKKGLLSE MKKKGRAFFG TMDTLPPPTD DPMINEIGQF QSFAEKNIFQ
101 SRKMWIVLFG SALAHGCVL ITRLVSDRSK VPSLELIFIR SVFQVLSVLV
151 VCYYQEAPFG PSGYRLRLEF YGVCNVISIT CAYTSFSIVP PSNGTMMWRA
201 TTTVFSAILA FLLVDEKMAY VDMATVVCSI LGVCLVMIPN IVDEDNSLLN
251 AWKEAFGYTM TVMAGLTAL SMIVYRSIKE KISMWTALEF FGWTGTIWGI
301 STMFILOEPI IPLDGETWSY LIAICVCSTA AFLGVVYALD KFHPALVSTV
351 QHLEIVVAMV LQLLVLIHIF SIYDVFGGVI IMISVFVLAV YKLYWRNLRR
401 QDYQEILDSP IK
  
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64k24, frame 3

TREMBLNEW:AF016712_1 gene: "AMAC1"; product: "testicular condensing enzyme"; Mus musculus testicular condensing enzyme (AMAC1) mRNA, complete cds., N = 1, Score = 191, P = 1.9e-12

TREMBL:BMAJ733_6 product: "hypothetical protein"; Bacillus megaterium bgaM gene, N = 1, Score = 137, P = 1.6e-06

PIR:G71841 hypothetical protein jhp1155 - Helicobacter pylori (strain J99), N = 1, Score = 129, P = 1.3e-05

>TREMBLNEW:AF016712_1 gene: "AMAC1"; product: "testicular condensing enzyme"; Mus musculus testicular condensing enzyme (AMAC1) mRNA, complete cds.

Length = 362

HSPs:

Score = 191 (28.7 bits), Expect = 1.9e-12, P = 1.9e-12
 Identities = 39/105 (37%), Positives = 66/105 (62%)

Query: 289 FTFGWTGTIWGISTMFILOEPIIPLDGETWSYLIAICVCSTAFLGVVYALDKFHPALVS 348
 F FG G + + +F+LQ P++P D +WS ++A+ + + +F+ V YA+ K HPALV
 Sbjct: 248 FLFGLVGLMVSVPGLFVLQTPVLPQDTLSWSCVAVGGLLALVSFVCSYAVTKAHPALVC 307

Query: 349 TVQHLEIVVAMVLQLLVLH--IFPSIYDVFGGVIIMISVFVLAVGYKL 393
 V H E+VVA++LQ VL+ + PS D+ G +++ S+ ++ L
 Sbjct: 308 AVLHSEVVVALMLQYYVLYETVAPS--DIMGAGVVLGSAIITAQNL 352

Pedant information for DKFZphfbr2_64k24, frame 3

Report for DKFZphfbr2_64k24.3

```

[LENGTH]      412
[MW]           46449.87
[pI]           6.99
[HOMOL]        TREMBL:AF016712_1 gene: "AMAC1"; product: "testicular condensing enzyme"; Mus
musculus testicular condensing enzyme (AMAC1) mRNA, complete cds. 8e-14
[PROSITE]      MYRISTYL 6
[PROSITE]      CK2_PHOSPHO_SITE 3
[PROSITE]      PKC_PHOSPHO_SITE 4
[PROSITE]      ASN_GLYCOSYLATION 1
[KW]           TRANSMEMBRANE 5
  
```

SEQ MDTSPSRKYPVKKRVKIHPNTVMVKYTSHYPQPGDDGYEINEGYGNFMEENPKKGLLSE

```

PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhh
MEM  .....

SEQ  MKKKGRAFFGTMDTLPPTEDPMINEIGQFQSFAEKNIFQSRKMWIVLFGSALAHGCVAL
PRD  hhhhccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhh
MEM  .....

SEQ  ITRLVSDRSKVPSSLELIFTRSVFQVLSVLVVCYYQEAPFGPSGYRLRLFFYGVCNVISIT
PRD  chhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ  CAYTSFSIVPPSNGTTMWRATTTVFSAILAFLLVDEKMAYVDMATVVCSILGVCCLVMIPN
PRD  ecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  IVDEDNSLLNAWKEAFGYTMTVMAGLTTALSMIVYRSIKEKISMWTALFTFGWTGTIWI
PRD  cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ  STMFILQEPIIPLDGETWSYLIAICVCSTAAFLGVYALDKFHPALVSTVQHLEIVVAMV
PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhh
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ  LQLLVLHIFPSIYDVFGGVIIMISVFLAGYKLYWRNLRRQDYQEILDSPK
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

```

Prosites for DKFZphfbr2_64k24.3

PS00001	193->197	ASN_GLYCOSYLATION	PDOC00001
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	101->104	PKC_PHOSPHO_SITE	PDOC00005
PS00005	126->129	PKC_PHOSPHO_SITE	PDOC00005
PS00005	277->280	PKC_PHOSPHO_SITE	PDOC00005
PS00006	92->96	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	371->375	CK2_PHOSPHO_SITE	PDOC00006
PS00008	70->76	MYRISTYL	PDOC00008
PS00008	88->94	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	265->271	MYRISTYL	PDOC00008
PS00008	295->301	MYRISTYL	PDOC00008
PS00008	334->340	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_64k24.3)

DKFZphfbr2_6a17

group: brain derived

DKFZphfbr2_6a17 encodes a novel 100 amino acid protein with very weak similarity to human finger protein zFOC1.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 1424 bp

Poly A stretch at pos. 1405, polyadenylation signal at pos. 1389

```
1 GGGACTGAGG GGGTGGGCTT ACTCCCTGGG CAGTCTTGGG GGCCAGAGCT
51 GAGGCCAGTC CATATTACAG TGGCTGGGCT GTTTTTCCTA GTAGCCCCCTA
101 GCATTGGCTG GGATTCCTGT TCCTGGGTGC GCCTCCACCT CCCTTCTGAT
151 GCTTCCTGGC TATGGTGGGG TGGGAACCTC AGTTTCCCCC AAAGTCTTCC
201 CTGGATGCTG GCTTCAGGTT GAAGACCCTG GTTCTTCCAG TTCCTCACGG
251 GTTAGGTAGG GGCCTCTGCA TCACCTTCAG AATCAGTTCC AACCCCCACT
301 CTCCTTAGGC TTTGTGCTCT GCTCTGCCCT GCCAGGCTGC CCTTGTCCAT
351 GTGAGTAGCA TGGCGGGGTG GTGGGGACGG CAGTGGTGAT GAAGGGGGTG
401 CACCACAGGC CTCATGAAGC AGTTCCACAC TGGCGGTGTC GCTGGGGCGT
451 GGCCACCACA GAGCACATGG CTGTGTCTAG GCGCAAGCAC TTTAGCAGTA
501 TCTGTTTACA TGGCCAAGGA TCAAGCCGAC TACCTGTGCT GTCTACTGGG
551 ACAGCAGTCT CCGAGCTACT CCGTACCTCC CTCTGCCAGG TCGTGGAGTT
601 AGGCCCCAGT CCCTACTTGT CACTGGTTCC CACTGTGCTC CTAAGTGTGC
651 AGCACCTGGG AGCTCTGGCC TGGGGCTGGA GGCCCTGGTA GGAGCTGCAG
701 TTGGAGGCCG TTCTGTGCCC AGCAGCGGTG AGCGGCTCCC ATGGGCCCTG
751 TGTCTGCAGG GAGCCAGGGC TCGGGCACAT GTGCTGTGAA ACTGGCACCC
801 ACCTGGCGTG CTGCTGCCGC CACTTGCTTC CTGCAGCACC TCCTACCCCTG
851 CTCCGTGTCC TCCCTCTCCC CGCGCCTGGC TCAGGAGTGC TGGAAAAGCT
901 CACGCCCTCG CTTGGGAGCC TGGCCTCTTG ATATACCTCG AGCTTCCCCT
951 GTGCTCCCCA GCCCCAGGAC CACTGGCCCC TTGGCCTGAG GGGCTGGGGG
1001 CCCCACGACC TGCAGCGTCG AGTCCGGGAG AGAGCCCCGA GCGGCGTGCC
1051 ATCTCGGCTC GGCCTTGCTG AGAGCCTCCG CCCTGGCTTT CTCCCTGTCT
1101 GGTTTCAGTG GCTCACGTTG GTGCTACACA GCTAGAATAG ATATATTAG
1151 AGAGAGAGAT ATTTTAAAGA CAAAGCCAC AATTAGCTGT CCTTTAACAC
1201 CGCAGAACCC CCTCCAGAA GAAGAGCGAT CCCTCGGACG GTCCGGGCGG
1251 GCACCCCTCAG CCGGGCTCTT TGCAGAAAGCA GCACCGCTGA CTGTGGGCCC
1301 GGCCTCAGA TGTGTACATA TACGGCTATT TCCTATTTTA CTGTTCTTCA
1351 GATTTAGTAC TTGTAATAA ACACACACAT TAAGGAGAGA TTAACATT
1401 TTGCCAAAAA AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 389 bp to 688 bp; peptide length: 100
Category: putative protein

```
1 MKGVHHRPHE AVPTWACGWG VATTEHMAVS RRKHFSSICL HAQSSRLPV
51 LSTGTAVSEL LRTSLCQVVE LGPSPYLSLV PTVLLTVQHL GALAWGWRPW
```

BLASTP hits

Entry S70007 from database PIR:
finger protein zfOC1 - human (fragment)
Length = 183
Score = 62 (21.8 bits), Expect = 0.24, Sum P(2) = 0.22
Identities = 18/47 (38%), Positives = 24/47 (51%)

Alert BLASTP hits for DKFZphfbr2_6a17, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_6a17, frame 2

Report for DKFZphfbr2_6a17.2

[LENGTH] 100
[MW] 10944.82
[pI] 9.49
[PROSITE] MYRISTYL 2
[PROSITE] PKC_PHOSPHO_SITE 2
[KW] Alpha_Beta

SEQ MKGVHHRPHEAVPTWACGWGVATTEHMAVSRKHFSSICLHAQGSSRLPVLSTGTAVSEL
PRD cccccccccccccccccccccchhhhhhhhhccccceccccccccceccccchhhh

SEQ LRTSLCQVVELGSPYLSLVPTVLLTVQHLGALAWGWRPW
PRD hhhhheeeeeccccceecchhhhhhhhhchhhhhcccc

Prosites for DKFZphfbr2_6a17.2

PS00005	30->33	PKC_PHOSPHO_SITE	PDOC00005
PS00005	45->48	PKC_PHOSPHO_SITE	PDOC00005
PS00008	20->26	MYRISTYL	PDOC00008
PS00008	54->60	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_6a17.2)

DKFZphfbr2_6b24

group: metabolism

DKFZphfkd2_6b24 encodes a novel 334 amino acid protein with similarity to several bacterial dTDP-4-dehydrorhamnose reductases (EC 1.1.1.133).

The novel protein seems to be a human enzyme similar to dTDP-4-dehydrorhamnose reductases. EC 1.1.1.133 catalyses the reaction: dTDP-6-deoxy-L-mannose + NADP(+) \rightleftharpoons dTDP-4-dehydro-6-deoxy-L-mannose + NADPH.

The new protein can find application in modulation of rhamnose metabolism and as a new enzyme for biotechnologic production processes.

similar to dTDP-6-deoxy-L-mannose-dehydrogenases

complete cDNA, EST hits, complete cds
Nucleotide sugars metabolism seems to be a dehydrogenase
localisation: region of primer A missing

Sequenced by AGOWA

Locus: /map="5"

Insert length: 2054 bp

Poly A stretch at pos. 2028, polyadenylation signal at pos. 2015

```
1 GGGGGAGGCC CGCGTCGATC CTGGGTTGGA GGAGGTGGCG GCCGCTGAGG
51 CTGCGGCGTG AAGACGGCGG GCATGGTGGG CGCGGAGAAA GAGCTCTCTA
101 TACACTTTGT TCCCGGCGAGC TGTCGGCTGG TGGACGAGGA AGTTAACATC
151 CCTAATAGGA GGGTTCCTGGT TACTGGTGCC ACTGGGCTTC TTGGCAGAGC
201 TGTACACAAA GAATTTTCAGC AGAATAATTG GCATGCAGTT GGCTGTGGTT
251 TCAGAAGAGC AAGACCAAAA TTTGAACAGG TTAATCTGTT GGATTCTAAT
301 GCAGTTCATC ACATCATTCA TGATTTTCAG CCCCATGTTA TAGTACATTG
351 TGCAGCAGAG AGAAGACCAG ATGTTGTAGA AAATCAGCCA GATGCTGCCT
401 CTCAACTTAA TGTGGATGCT TCTGGGAATT TAGCAAAGGA AGCAGCTGCT
451 GTTGGAGCAT TTCTCATCTA CATTAGCTCA GATTATGTAT TTGATGGAAC
501 AAATCCACCT TACAGAGAGG AAGACATACC AGCTCCCCTA AATTTGTATG
551 GCAAAACAAA ATTAGATGGA GAAAAGGCTG TCCTGGAGAA CAATCTAGGA
601 GCTGCTGTTT TGAGGATTCC TATTCTGTAT GGGGAAGTTG AAAAGCTCGA
651 AGAAAGTGA GTGACTGTTA TGTTTGATAA AGTGCAGTTC AGCAACAAGT
701 CAGCAAACAT GGATCACTGG CAGCAGAGGT TCCCCACACA TGTCAAAGAT
751 GTGGCCACTG TGTGCCGGCA GCTAGCAGAG AAGAGAATGC TGGATCCATC
801 AATTAAGGGA ACCTTTCAC TGTCTGGCAA TGAACAGATG ACTAAGTATG
851 AATGGCATG TGCATTTGCA GATGCCTTCA ACCTCCCCAG CAGTCACTTA
901 AGACCTATTA CTGACAGCCC TGTCTTAGGA GCACAACGTC CGAGAAATGC
951 TCAGCTTGAC TGCTCCAAAT TGGAGACCTT GGGCATTGGC CAACGAACAC
1001 CATTTCGAAT TGAATCAAA GAATCACTTT GGCTTTCCCT CATTGACAAG
1051 AGATGGAGAC AAACGGTCTT TCATTAGTTT ATTTGTSTTG GGTTCCTTTT
1101 TTTTAAAT GAAAAGTATA GTATGTGGCC CTTTAAAG AACAAAGGAA
1151 ATAGTTTTGT ATGAGTACTT TAATGTGTAC TCTTAGGATC TTTGAGGTAA
1201 ATGATGCTCT TGCAGTAGTG AAATTGTCTA AAGAACTAA AGGGCAGTCA
1251 TGCCCTGTTT GCAGTAATT TTCTTTTAT CATTATGTTT GTCCTGGCTA
1301 AACTTGGAGT TTGAGTATAG TAAATTATGA TCCTAAATA TTTGAGGGTC
1351 AGGATGAAGC AGATCTGCTG TAGACTTTTC AGATGAAAT GTTCATTCTC
1401 GTAACCTCCA TATTTTCAGG ATTTTGAAG CTGTTGACCA TTTCATGTTG
1451 ATTATTTTAA ATTGTGTGGA ATAGTATAAA AATCATTGGT GTTCATTATT
1501 TGCTTTGCCT GAGCTCAGAT CAAAATGTTT GAAGAAAGGA ACTTTATTTT
1551 TGCAAGTTAC GTACAGTTTT TATGCTTGAG ATATTTCAAC ATGTTATGTA
1601 TATTGGAAC TCTACAGCTT GATGCCTCCT GCTTTTATAG CAGTTTATGG
1651 GGAGCACTTG AAAGAGCGTG TGTACATGTA TTTTCTTCT AGGCAACAT
1701 TGAATGCAAA CGTGTATTT TTTAATATAA ATATATAACT GTCCTTTTCA
1751 TCCCATGTTG CCGCTAAGTG ATATTTTATA TGTGTGGTTA TACTGATAAT
1801 AATGGGCCCT GTAAGTCTTT TCACCATTCA TGAATAATAA TAAATATGTA
1851 CTGCTGGCAT GTAAATGCTT GTTTCTTGT ATTTACTTCT TTTTAAAAA
1901 TGAAGGACC AAACCTCTAA ACTAATTGTT CTTTGTGTC TTTAATTTT
1951 AAAAATTACA TTCTCTGAT GTAACATGTG ATACATACAA AAGAATATAG
2001 TTTAATATGT ATTGAAATAA AACACAATAA AATTAAAAAA AAAAAAAA
2051 AAAA
```

BLAST Results

Entry G37115 from database EMBL:
SHGC-56899 Human Homo sapiens STS genomic.
Score = 446, P = 4.6e-14, identities = 90/91

Medline entries

99109950:
The metabolism of 6-deoxyhexoses in bacterial and animal cells.

Peptide information for frame 1

ORF from 73 bp to 1074 bp; peptide length: 334
Category: similarity to known protein

```

1 MVGREKELSI HFVPGSCRLV EEEVNIPNRR VLVGTATGLL GRAVHKEFQQ
51 NNWHAVGCGF RRARPKFEQV NLLDSNAVHH IIHDFQPHVI VHCAAERRPD
101 VVENQPDAAAS QLNVDASGNL AKEAAAVGAF LIYISSDYVF DGTNPPYREE
151 DIPAPLNLYG KTKLDGEKAV LENNLGA AVL RIPILYGEVE KLEESAVTVM
201 FDKVQFSNKS ANMDHWQORF PTHVKDVATV CRQLAEKRML DPSIKGTFHW
251 SGNEQMTKYE MACAIADAFN LPSSHLRPIT DSPVLGAQRP RNAQLDCSKL
301 ETLGIGQRTF FRIGIKESLW PFLIDKRWRQ TVFH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_6b24, frame 1

PIR:T00104 probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) -
Actinobacillus actinomycetemcomitans, N = 1, Score = 293, P = 6.4e-26

TREMBL:SSU51197_21 gene: "zhsD"; product:
"dTDP-6-deoxy-L-mannose-dehydrogenase"; Sphingomonas S88 sphingan
polysaccharide synthesis (spsG), (spsS), (spsR), glycosyl transferase
(spsQ), (spsI), glycosyl transferase (spsK), glycosyl transferase
(spsL), (spsJ), (spsF), (spsD), (spsC), (spsE), Urf 32, Urf 26,
ATP-binding cassette trans>., N = 1, Score = 291, P = 1e-25

SWISSPROT:RFBD_RHISN PROBABLE DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC
1.1.1.133) (DTDP-4-KETO- L-RHAMNOSE REDUCTASE) (DTDP-6-DEOXY-L-MANNOSE
DEHYDROGENASE) (DTDP-L- RHAMNOSE SYNTHETASE)., N = 1, Score = 283, P =
7.4e-25

>PIR:T00104 probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) -
Actinobacillus actinomycetemcomitans
Length = 294

HSPs:

Score = 293 (44.0 bits), Expect = 6.4e-26, P = 6.4e-26
Identities = 89/276 (32%), Positives = 151/276 (54%)

```

Query:   30 RVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNNLLDSNAVHHIIHDFQPHV 89
          R+L+TGA G LGR++ K   N   + V           F +++++ + + V II F+P+V
Sbjct:   3 RLLITGAGGQLGRSLAKLLVDNGRYEV-----LALDFSELDITNKDMVFSIIDSFKPNV 56

Query:   90 IVHCAAERRPDVVENQPDAAASQLNVDASGNLAKEAAAVGAFLIYISSDYVFDG-TNPPYR 148
          I++ AA   D E + + +A +NV   LA+ A   + ++++S+DYVFDG + Y+
Sbjct:   57 IINAAAYTSVDQAELEVSSAYSNNVRGVQYLAEAAIRHNSAILHVSTDYVFDGYKSGKYK 116

Query:  149 EEDIPAPLNLYGKTKLDGEKAVLENNLGA AVL RIPILYGEVEKLEESAVTVMFDKVQFSN 208
          E DI  PL +YGK+K +GE+ +L + + +LR   +GE   + V M ++ +
Sbjct:  117 ETDIIHPLCVYGKSKAEGERLLLTLSPKSIILRTSWTFGEYGN---NFVKTML-RLAKNR 172

Query:  209 KSANMDHWQORFPTHVKDVATVCRQLAEKRMLDPSIK-GTFHWSGNEQMTKYEMACAIAD 267
          +   Q   PT+  D+A+V  Q+AEK ++  ++K G +H++G  ++ Y+ A AI D
Sbjct:  173 DILGVVADQIGGPTYSGDIASVLIIQIAEKIIVGETVKYGIYHFTGEPCVSWYDFAIAIFD 232

Query:  268 AF-----NLPSSHLRPITDSPVLGAQRP RNAQLDCSKLE-TLGI 305
          N+P +           D P L A+RP N+ LD +K++   GI
Sbjct:  233 EAVAQKVLENVPLVNAITADYPTL-AKRPANSCLDLTKIQQAFCI 277

```


Report for DKFZphfbr2_6b24.1

SEQ PRD	MVGREKELSIHFVPGSCLRVEEVNIPNRRVLVTGATGLLGRAVHKEFQNNWNHAVGCGF ccccceeeccccceeeccccccccceeeccccchhhhhhhhhhhccceeeeeecc
SEQ PRD	RRARPKFEQVNLDSNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAAASQLNVDASGNL ccccccccccccchhhhhhhhhhhccceeeehhhhhhhhhhhhhhhhhhhhhhhccchhh
SEQ PRD	AKEAAAVGAFLIYISSDYVFDGTPPYREEDIAPNLNLYGKTKLDGEKAVLENNLGAAVL hhhhhhhhhhheeeeeccccccccccccccccccccccccchhhhhhhhhccccccceee
SEQ PRD	RIPILYGEVERKEESAIVTMFDKVVQFSNKSANMDHWQQRFPETHVKDVATVCRQLAEKRML eeeeeeccccccccchhhhhhhhhhhhhccceeeccccccccccchhhhhhhhhhhhhhhhh
SEQ PRD	DPSIKGTFHWSGNEQMTKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL ccccceeeccccccccchhhhhhhhhhhhhccceccccccccccccccccccccchhhhhh
SEQ PRD	ETLGIGQRTFFRIGIKESLWPFLLDKRWQRTVFH hhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhccccc

PS000001	208->212	ASN_GLYCOSYLATION	PDOC000001
PS000005	16->19	PKC_PHOSPHO_SITE	PDOC000005
PS000005	207->210	PKC_PHOSPHO_SITE	PDOC000005
PS000005	243->246	PKC_PHOSPHO_SITE	PDOC000005
PS000006	162->166	CK2_PHOSPHO_SITE	PDOC000006
PS000006	251->255	CK2_PHOSPHO_SITE	PDOC000006
PS000006	257->261	CK2_PHOSPHO_SITE	PDOC000006
PS000006	298->302	CK2_PHOSPHO_SITE	PDOC000006
PS000008	314->320	MYRISTYL	PDOC000008

298

DKFZphfbr2_6i20

group: brain derived

DKFZphfbr2_6i20 encodes a novel 296 amino acid protein with similarity to ribosomal protein L15 precursor of *S. cerevisiae* mitochondria.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to ribosomal protein L15 precursor, mitochondrial

complete cDNA, complete cds, EST hits
potential mitochondrial L15 ribosomal protein

Sequenced by AGOWA

Locus: /map="377.5 cR from top of Chr8 linkage group"

Insert length: 1122 bp

Poly A stretch at pos. 1099, polyadenylation signal at pos. 1071

```

1  GGGGGCCCTT  GAAAGTCTT  GGATCTGCGG  GTTATGGCCG  GTCCCTTGCA
51  GGGCGGTGGG  GCCCCGGCCC  TGGACCTACT  CCGGGGCCTG  CCGCGTGTGA
101  GCCTGGCCAA  CTTAAAGCCG  AATCCCGGCT  CCAAGAAACC  GGAGAGAAGA
151  CCAAGAGGTC  GGAGAAGAGG  TAGAAAATGT  GGCAGAGGCC  ATAAAGGAGA
201  AAGGCAAAGA  GGAACCCGGC  CCCGCTTGGG  CTTTGAGGGA  GGCCAGACTC
251  CATTTTACAT  CCGAATCCCA  AAATACGGGT  TTAACGAAGG  ACATAGTTTC
301  AGACGCCAGT  ATAAGCCTAT  GAGTCTCAAT  AGACTGCAGT  ATCTTATTGA
351  TTTGGGTCCT  CTTGATCCTA  CTCAACCTAT  TGACTTAACC  CAGCTTGTCa
401  ATGGGAGAGG  TGTGACCATC  CAGCCACTTA  AAAGGGATTA  TGATGTCCAG
451  CTGGTTGAGG  AGGGTGCTGA  CACCTTTACG  GCAAAAGTTA  ATATTGAAGT
501  ACAGTTGGCT  TCAGAACTAG  CTATTGCTGC  CATTGAAAAA  AATGGTGGTG
551  TTGTTACTAC  AGCCTTCTAT  GATCCAAGAA  GTCTGGACAT  TGTATGCAAA
601  CCTGTTCAT  TCTTTCTTCG  TGGACAACCC  ATTCCAAAAA  GAATGCTTCC
651  ACCAGAAGAA  CTGGTACCAT  ATTACTGA  TGCAAAGAAC  CGTGGGTACC
701  TGGCGGATCC  TGCCAAATTT  CCTGAAGCAC  GACTTGAAC  CGCCAGGAAG
751  TATGGTTATA  TCTTACCTGA  TATCACTAAA  GATGAACCTC  TCAAAATGCT
801  CTGTACTAGG  AAGGATCCAA  GGCAGATTTT  CTTTGGTCTT  GCTCCAGGAT
851  GGGTGGTGAA  TATGGCCGAT  AAGAAAATCC  TAAAACCTAC  AGATGAAAAA
901  CTCCTTAAGT  ATTATACCTC  ATGAATTCCC  GTCCAAGGAA  GCAGAGTTGT
951  TAAAGAGTAC  TGGAAATAGG  GCTGAAGGAT  CTATATTCCC  TTATTGCATT
1001  TTCCTTATGT  ATAATTTTCC  AGATGGTGAT  GTTACTTTTC  AGTCTACTCA
1051  TATGTCTCAT  TTTTATCTAA  AATTAAATGG  CAGGAAACAA  GGACTGCATA
1101  GAGAAAAAAA  AAAAAAAA  AA

```

BLAST Results

Entry HS500354 from database EMBL:
human STS WI-12392.
Length = 426
Minus Strand HSPs:
Score = 1791 (268.7 bits), Expect = 1.1e-74, P = 1.1e-74
Identities = 375/384 (97%)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 34 bp to 921 bp; peptide length: 296
Category: strong similarity to known protein

1 MAGPLQGGGA RALDLLRGLP RVSLANLKP N PGSKKPERRP RGRRRGRKCG

DKFZphfkd2_3i13

group: transmembrane protein

DKFZphfkd2_3i13 encodes a novel 406 amino acid protein with *C. elegans* cosmid Y37D8A and *A. thaliana* H71412 hypothetical protein.

The novel protein contains 3 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of kidney-specific genes and as a new marker for kidney cells.

similarity to *A.thaliana* and *C.elegans*;
membrane regions: 3

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: /map="17"

Insert length: 2052 bp

Poly A stretch at pos. 2032, no polyadenylation signal found

```
1 AGTGACGTGA GCGGGTTCCG GTTGTCTGGA GCCCAGCGGC GGGTGTGAGA
51 GTCGGTAAGG AGCAGCTTCC AGGATCCTGA GATCCGGAGC AGCCGGGGTC
101 GGAGCGGCTC CTCAAGAGTT ACTGATCTAT GAAATGGCAG AGAATGGAAA
151 AAATTGTGAC CAGAGACGTG TAGCAATGAA CAAGGAACAT CATAATGGAA
201 ATTTACAGCA CCCCTCTTCA GTGAATGAAA AGAAGAGGAG GGAGCGGGAA
251 GAAAGGCAGA ATATTGTCCT GTGGAGACAG CCGCTCATT CTTGCAGTA
301 TTTTCTCTG GAAATCCTTG TAATCTTGAA GGAATGGACC TCAAAATTAT
351 GGCATCGTCA AAGCATTGTG GTGTCTTTT TACTGCTGCT TGCTGTGCTT
401 ATAGCTACGT ATTATGTTGA AGGAGTGCAT CAACAGTATG TGCAACGTAT
451 AGAGAAACAG TTTCTTTTGT ATGCCTACTG GATAGGCTTA GGAATTTTGT
501 CTTCTGTTGG GCTTGGAAAC GGGCTGCACA CCTTCTGCT TTATCTGGGT
551 CCACATATAG CCTCAGTTAC ATTAGCTGCT TATGAATGCA ATTCAAGTTAA
601 TTTTCCCGAA CCACCTTATC CTGATCAGAT TATTGTCCA GATGAAGAGG
651 GCACTGAAGG AACCATTTTT TTGTGGAGTA TCATCTCAA AGTTAGGATT
701 GAAGCCTGCA TGTGGGGTAT CGGTACAGCA ATCGGAGAGC TGCTCCATA
751 TTTTCATGGC AGAGCAGCTC GCCTCTCAGG TGCTGAACCA GATGATGAAG
801 AGTATCAGGA ATTTGAAGAG ATGCTGGAAC ATGCAGAGTC TGCACAAGAC
851 TTTGCCTCCC GGGCCAAACT GGCAGTTCAA AAAGTAGTAC AGAAAGTTGG
901 ATTTTGTGGA ATTTTGGCCT GTGCTTCAAT TCCAAATCCT TTATTTGATC
951 TGGCTGGAAT AACGTGTGGA CACTTCTGG TACCTTTTGG GACCTTCTTT
1001 GGTGCAACCC TAATTGAAA AGCAATAATA AAAATGCATA TCCAGAAAAT
1051 TTTTGTATA ATAACATTCA GCAAGCACAT AGTGGAGCAA ATGGTGGCTT
1101 TCATTGGTGC TGTCCCGGGC ATAGGTCCAT CTCTGCAGAA GCCATTTTCA
1151 GAGTACCTGG AGGCTCAACG GCAGAAGCTT CACCACAAA GCGAAATGGG
1201 CACACCCAGG GGAGAAAACG GGTGTCTCTG GATGTTTGA AAGTTGGTCG
1251 TTGTATGGT GTGTACTTTC ATCCTATCTA TCATTAATC CATGGCACAA
1301 AGTTATGCCA AACGAATCCA GCAGCGGTTG AACTCAGAGG AGAAACTAA
1351 ATAAGTAGAG AAAGTTTAA ACTGCAGAAA TTGGAGTGA TGGGTCTGTC
1401 CTAAATTTGG GAGGACTCCA AGCCGGGAAG GAAATTTCCC TTTTCCAACC
1451 TGTATCAATT TTTACAACCT TTTTCTGAA AGCAGTTTAG TCCATACTTT
1501 GCACTGACAT ACTTTTCTCT TCTGTGCTAA GGTAAGGTAT CCACCTCGA
1551 TGCAATCCAC CTTGTGTTTT CTTAGGGTGG AATGTGATG TCAGCAGCAA
1601 ACTTGAACA GACTGGCCTT CTGTTTGTTA CTTTCAAAG GCCACATGA
1651 TACAATTAGA GAATTCCCAC CGCACAAAAA AAGTTCTTAA GTATGTTAAA
1701 TATGTCAAGC TTTTATAGGCT TGTCACAAAT GATTGCTTTG TTTTCTAAG
1751 TCATCAAAAT GTATATAAAT TATCTAGATT GGATAACAGT CTTGCATGTT
1801 TATCATGTTA CAATTTAATA TTCCATCCTG CCCAACCTT CCTCTCCAT
1851 CCTCAAAAAA GGGCCATTTT ATGATGCATT GCACACCTC TGGGGAAATT
1901 GATCTTTAAA TTTTGAACA GTATAAGGAA AATCTGGTTG GTGTCTTACA
1951 AGTGAGCTGA CACCATTTTT TATTCGTGTG ATTTAGGATG AAGTCTTGAA
2001 AAAAATTTA TAAAGACATC TTTAATCATT CCAAAAAAAA AAAAAAAA
2051 AA
```

BLAST Results

Entry AC004686 from database EMBL:
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone
hRPC.1073 F15; HTGS phase 1, 8 unordered pieces.
Score = 4142, P = 6.1e-199, identities = 830/832

```

SEQ      KWVTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDVPVG
SEG      .....
PRD      hhhhhccccccccchhhhhhhhhhhccceeeeecccccccccccccccccccccccccccccc
MEM      .....

SEQ      YPSLQVELETPTGLHYTPPTPFQDDYFSDISSIESPLRTPSRLSDGLVPSQGNIEHSAD
SEG      .....
PRD      ccccccccccccccccccccccccccccccecccccccccccccccccccccccccccccc
MEM      .....

SEQ      GPPVVTAEDASLEDSKLEDSVPLTEMPEAVM
SEG      .....
PRD      ccccccccccccccccccccccccccccccc
MEM      .....

```

(No Prosite data available for DKFZphfkd2_24p5.3)

(No Pfam data available for DKFZphfkd2_24p5.3)

Sbjct: 781 GPPVVTAEDTSLEDSKMDSDSVTVTD 805

Pedant information for DKFZphfkd2_24p5, frame 3

Report for DKFZphfkd2_24p5.3

{LENGTH} 811
{MW} 90104.66
{pI} 5.40
{HOMOL} TREMBL:MMANK3A_1 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial
ankyrin 3 (Ank3) 5kb isoform mRNA, complete cds. 0.0
{BLOCKS} BL50017B Death domain proteins profile
{PIRKW} phosphoprotein 0.0
{PIRKW} alternative splicing 0.0
{PIRKW} peripheral membrane protein 0.0
{PIRKW} cytoskeleton 0.0
{SUPFAM} ankyrin 0.0
{SUPFAM} ankyrin repeat homology 0.0
{SUPFAM} unassigned ankyrin repeat proteins 0.0
{KW} TRANSMEMBRANE 2
{KW} LOW_COMPLEXITY 1.73 %

SEQ MALPQSEDAMTGDYDKYLGPDQLKELGDDSLPAEGYMGFSLGARSASLSRFSSDGSYTLN
SEG
PRD ccc
MEM

SEQ RSSYARDSMMIEELLVPSKEQHLTFTRFDSDSLRLHYSWAADTLNVLNLPSPHSGFLV
SEG
PRD cccchhhhhhhhhheeeehhhhhhhhhhhcccccccccccccccccccccccccccccccccc
MEMMMMMMMMMMMMM

SEQ SFMVVDARGGSMRGRSRHHGMRIIIPPRKCTAPTRITCRLVKKRHLANPPPMVEGEGLASRL
SEGxxxxxxxxxxxxxxxx.....
PRD eeeeecc
MEM MMMMMMMMMMMMMMMMMMM.....M

SEQ VEMGPAGAQFLGPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFDSKNEDELTELLNG
SEG
PRD ecc
MEM MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ MDEELDSPEELGKKRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF
SEG
PRD cccccchhhhhhhhhheeeeeecc
MEM

SEQ PEGALTKRIRVGLQAQVPDEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS
SEG
PRD ccchhhhhhhhhhhhhcc
MEM

SEQ GEGVSNYKGDTPNLRLLCSITGGTSPAQWEDITGTPLTFIKDCVSFTTNVSARFWLA
SEG
PRD ccc
MEM

SEQ DCHQVLETVGLATQLYRELICVPYMAKFVVFAMNDPVESSLRCFCMTDDKVDKTLEQQE
SEG
PRD cchhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhheeeccccchhhhhhhhhccccchhhhhhhhh
MEM

SEQ NFEEVARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYFVKENRLPFSIKIRDTSQ
SEG
PRD ceeeeccccccccccccccccccccccccccccccccccccchhhhhhhhhchhhhhhhccceeecccc
MEM

SEQ EPCGRSLFLKEPKTKGLPQTAVCNLNLITLPAHKKIEKTPDGRQSFASLALRKRYSYLTEP
SEG
PRD ccc
MEM

SEQ GMSPQSPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMLK
SEG
PRD cccccchhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhccceeeccccchhhhhhhhh
MEM

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_24p5, frame 3

TREMBL:MMANK3A_1 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (Ank3) 5kb isoform mRNA, complete cds., N = 1, Score = 4022, P = 0

TREMBL:MMANK3B_3 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (7kb isoform) mRNA, complete cds., N = 1, Score = 4005, P = 0

TREMBL:MMANK3B_4 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (7kb isoform) mRNA, complete cds., N = 1, Score = 4005, P = 0

>TREMBL:MMANK3A_1 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (Ank3) 5kb isoform mRNA, complete cds.
Length = 1,094

HSPs:

Score = 4022 (603.5 bits), Expect = 0.0e+00, P = 0.0e+00
Identities = 769/805 (95%), Positives = 783/805 (97%)

Query: 1 MALPQSEDAMTGDYDKYLGPDQLKELGDDSLPAEGYMGFSLGARSASLSRFSDDGSYTLN 60
MALP SEDA+TGDTDKYLGPDQLKELGDDSLPAEGY+GFSLGARSASLSRFSDD SYTLN
Sbjct: 1 MALPHSEDAITGDTDKYLGPDQLKELGDDSLPAEGYVGFSLGARSASLSRFSDDRSYTLN 60

Query: 61 RSSYARDSMMIEELLVPSKEQHLTFTRFSDSLRHYSWAADTLDNVNLVPSPIHSGFLV 120
RSSYARDSMMIEELLVPSKEQHLTFTRFSDSLRHYSWAADTLDNVNLV SP+HSGFLV
Sbjct: 61 RSSYARDSMMIEELLVPSKEQHLTFTRFSDSLRHYSWAADTLDNVNLVSSPVHSGFLV 120

Query: 121 SFMVDARGGSMRGSRRHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL 180
SFMVDARGGSMRGSRRHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL
Sbjct: 121 SFMVDARGGSMRGSRRHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL 180

Query: 181 VEMGPAGAQLGPPVIVEIPHEGSMRGKERELIVLRSENGETWKEHQFDSKNEDLTELLNG 240
VEMGPAGAQLGPPVIVEIPHEGSMRGKERELIVLRSENGETWKEHQFDSKNEDL ELLNG
Sbjct: 181 VEMGPAGAQLGPPVIVEIPHEGSMRGKERELIVLRSENGETWKEHQFDSKNEDLAELLNG 240

Query: 241 MDEELDSPEELGKKRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF 300
MDEELDSPEELG KRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF
Sbjct: 241 MDEELDSPEELGKKRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF 300

Query: 301 PEGALTKRIRVGLQAQPVPEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS 360
PEGALTKRIRVGLQAQPVPEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS
Sbjct: 301 PEGALTKRIRVGLQAQPVPEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS 360

Query: 361 GEGVSNYKGDTPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSAREWLA 420
GEGVSNYKGD TPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSAREWLA
Sbjct: 361 GEGVSNYKGDATPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSAREWLA 420

Query: 421 DCHQVLETVGLATQLYRELICVPYMAKFVVFVAKMNDPVESSLRCFCMTDDKVDKTEQQE 480
DCHQVLETVGLA+QLYRELICVPYMAKFVVFVAK NDPVESSLRCFCMTDD+VDKTEQQE
Sbjct: 421 DCHQVLETVGLASQLYRELICVPYMAKFVVFVAKTNDPVESSLRCFCMTDDRVDKTEQQE 480

Query: 481 NFEEVARSKDIEVLEGGPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ 540
NFEEVARSKDIEVLEGGPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ
Sbjct: 481 NFEEVARSKDIEVLEGGPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ 540

Query: 541 EPCGRSLFLKEPKTTKGLPQTAVCNLNLITLPAHKKIEKTDGROSFASLALRKRYSYLTEP 600
EPCGRSLFLKEPKTTKGLPQTAVCNLNLITLPAHKK EK D RQSFASLALRKRYSYLTEP
Sbjct: 541 EPCGRSLFLKEPKTTKGLPQTAVCNLNLITLPAHKKAEKADRRQSFASLALRKRYSYLTEP 600

Query: 601 GMSPOQPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNLSISQSFMLK 660
GMSPOQPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNLSISQSFMLK
Sbjct: 601 GMSPOQPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNLSISQSFMLK 660

Query: 661 KWTTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDVPDG 720
KWTTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDVPDG
Sbjct: 661 KWTTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDVPDG 720

Query: 721 YPSLQVELETPTGLHYTPPTPFQDDYFSDISSIESPLRTPSRSLDGLVPSQGNIEHSAD 780
+PS QVELETPT GL++TTP PFQDD+FSDISSIESP RTPSRSLDGLVPSQGNIEH
Sbjct: 721 HPSFQVELETPTGLHYTPPTPFQDDHFSDISSIESPFTPTSRSLDGLVPSQGNIEHPTG 780

Query: 781 GPPVVTAEDASLEDSKLEDSVPLTE 805
GPPVVTAED SLEDSK++DSV +T+

```

2401 ATGGAAATAT TTCAGGCACC AGAAGTTTGG CAGATGAGAA CAATGTTTTT
2451 CATGACCCTG TTGATGGTTA TCCTTCCCTT CAAGTGGAAAC TGGAAACCCC
2501 CACAGGGTGG CACTACACAC CACCTACCCC TTTCCAGCAA GATGATTATT
2551 TTAGTGATAT CTCTAGCATA GAATCTCCCC TTAGAACCCC TAGTAGACTG
2601 AGTGATGGGC TAGTGCCTTC CCAGGGGAAC ATAGAGCATT CCGCAGATGG
2651 ACCTCCAGTC GTAACGTCAG AAGACGCTTC CTTAGAAGAC AGCAAACCTGG
2701 AAGACTCAGT GCCTTTAACA GAAATGCCTG AAGCAGTGAT GTAGATGAGA
2751 GCCAGTTGGA GAATGTATGT CTGAGTTGGC AGAATGAGAC ATCAAGTGGG
2801 AACCTAGAGT CCTGCGCTCA AGCTCGAAGA GTAACGCTGG GGTACTAGA
2851 TCGACTGGAT GACAGCCCTG ACCAGTGTAG AGATTCCATT ACCTCATATC
2901 TCAAAGGAGA AGCTGGCAAA TTTGAAGCAA ATGGAAGCCA TACAGAAATC
2951 ACTCCAGAGG CAAAGACAAA ATCTTACTTT CCAGAATCCC AAAATGATGT
3001 AGGAAACAG AGTACCAAGG AACTCTGAA ACCAAAAATA CATGGATCTG
3051 GTCATGTTGA AGAACCAGCA TCACCACTAG CAGCATATCA GAAATCTCTA
3101 GAAGAAACCA GCAAGCTTAT AATAGAAGAG ACTAAACCCG GTGTGCCTGT
3151 CAGTATGAAA AAGATGAGTA GGAATCTCC AGCAGATGGC AAGCCAAGGC
3201 TTAGCCTCCA TGAAGAAGAG GGGTCCAGTG GGTCTGAGCA AAAGCAGGGA
3251 GAAGGTTTGA AGGTGAAAAC GAAGAAAGAA ATCCGGCATG TGGAAAAGAA
3301 GAGCCACTCG TAACAGCGAA CGGTCAGTCA AGGATCATAA GTTTTACTG
3351 CCAGTATTGA GAAATTCGTG GAAGAAATGT CAGCAGGAAG TAAAAATTCA
3401 CCGAGAAGTG TGTGTGTGTT CGCTGCTTCC ACACATTAAT GGCATGATTT
3451 TTTTATGCA AAAAAAAAAA

```

BLAST Results

Entry MMANK3A_1 from database TREMBL:
Ank3"; product: "ankyrin 3"; Mus mu... +3 4022 0.0 2

Entry HS13616 from database EMBL:
Human ankyrin G (ANK-3) mRNA, complete cds.
Length = 14,770
Plus Strand HSPs:
Score = 8505 (1276.1 bits), Expect = 0.0, Sum P(3) = 0.0
Identities = 1799/1873 (96%)

Medline entries

95394457:
Chromosomal localization of the ankyrinG gene
(ANK3/Ank3) to human 10q21 and mouse 10.

95138209:
A new ankyrin gene with neural-specific isoforms, localized at the
axonal initial segment and node of Ranvier

Peptide information for frame 3

ORF from 309 bp to 2741 bp; peptide length: 811
Category: known protein
Classification: unset

```

1 MALPQSEDAM TGDTDKYLGP QDLKELGDDS LPAEGYMGFS LGARSASLRS
51 FSSDGSYTLN RSSIYARDSMM IEELLVPSKE QHLTFTREFD SDSLRHYSWA
101 ADTLDNVNLV PSPIHSGFLV SFMVDARGGS MRGSRHHGMR IIPPRKCTA
151 PTRITCRLVK RHKLANPPPM VEGEGLASRL VEMGPAGAQQ LGPVIVEIPH
201 FGSMRGKERE LIVLRSENGE TWKEHQFDSK NEDLTELENG MDEELDSPEE
251 LGKKRICRII TKDFPQYFAV VSRIKQESNQ IGPEGGILSS TTVPLVQASF
301 PEGALTKRIR VGLOAQPVDP EIVKKILGNK ATFSPIVTVE PRRRKFKHPI
351 TMTIPVPPPS GEGVSNKYKG DTTPNLRLLC SITGGTSPAQ WEDITGTTFP
401 TFIKDCVSTF TNVSARFWLA DCHOVLETVG LATQLYRELI CVPYMAKFVV
451 FAKMNDPVES SLRCFCMTDD KVDKTLQQE NFEEVARSKD IEVLEGGPIY
501 VDCYGNLAPL TKGGQQLVFN FYSFKENRLP FSIKIRDTSQ EPCGRLSFLK
551 EPKTTKGLPQ TAVCNLNLITL PAHKKIEKTD GRQSFASLAL RKRYSYLTET
601 GMSPOQSPCR TDIRMAIVAD HLGLSWTELA RELNFSVDEI NQIRVENPNS
651 LISQSFMLK KWTTRDGNKA TTDALTSVLT KINRIDIVTL LEGPIFDYGN
701 ISGTRSFAD E NNVFHDPVDG YPSLQVELET PTGLHYTPPT PFQDDYFSD
751 ISSIESPLRT PSRLSDGLVP SQGNIEHSAD GPPVVTAEDA SLEDSKLEDS
801 VPLTEMPEAV M

```

BLASTP hits

DKFZphfkd2_24p5

group: intracellular transport and trafficking

DKFZphfkd2_24p5 encodes a novel 811 amino acid protein which is a novel splice variant of human ankyrin G.

The ankyrin 3 gene encodes a novel ankyrin, which is expressed in multiple tissues, with very high expression at the axonal initial segment and nodes of Ranvier of neurons in the central and peripheral nervous systems. Ankyrin G shows several tissue-specific alternative mRNA processing. The different ankyrin G proteins participate in maintenance/targeting of ion channels and cell adhesion molecules to nodes of Ranvier and axonal initial segments.

The new protein can find application in modulating the structure and membrane topology of Ranvier nodes and other neuronal cell membranes.

Human ankyrin G (ANK-3) new splice variant

splice variant
potential frame shift at 2720 was checked
see BLASTX

Sequenced by EMBL

Locus: /map="10q21"

Insert length: 3470 bp
Poly A stretch at pos. 3459, no polyadenylation signal found

```

1 AGCTTTAAAA GGATGTCTGC GAAGTGGTCA AAAGGATCTT AACCTCAATT
51 AAGTGGGGTT TTTTAAAAAG ATTTTGTGGG GGGCCTGAAA TTTTGAAAAT
101 CTTGGAACCTC TGAGTGGGGA AAGATGTATA ATTCTCAAT TGCCTACGAG
151 GATATCAAGA TGCTGAGAGG AATTCAGCGG TGGTGAAGAG AGTGGATACA
201 AACCAAGGGAT TGGTTTCCTT GAGCTGTTT GGAGGTGAT TCTAAATCAC
251 TGCTTAAGGA ATTCTGGAA ACATCAGGAA AACATTGAT CATCCAAGCC
301 TAGTGGAAAT GGGCTTACCG CAGAGTGAAG ATGCAATGAC CGGGGACACA
351 GACAAATATC TTGGGCCACA GGACCTTAAG GAATTGGGTG ATGATTCCCT
401 GCCTGCAGAG GGTACATGG GCTTTAGTCT CGGAGCGCGT TCTGCCAGCC
451 TCCGCTCCTT CAGTTCGGAT GGGTCTTACA CCTTGAACAG AAGCTCCTAT
501 GCACGGGACA GCATGATGAT TGAAGAACTC CTCGTGCCAT CCAAAGAGCA
551 GCATCTAACA TTCACAAGGG AATTTGATTC AGATTCTCTT AGACATTACA
601 GCTGGGCTGC AGACACCTTA GACAATGTCA ATCTTGTTC AAGCCCCATT
651 CATTCTGGGT TTCTGGTTAG CTTTATGGTG GACGCGAGAG GGGGCTCCAT
701 GAGAGGAAGC CGTCATCACG GGATGAGAAT CATCATTCCT CCACGCAAGT
751 GTACGGCCCC CACTCGAATC ACCTGCCGTT TGGTAAAGAG ACATAAACTG
801 GCCAACCCAC CCCCCATGGT GGAAGGAGAG GGATTAGCCA GTAGGCTGGT
851 AGAAATGGGT CCTGCAGGGG CACAATTTT AGGCCCTGTC ATAGTGGAAA
901 TCCCTCACTT TGGGTCCATG AGAGGAAAAG AGAGAGAACT CATTGTTCTT
951 CGAAGTGAAA ATGGTGAAAC TTGGAAGGAG CATCAGTTG ACAGCAAAAA
1001 TGAAGATTTA ACCGAGTTAC TTAATGGCAT GGATGAAGAA CTGTATAGCC
1051 CAGAAGAGTT AGGGAAAAAG CGTATCTGCA GGATTATCAC GAAAGATTTC
1101 CCCCAGTATT TTCCAGTGGT TTCCCGGATT AAGCAGGAAA GCAACCAGAT
1151 TGGTCTTGAA GGTGGAATTC TGAGCAGCAC CACAGTCCCC CTGTTCAG
1201 CATCTTTCCC AGAGGGTGCC CTAACATAAA GAATTCGAGT GGGCCTCCAG
1251 CCCCAGCCTG TTCCAGATGA AATTGTGAAA AAGATCCTTG GAAACAAAGC
1301 AACTTTTAGC CCAATTGTCA CTGTGGAACC AAGAAGACGG AAATTCCATA
1351 AACCAATCAC AATGACCATT CCGGTGCCCC CGCCCTCAGG AGAAGGTGTA
1401 TCCAATGGAT ACAAAGGGGA CACTACACCC AATCTGCGTC TTCTCTGTAG
1451 CATTACAGGG GGCACCTCGC CTGCTCAGTG GGAAGACATC ACAGGAACAA
1501 CTCCTTTGAC GTTTATAAAA GATTGTGTCT CCTTTACAA CAATGTTTCA
1551 GCCAGATTTT GGCTTGCGA CTGCCATCAA GTTTTAGAAA CTGTGGGGTT
1601 AGCCACGCAA CTGTACAGAG AATTGATATG TGTTCATAT ATGGCCAAAT
1651 TTGTTGTTTT TGCCAAAATG AATGATCCCC TAGAATCTTC CTGCGATGT
1701 TTCTGCATGA CAGATGACAA AGTGGACAAA ACTTTAGAGC AACAAAGAGAA
1751 TTTTGAGGAA GTCGCAAGAA GCAAAGATAT TGAGGTTCTG GAAGGAAAAC
1801 CTATTTATGT TGATTTGTTT GGAATTTGG CCCCATTAC CAAAGGAGGA
1851 CAGCAACTTG TTTTAACTT TTATCTTTC AAAGAAAATA GACTGCCATT
1901 TTCCATCAAG ATTAGAGACA CCAGCCAAGA GCCCTGTGGT CGTCTGTCTT
1951 TTCTGAAAGA ACCAAAGACA ACAAAGGAC TGCCCTCAAC AGCGGTTTGC
2001 AACTTAAATA TCACCTGCC AGCACATAAA AAGATTGAGA AAACAGATGG
2051 ACGACAGAGC TCGCATCCT TAGCTTTACG TAAGCCCTAC AGCTACTTGA
2101 CTGAGCCTGG AATGAGTCCA CAGAGTCCAT GTGAACGGAG AGATATCAGG
2151 ATGGCAATAG TAGCCGATCA CCTGGGACTT AGTTGGACAG AACTGGCAAG
2201 GGAACCTGAA TTTTCAGTGG ATGAAATCAA TCAAATACGT GTGGAAAATC
2251 CAAATCTCTT AATTTCTCAG AGCTTCATGT TTTTAAAAAA ATGGGTTACC
2301 AGAGACGGAA AAAATGCCAC AACTGATGCC TTAACCTCGG TCTTGACAAA
2351 AATTAATCGA ATAGATATAG TGACACTGCT AGAAGGACCA ATATTTGATT

```


SEQ GQKVIAPENLPPLTPYCRRLNFGCLDDIGHGIKDLSTQLSRTGTLRSRSIKAPATPASA
SEG
laboA

SEQ TLGRPPRIPEPVHLPVVPDGRLSAASSASSLASAGSAEGVGGAPTPKGQAAPPAPPLPSS
SEGxx
laboA

SEQ LDPPPPPAAEVEVFQRPPTLEELSPPPPDEELPLPLDLPPPPPLDGDDELGLPPPPPGFGPD
SEG xxx
laboA

SEQ EPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRYSDGWCEGVSSEGTGFFPGN
SEG xx.....
laboAEECCCBCCCTTTBCCBTTEEEEEEEETTTTEEEEEETTEEEEEEGG

SEQ YVEPSC
SEG
laboA GEEE..

Prosites for DKFZphfd2_24n20.3

PS00001	22->26	ASN_GLYCOSYLATION	PDOC00001
PS00004	339->343	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	14->17	PKC_PHOSPHO_SITE	PDOC00005
PS00005	41->44	PKC_PHOSPHO_SITE	PDOC00005
PS00005	72->75	PKC_PHOSPHO_SITE	PDOC00005
PS00005	167->170	PKC_PHOSPHO_SITE	PDOC00005
PS00005	170->173	PKC_PHOSPHO_SITE	PDOC00005
PS00005	225->228	PKC_PHOSPHO_SITE	PDOC00005
PS00005	321->324	PKC_PHOSPHO_SITE	PDOC00005
PS00005	338->341	PKC_PHOSPHO_SITE	PDOC00005
PS00006	14->18	CK2_PHOSPHO_SITE	PDOC00006
PS00006	239->243	CK2_PHOSPHO_SITE	PDOC00006
PS00006	258->262	CK2_PHOSPHO_SITE	PDOC00006
PS00006	308->312	CK2_PHOSPHO_SITE	PDOC00006
PS00006	321->325	CK2_PHOSPHO_SITE	PDOC00006
PS00006	328->332	CK2_PHOSPHO_SITE	PDOC00006
PS00008	21->27	MYRISTYL	PDOC00008
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	94->100	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	215->221	MYRISTYL	PDOC00008
PS00008	332->338	MYRISTYL	PDOC00008

Pfam for DKFZphfd2_24n20.3

HMM_NAME Src homology domain 3

HMM *pyVIALYDYqAqdpDELSFkEGDIIiIIEdsDD.WWrgRnnnTNGQEGW
++V+ LY+Y++Q ++ELSF EG +I + + D W++G + +G+

Query 311 EKVVTLTPYTSQKDNELSFSEGTVICVTRRYSDGWCEGVSSE---GTGF 356

HMM IPSNYVEPI*
+P NYVEP

Query 357 FPGNYVEPS 365

Medline entries

97163405:
Isolation and characterization of e3B1, an eps8 binding protein that regulates cell growth.

98256293:
Identification of a candidate human spectrin Src homology 3 domain-binding protein suggests a general mechanism of association of tyrosine kinases with the spectrin-based membrane skeleton.

Peptide information for frame 3

ORF from 300 bp to 1397 bp; peptide length: 366
Category: strong similarity to known protein

```

1 MAELQQLQEF EIPTGREALR GNHSALLRVA DYCEDNYVQA TDKQKALEET
51 MAFTTQALAS VAYQVGNLAG HTLRMLDLQG AALRQVEARV STLGMVMNMH
101 MEKVARREIG TLATVQRLPP GQKVIAPENL PPLTPYCRRP LNFGCLDDIG
151 HGIKDLSTQL SRTGTLRSRKS IKAPATPASA TLGRPPRIPE PVHLPVVPDG
201 RLSAASSASS LASAGSAEGV GGAPTPKGQA APPAPPLPSS LDPPPPPAAV
251 EVFQRPPTLE ELSPPPPDEE LPLPLDLPPP PPLDGDELGL PPPPPGFGPD
301 EPSWVPASYL EKVVTLYPYT SQKDNELSFS EGTVICVTRR YSDGWCEGVS
351 SEGTFGFFGN YVEPSC

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_24n20, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_24n20, frame 3

Report for DKFZphfkd2_24n20.3

```

{LENGTH}      366
{MW}           38947.21
{pI}           4.93
{HOMOL}        TREMBL:U87166_1 gene: "SSH3BP1"; product: "spectrin SH3 domain binding protein
1"; Homo sapiens spectrin SH3 domain binding protein 1 (SSH3BP1) mRNA, complete cds. 3e-48

{FUNCAT}       10.99 other signal-transduction activities [S. cerevisiae, YGR136w] 9e-06
{FUNCAT}       30.10 nuclear organization [S. cerevisiae, YGR136w] 9e-06
{FUNCAT}       99 unclassified proteins [S. cerevisiae, YPR154w] 3e-05
{FUNCAT}       30.04 organization of cytoskeleton [S. cerevisiae, YDR388w] 2e-04
{FUNCAT}       03.04 budding, cell polarity and filament formation [S. cerevisiae, YDR388w]
2e-04
{FUNCAT}       06.10 assembly of protein complexes [S. cerevisiae, YDR162c] 4e-04
{BLOCKS}       BL50002B Src homology 3 (SH3) domain proteins profile
{SUPFAM}       SH3 homology 6e-17
{PROSITE}      MYRISTYL 6
{PROSITE}      CAMP_PHOSPHO_SITE 1
{PROSITE}      CK2_PHOSPHO_SITE 6
{PROSITE}      PKC_PHOSPHO_SITE 8
{PROSITE}      ASN_GLYCOSYLATION 1
{PFAM}         Src homology domain 3
{KW}           Irregular
{KW}           3D
{KW}           LOW_COMPLEXITY 24.04 %

```

```

SEQ  MAELQQLQEF EIPTGREALRGNHSALLRVADYCEDNYVQATDKQKALEETMAFTTQALAS
SEG  .....
laboA .....

SEQ  VAYQVGNLAGHTLRMLDLQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPP
SEG  .....
laboA .....

```

DKFZphfkd2_24n20

group: intracellular transport and trafficking

DKFZphfkd2_24n20.3 encodes a novel 366 amino acid protein with similarity to human eps8 binding protein e3B1 and spectrins.

The new protein contains an Src homology domain 3 and is similar to human eps8 SH3 domain binding protein 1 (e3B1) and spectrins. Eps8 is a substrate of receptor tyrosine kinases involved in mitogenic signaling. Spectrin is part of the submembrane cytoskeletal network in the human erythrocyte ghost. Nonerythroid spectrins are proposed to have roles in cell adhesion, establishment of cell polarity, and attachment of other cytoskeletal structures to the plasma membrane. The new protein seems to be part of the signalling pathway between tyrosine kinases and the membrane/cyto skeleton.

The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamics.

strong similarity to eps8 binding protein e3B1

complete cDNA, complete cds, few EST hits
potential start at Bp 300, but there are ATGs in other frames in 5' region of the cDNA

Sequenced by GBF

Locus: /map="17"

Insert length: 1719 bp

Poly A stretch at pos. 1699, polyadenylation signal at pos. 1680

```

1 GGGGACAGCT GCCCGACCT TGGCTTCCTC TGCTGGGTGG GATTGGGGGC
51 TGGGCCCCCA AATGGGCCCC TGGCTTCCCC CTTCCTCTGG GCAGGGGACA
101 GAGAGACACA GGCTCGGGGA GCAGGACTGA CTTCTCTTTG TCCCGGAATG
151 AGCATGCCTG CCCTTTGCAA GCAGGTTTGG GTCTCACGCA GAGGAAACCA
201 AAAGCAATAA GAGGAGGGA AGGCAGAGCA ACCAATCAAG GGCAGGGTGA
251 GACTCAAAAC GAGCGGGCTC CCTGGGGAGC CAGACAGAGG CTGGGGGTGA
301 TGGCGGAGCT ACAGCAGCTG CAGGAGTTTG AGATCCCCAC TGGCCGGGAG
351 GCTCTGAGGG GCAACACAG TGCCTGCTG CGGGTCGCTG ACTACTGCGA
401 GGACAACATAT GTGCAGGCCA CAGACAAGCA GAAGGCGCTG GAGGAGACCA
451 TGGCCTTCAC TACCCAGGCA CTGGCCAGCG TGGCCTACCA GGTGGGCAAC
501 CTGGCCGGGC ACACCTCTGG CATGTTGGAC CTGCAGGGGG CCGCCCTGCG
551 GCAGGTGGAA GCCCGTGTA GACGCTGGC CCAGATGGTG AACATGCATA
601 TGGAGAAGGT GGCCCGAAGG GAGATCGGCA CCTTAGCCAC TGTCCAGCGG
651 CTGCCCCCGG GCCAGAAGGT CATCGCCCCA GAGAACCTAC CCCCTCTCAC
701 GCCCTACTGC AGGAGACCCC TCAACTTTGG CTGCCTGGAC GACATTGGCC
751 ATGGGATCAA GGACCTCAGC ACGCAGCTGT CAAGAACAGG CACCCTGTCT
801 CGAAAGAGCA TCAAGGCCCC TGCCACACCC GCCTCCGCCA CCTTGGGGAG
851 ACCGCCCCGG ATTCCCGAGC CAGTGCACCT GCCGGTGGTG CCGCAGCGCA
901 GACTCTCCGC CGCTCCTCTT GCGTCTTCCC TGGCCTCGGC CGGCAGCGCC
951 GAAGGTGTCT GTGGGGCCCC CACGCCAAG GGGCAGGCAG CACCTCCAGC
1001 CCCACCTCTC CCCAGCTCCT TGGACCCACC TCCTCCACCA GCAGCCGTCG
1051 AGGTGTTCCA GCGGCTCCC ACGCTGGAGG AGTTGTCCCC ACCCCCACCG
1101 GACGAAGAGC TGCCCTTGCC ACTGGACCTG CCTCTCTCTC CACCCCTGGA
1151 TGGAGATGAA TTGGGGCTGC CTCCACCCCC ACCAGGATT TGGGCTGATG
1201 AGCCAGCTG GGTGCCTGCC TCATACTTGG AGAAAGTGGT GACACTGTAC
1251 CCATACACCA GCCAGAAGGA CAATGAGCTC TCCTTCTCTG AGGGCACTGT
1301 CATCTGTGTC ACTCGCCGCT ACTCCGATGG CTGGTGCGAG GGCCTCAGCT
1351 CGGAGGGGAC TGGATTCTTC CCTGGGAAC ATGTGGAGCC CAGCTGCTGA
1401 CAGCCAGGG CTCTCTGGGC AGCTGATGTC TGCACTGAGT GGGTTTCATG
1451 AGCCCAAGC CAAACACAGC TCCAGTCACA GCTGGACTGG GTCTGCCCCA
1501 CTCTTGGGCT GTGAGCTGTG TTCTGTCTCT CCTCCCACG GAGGGAGAAG
1551 GGGTCTTGGG GAGAGAGAAT TTATCCAGAG GCCTGCTGCA GATGGGGAAG
1601 AGCTGGAAAC CAAGAAGTTT GTCAACAGAG GACCCTACT CCATGCAGGA
1651 CAGGGTCTCC TGCTGCAAGT CCCAACTTTG AATAAACAG ATGATGTCCA
1701 AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

Entry AC004797 from database EMBL:
Homo sapiens chromosome 17, clone hRPC.62_0_9, complete sequence.
Score = 2316, P = 5.9e-255, identities = 464/465
7 exons Bp. 93317-110902

ORF from 299 bp to 892 bp; peptide length: 198
Category: putative protein

1 MADTQCCPPP CEFISSAGTD LALGMGWDAT LCLLPFTGFG KCAGIWNHMD
51 EEPDNGDDRG SRRTTGQGRK WAAHGTMAAP RVHTDYHPPG GSACSSVKVR
101 SHVGHTGVFF FVDQDPLAVS LTSQSLIPPL IKPGLLKAWG FLLCAQPSA
151 NGHSLCCLLY TDLVSSHELSPFRALCLGPS DAPSACASCN CLASTYYL

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_24e23, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_24e23, frame 2

Report for DKFZphfkd2_24e23.2

{LENGTH} 198
{MW} 20948.98
{pI} 6.01
{PROSITE} MYRISTYL 5
{PROSITE} AMIDATION 1
{PROSITE} CAMP_PHOSPHO_SITE 1
{PROSITE} CK2_PHOSPHO_SITE 1
{PROSITE} PKC_PHOSPHO_SITE 2
{KW} All_Beta
{KW} LOW_COMPLEXITY 6.06 %

SEQ MADTQCCPPPCEFISSAGTDLALGMGWDATLCLLPFTGFGKCAGIWNHMDDEPDNGDDRG
SEG
PRD ccc

SEQ SRRTTGQGRKWAHGTMAAPRVHTDYHPPGGSACSSVKVRSHVGHTGVFFVVDQDPLAVS
SEG
PRD ccc

SEQ LTSQSLIPPLIKPGLLKAWGFLLLCAQPSANGHSLCCLLYTDLVSSHELSPFRALCLGPS
SEGxxxxxxxxxxxxx.....
PRD eccccccccccccchhhhhhhhhcc

SEQ DAPSACASCNCLASTYYL
SEG
PRD ccccccccccccccccccccc

Prosites for DKFZphfkd2_24e23.2

PS00004	62->66	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	61->64	PKC_PHOSPHO_SITE	PDOC00005
PS00005	96->99	PKC_PHOSPHO_SITE	PDOC00005
PS00006	165->169	CK2_PHOSPHO_SITE	PDOC00006
PS00008	18->24	MYRISTYL	PDOC00008
PS00008	60->66	MYRISTYL	PDOC00008
PS00008	89->95	MYRISTYL	PDOC00008
PS00008	91->97	MYRISTYL	PDOC00008
PS00008	134->140	MYRISTYL	PDOC00008
PS00009	67->71	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfkd2_24e23.2)

DKF2phfkd2_24e23

group: kidney derived

DKF2phfkd2_24e23 encodes a novel 198 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

unknown

complete cDNA, complete cds, 1 EST hit,
many ATGs in front of the ORF

Sequenced by GBF

Locus: unknown

Insert length: 1723 bp

Poly A stretch at pos. 1695, no polyadenylation signal found

```
1 GGGGGATTTT CGATCATGAC AACGATAGCA ATTGATATAC CTTCAAAATA
51 CGTGTCCAGT GAGTGTGTGAT TGTGTGTGGT TTCTCTAGGA GACCGTGTTC
101 ATGCAACACA GCATTATTTT ACCGCCTTTA CCCCAGCTTC TTCATACACA
151 TGCACCTTGT CAGGGGCTCTT TGGCTGAAGA GAAGTTAGAA GTTCCAGAT
201 ATGGAGGGGT ATTTTCAGCA GATATGCCCA CCGCCATGGT TTGTGACGCT
251 CTGTAGGGTG GTCTTGCACC CTGCTCACTG CTGGCATCAC CTGAGCCTAT
301 GGCAGATACC CAGTGCTGCC CGCCACCATG TGAATTCATC AGCTCTGCAG
351 GCACAGACCT TGCACATAGGA ATGGGCTGGG ACGCCACCTT CTGCCTCTTA
401 CCATTCACCT GGTTTGGCAA GTGTGCTGGG ATCTGGAATC ACATGGATGA
451 GGAACCCGAT AATGGTGACG ACCGAGGTAG CAGGCGAACC ACTGGCCAGG
501 GCAGGAAAGT GGCAGCTCAC GGGACTATGG CTGCACCGCG GGTTCCATACC
551 GACTACCATC CTGGAGGTGG GAGCGCATGC TCATCTGTAA AAGTCCGGTC
601 CCACGTTGGA CACACCGGGG TCTTCTTCTT TGTGACCAG GATCCTCTGG
651 CAGTGTCTTT AACAAGCCAG AGTCTGATCC CACCGCTCAT AAAGCCAGGG
701 TTGTTGAAAG CTTGGGGCTT CCTCCTCCTC TGTGCGCAGC CCTCAGCAAA
751 CGGTCACAGC CTGTGCTGTC TGCTGTACAC CGACTTGGTA TCATCCCATG
801 AACTGTCCCC CTTTCGTGCT CTGTGCTTAG GGCCCTCTGA TGCCCCATCT
851 GCCTGCCGCT CCGCAACTG TTTAGCAAGC ACCTATTATC TATAGGTGTC
901 TGGGGTGCTG GGCAGGCGCA ATCGCTCCTA TTACTTTCTG CCCTGGGGAC
951 GTCCTGTTTT CCCACCTACC CCTGTAACGC CTCTGCTCTG CCTTCCCATC
1001 TGGGGGGCTA ACGCCATCCC ACAAGGGCTG GGCTGTCCGT TCAGAAGAGA
1051 AACTGGGAAG GGCCTTGAG GACCTGTGTC CAGGCAGGGT GGACAAGGGC
1101 TTTGTGCAAG GAGCTCCTCT CCCATCTTTG TGTCCTGACA GCCGTGACCG
1151 TGACCCCTCA AAGCAGAGCC AGTAGTGATC AGTATCCTGC TGCTTCAAGC
1201 CTGCACGGTC CTCTTCTCCT CTCCGCACAT CTGCATGCCT GTCAAACCCA
1251 GAGTAGTTTG GGGCCTGGTA AACAGAGGGA AGTTGGCTGG AGGAGGCCAG
1301 TCAGGAGTGC AAGAACCCTG CGTACTCTGT CCCACGTGGA TAAAGTCTCT
1351 AATTCCAGTC TGAGGTGAAT TCTTAGAGAG TGCTTTTATT TAATGTTTGC
1401 TTTATGCATT TCCCCTGCAG CTGTGACTAA TTGTGGAACA GCATACATTT
1451 TGTTTTGAGA CTCTCTTGAG ATTTTCTGAG CAGTGTAAGG TCTACCCAT
1501 TTTCTCTCA GCATCAGAGA AGGCAGAAAG CAAGAGAAAG GAATGCAATG
1551 TGAGCAAGGC CAGGCACACT TGTGCTACTG CAGTTGGCAA GAATGGAGTC
1601 TAATCCCAGC ACTTTGGGAG GCCGAGGCGG GTGGATCACC TGAGGTCAGG
1651 AATTTGAGAC CAACCTGGCC AACATGTTGA AACCTCCTCT GTACTAAAAA
1701 TACAAAAAAA AAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

```

SEQ  FAFEEAIGYMCCPFVLDDKGVSAAVISAEELASFLATKNLSLSQOLKAIYVEYGYHITKAS
PRD  hhhhhccccccccccccccccchhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhcccc

SEQ  YFICHDOETIKKLFENLRNYDGKNYPKACGKFEISAIRDLTTGYDDSQPDKKAVLPTSK
PRD  eeecccchhhhhhhhhhhhhhhhhccccccccchhhhhhhcccccccccccccccccccccccc

SEQ  SSQMITFTFANGGVATMRTSGTEPKIKYYAELCAPPGNSDPEQLKKELNELVSAIEEHFF
PRD  cccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  QPQKYNLQPKAD
PRD  ccccccccccccc

```

Prosites for DKFZphfkd2_24b15.1

PS00001	458->462	ASN_GLYCOSYLATION	PDOC00001
PS00002	7->11	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00005	117->120	PKC_PHOSPHO_SITE	PDOC00005
PS00005	290->293	PKC_PHOSPHO_SITE	PDOC00005
PS00005	358->361	PKC_PHOSPHO_SITE	PDOC00005
PS00005	380->383	PKC_PHOSPHO_SITE	PDOC00005
PS00005	489->492	PKC_PHOSPHO_SITE	PDOC00005
PS00005	538->541	PKC_PHOSPHO_SITE	PDOC00005
PS00005	556->559	PKC_PHOSPHO_SITE	PDOC00005
PS00006	186->190	CK2_PHOSPHO_SITE	PDOC00006
PS00006	210->214	CK2_PHOSPHO_SITE	PDOC00006
PS00006	343->347	CK2_PHOSPHO_SITE	PDOC00006
PS00006	358->362	CK2_PHOSPHO_SITE	PDOC00006
PS00006	523->527	CK2_PHOSPHO_SITE	PDOC00006
PS00006	528->532	CK2_PHOSPHO_SITE	PDOC00006
PS00006	560->564	CK2_PHOSPHO_SITE	PDOC00006
PS00006	579->583	CK2_PHOSPHO_SITE	PDOC00006
PS00006	593->597	CK2_PHOSPHO_SITE	PDOC00006
PS00008	6->12	MYRISTYL	PDOC00008
PS00008	61->67	MYRISTYL	PDOC00008
PS00008	100->106	MYRISTYL	PDOC00008
PS00008	159->165	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008
PS00008	257->263	MYRISTYL	PDOC00008
PS00008	344->350	MYRISTYL	PDOC00008
PS00008	348->354	MYRISTYL	PDOC00008
PS00008	440->446	MYRISTYL	PDOC00008
PS00008	552->558	MYRISTYL	PDOC00008
PS00710	159->174	PGM_PMM	PDOC00589
PS00213	346->358	LIPOCALIN	PDOC00187
PS00213	344->358	LIPOCALIN	PDOC00187

Pfam for DKFZphfkd2_24b15.1

```

HMM_NAME      Phosphoglucomutase and phosphomannomutase phosphoserine
HMM            *GvnVIdIGQNGMMPTPMIYFaIRTYKhmcmggGIMITaSHNPGGPDnDN
               G+ V + ++PTP + F + H+++ +GIMITASHNP DN
Query         132 GIPVYLFs---DITPTFPVPFTVS---HLKLCAGIMITASHNP--KQ-DN 172
HMM            GIK*
               G+K
Query         173 GYK 175

```

Query: 311 DTKARIVLANDPDADRLAVAQKQDSGEWRFVSGNELGALLGWLFTSWKEKNQDRSALK 370
 DK + ++LANDPDADR+ +AEKQ GEWRFV+GNE+GAL+ WW++T+W++ N + A K
 Sbjct: 298 DKNGSTVILANDPDADRIQMAEKQKDGGEWRFVFTGNEMGALITWWIWTNWRKANPNADASK 357

Query: 371 DTYMLSSTVSSKILRAIALKEGFHFEETLTGFKWMGNRAKQLIDQGKTVLFAFEEAIGYM 430
 Y+L+S VSS+I++ IA EGF E TLTGFKWMGNRA++L G V+ A+EE+IGYM
 Sbjct: 358 -VYILNSAVSSQIVKTIADAEGFKNETTTLTGFKWMGNRAEELRADGNQVILAWESIGYM 416

Query: 431 CCP-FVLDDKGVSAAVISAEASFLATKNLSLSQLKAIYVEYGYHITKASYFICHQDET 489
 P +DKDGVSA + AE+A+FL + SL QL A+Y YG+H+ +++Y++ E
 Sbjct: 417 --PGHTMDKGVSAAVFAEIAAFLHAEGKSLQDQLYALYNRVGFHLVRSTYWMVPAPEV 474

Query: 490 IKKLFENLRNYDGKNYPKACGKFEISAIRDLTTGYDDSQPKKAVLPTSKSSQMITFTF 549
 KKLF LR D K +P G+ E++++RDLT GYD+S+PD K VLP S SS+M+TF
 Sbjct: 475 TKKLFSTLRA-DLK--FPTKIGEAEEVASVRDLTIGYDNSKPDNKPVLPLSTSEMVTFFL 531

Query: 550 ANGGVATMRTSGTEPKIKYIAELCAPPGNS--DPEQLKKELNELVSAIEEHFFQPKYKYL 607
 G V T+R SGTEPKIKYY EL PG + D E + E++L + +PQ++ L
 Sbjct: 532 KTGSVTTLRASGTEPKIKYIELITAPGKTQNDLESVISEMDQLEKDVVATLLRPQQFGL 591

Query: 608 QPK 610
 P+
 Sbjct: 592 IPR 594

Pedant information for DKFZphfkd2_24b15, frame 1

Report for DKFZphfkd2_24b15.1

[LENGTH] 612
 [MW] 68311.58
 [pI] 6.28
 [HOMOL] TREMBL:CEY43F4B_5 gene: "Y43F4B.5"; Caenorhabditis elegans cosmid Y43F4B 1e-157

[FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae, YMR278w] 1e-111
 [FUNCAT] g carbohydrate metabolism and transport [H. influenzae, HI0740] 3e-66
 [FUNCAT] c energy conversion [M. genitalium, MG053] 4e-50
 [FUNCAT] m outer membrane and cell wall [H. influenzae, HI1463] 2e-04
 [BLOCKS] BL00607D cAMP phosphodiesterases class-II proteins
 [BLOCKS] BL00710 Phosphoglucomutase and phosphomannomutase phosphoserine signa
 [EC] 5.4.2.8 Phosphomannomutase 3e-56
 [EC] 5.4.2.2 Phosphoglucomutase 1e-09
 [PIRKW] isomerase 3e-56
 [PIRKW] intramolecular transferase 3e-56
 [SUPFAM] Methanobacterium thermoautotrophicum phosphomannomutase 1e-06
 [SUPFAM] probable phosphorylating protein ureC 9e-06
 [PROSITE] PGM_PMM1
 [PROSITE] MYRISTYL 10
 [PROSITE] LIPOCALIN 2
 [PROSITE] CK2_PHOSPHO_SITE 9
 [PROSITE] GLYCOSAMINOGLYCAN 1
 [PROSITE] PKC_PHOSPHO_SITE 8
 [PROSITE] ASN_GLYCOSYLATION 1
 [PFAM] Phosphoglucomutase and phosphomannomutase phosphoserine
 [KW] Alpha_Beta

SEQ MAAPEGSGLGEDARLDQETAQWLRLWDKNSLTLEAVKRLIAEGNKEELRKCFGARMEFGTA
 PRD cccccccccchhhhhhhhhhhhhhhccchhhhhhhhhhhhhcchhhhhhhhhhhhhccccc

SEQ GLRAAMGPGISRMNDLTIIQTQGFRCRYLEKQFSDLKQKQIVISFDARAHPSGGSSRRF
 PRD cccccccccccccccccccccchhhhhhhhhhhhhcccccceccccccccccccccccchhh

SEQ ARLAATTFISQGPVLYLFSIDITPTFPVFTVSHLKLKAGIMITASHNPKQDNGYKVYWDN
 PRD hhhhhhhhhhhcccccceccccccccchhhhhhhccccccecccccccccccccccccecc

SEQ GAQIISPHDKGISQAIEENLEPWPQAWDDSLIDSSPLLHNPSASINNDYFEDLKKYCFHR
 PRD cccccccccchhhhhhhhhhhhhhhcccccceccccccccccccccccchhhhhhhhhhhhhcc

SEQ SVNRETKVKFVHTSVHGVGHSFVQSAFAFDLVPPEAVPEQRDPDPEFPTVKYPNPPEGK
 PRD cccccccccccccccccchhhhhhhhhhhhhcccccceccccccccccccccccccccccccch

SEQ GVLTLFSALADKTKARIVLANDPDADRLAVAQKQDSGEWRFVSGNELGALLGWLFTSWK
 PRD hhhhhhhhhhhhhcccccceccccccccccccccccccccccccccccchhhhhhhhhhhhh

SEQ EKNQDRSALKDTYMLSSTVSSKILRAIALKEGFHFEETLTGFKWMGNRAKQLIDQGKTVL
 PRD hccccccccccccccccccccchhhhhhhhhhhhhcccccceccccccccchhhhhhhhhhhccccc

human STS WI-6820.

Score = 1261, P = 3.6e-52, identities = 253/254

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 31 bp to 1866 bp; peptide length: 612
Category: strong similarity to known protein

```

1  MAAPEGSGLG EDARLDQETA QWLRWDKNSL TLEAVKRLIA EGNKEELRKC
51 FGARMEFGTA GLRAAMGPGI SRMNDLTIIQ TTQGFRCYLE KQFSDLKQKG
101 IVISFDARAH PSSGGSSRRF ARLAATTFIS QGIPVYLFSD ITPTPFVFPFT
151 VSHLKLKAGI MITASHNPKQ DNGYKVYWDN GAQIISPHDK GISQAIEENL
201 EPWPQAWDDS LIDSSPLLHN PSASINNDYF EDLKKYCFHR SVNRETKVKF
251 VHTSVHGVGH SFVQSAFKAF DLVPPEAVPE QRDPDPEFPT VKYPNPEEGK
301 GVLTLFSALA DKTARIVLA NDPDADRLAV AEKQDSGEWR VFSGNELGAL
351 LGWWLFTSWK EKNQDRSALK DTYMLSSTVS SKILRAIALK EGFHFEETLT
401 GFKWMGNRAK QLIDQGKTVL FAFEEAIGYM CCPFVLDDKG VSAAVISAEAL
451 ASFLATKNLS LSQQLKAIYV EYGYHITKAS YFICHQDQETI KKLFFENLRNY
501 DGKNNYPKAC GKFEISAIRD LTTGYDDSQP DKKAVLPTSK SSOMITFTFA
551 NGGVATMRTS GTEPKIKYYA ELCAPPGNSD PEQLKKELNE LVSAIEEHFF
601 QPQKYNLQPK AD

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phfkd2_24b15, frame 1

TREMBL:CEY43F4B_5 gene: "Y43F4B.5"; Caenorhabditis elegans cosmid Y43F4B, N = 1, Score = 1431, P = 1.6e-146

TREMBL:SPCC1840_5 gene: "SPCC1840.05c"; product: "similarity to phosphomannomutases"; S.pombe chromosome III cosmid c1840., N = 1, Score = 1210, P = 4.2e-123

PIR:S54585 hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae), N = 1, Score = 1046, P = 1e-105

PIR:A71299 probable phosphomannomutase (manB) - syphilis spirochete, N = 1, Score = 697, P = 9.7e-69

>TREMBL:CEY43F4B_5 gene: "Y43F4B.5"; Caenorhabditis elegans cosmid Y43F4B
Length = 595

HSPs:

Score = 1431 (214.7 bits), Expect = 1.6e-146, P = 1.6e-146
Identities = 285/598 (47%), Positives = 393/598 (65%)

```

Query:   13  ARLDQETAQWLRWDKNSLTLEAVKRLIAEGNKEELRKC FGARMEFGTAGLRAAMGPGISR 72
          A+LD++ A WL WDKN    +++L+ E N + L+      R+ FGTAG+R+ M G R
Sbjct:   6  AKLDKQVADWLAWDKNDKRNREIQKLVDKENVDAKARMDTRLVFGTAGVRSMPQAGFGR 65

Query:   73  MNDLTIIQTTQGFRCYLEKQFSDLKQKGIVISFDARAH PSSGGSSRRFARLAATTFISQ 132
          +NDLTIIQ T GF R++   + K G+ I FD R +      SRRFA L+A F+
Sbjct:   66  LNDLTIIQITHGFARHMLNVYGOQPKN-GVATGFDGRYN-----SRRFAELSANVFVRNN 118

Query:   133 IPVYLFSDITPTPFVFPFTVSHLKLKAGIMITASHNPKQDNGYKVYWDN GAQIISPHDKGI 192
          IPVYLFs+++PTP V +   L AG++ITASHNPK+DNGYK YW NGAQII PHD I
Sbjct:   119 IPVYLFSEVSPTPVVSWATIKLGCDAGLIITASHNPKEDNGYKAYWSNGAQIIGPHDTEI 178

Query:   193 SQAIEENLEPWPQAWDDSLIDSSPLLHNPSASINNDYFEDLKKYCFHRSVNRETKVKFVH 252
          + E +P + WD S + SSPL H+   I+ YFE K F R +N T +KF +
Sbjct:   175 VRIKEAEPQPRDEYWDLSELKSSPLFHSADVVID-PYFEVEKSLNFTREINGSTPLKFTY 237

Query:   253 TSVHGVGHGSFVQSAFKAFDLVPPE--AVPEQRDPDPEFPTVKYPNPEEGKGVLTLSFALA 310
          ++ HG+G+ + + F F      +V EQ+DP+P+FPT+ +PNPEEG+ VLTL+ A
Sbjct:   238 SAFHGIGYHYTKRMFAEFGFPASSFISVAEQDPPNPDPFTIPFPNPEEGRKVI.TLAMETA 297

```


DKFZphfkd2_24b15

group: metabolism

DKFZphfkd2_24b15 encodes a novel 612 amino acid protein with similarity to bacterial and yeast phosphoglucomutase and phosphomannomutases.

The novel protein contains a phosphoserine signature typical for phosphoglucomutase (EC 5.4.2.2) or phosphomannomutase (EC 5.4.2.8). Thus, the protein seems to be taking part in the conversion of hexose phosphates.

The new protein can find application in modulation of hexose metabolism pathways and as a new enzyme for biotechnologic production processes.

similarity to phosphomannomutases

complete cDNA, complete cds, EST hits
potential start at bp 30 matches kozak consensus PyCnatG,

Sequenced by GBF

Locus: map="158.8 cR from top of Chr4 linkage group"

Insert length: 2204 bp

Poly A stretch at pos. 2186, no polyadenylation signal found

```

1 GGGCTCTGCA GCGGTAGCAC AAGCTCAGCG ATGGCGGCTC CAGAAGGCAG
51 CGGTCTAGGC GAGGACGCCC GGCTGGACCA GGAGACCGCC CAGTGGCTGC
101 GCTGGGACAA GAATTCCTTA ACTTTGGAGG CAGTGAAACG ACTAATAGCA
151 GAAGGTAATA AAGAAGAACT ACGAAAATGT TTTGGGGCCC GAATGGAGTT
201 TGGGACAGCT GGCCTCCGAG CTGCTATGGG ACCTGGAATT TCTCGTATGA
251 ATGACTTGAC CATCATCCAG ACTACACAGG GATTTTGCAG ATACCTGGAA
301 AAACGAATTCA GTGACTTAAA GCAGAAAGGC ATCGTGATCA GTTTTGACGC
351 CCGAGCTCAT CCATCCAGTG GGGGTAGCAG CAGAAGGTTT GCCCGACTTG
401 CTGCAACCAC ATTTATCAGT CAGGGGATTC CTGTGTACCT CTTTCTGAT
451 ATAACGCCAA CCCCTTTTGT GCCCTTCACA GTATCATT TGAACTTTG
501 TGCTGGAATC ATGATAACTG CATCTCACA TCCAAAGCAG GATAATGGTT
551 ATAAGGTCTA TTGGGATAAT GGAGCTCAGA TCATTTCCTC TCACGATAAA
601 GGGATTTCTC AAGCTATTGA AGAAAATCTA GAACCGTGGC CTCAGCTTG
651 GGACGATTCT TTAATTGATA GCAGTCCACT TCTCCACAAT CCGAGTGCTT
701 CCATCAATAA TGACTACTTT GAAGACCTTA AAAAGTACTG TTTCCACAGG
751 AGCGTGAACA GGGAGACAAA GGTGAAGTTT GTGCACCTT CTGTCCATGG
801 GGTGGGTGTC AGCTTTGTGC AGTCAGCTTT CAAGGCTTTT GACCTTGTTT
851 CTCTGAGGC TGTTCCTGAA CAGAGAGATC CGGATCCTGA GTTTCCAACA
901 GTGAAATACC CCAATCCCGA AGAGGGGAAA GGTGTCTTGA CTTTGTCTTT
951 TGCTTTGGCT GCAAAAACCA AGGCCAGAAT TGTTTGTAGT AACGACCCGG
1001 ATGCTGATAG ACTTGCTGTG GCAGAAAAGC AAGACAGTGG TGAATGGAGG
1051 TGTTTTTCAG GCAATGAGTT GGGGGCCCTC CTGGGCTGGT GGCTTTTTTAC
1101 ATCTTGGAAG GAGAAGAACC AGGATCGCAG TGCTCTCAAA GACACGTACA
1151 TGTGTCCAG CACCGTCTCC TCCAAAATCT TCGGGGCCAT TGCCTTAAAG
1201 GAAGTTTTTC ATTTTGAGGA AACATTAAC TGGCTTTAAGT GGATGGGAAA
1251 CAGAGCCAAA CAGCTAATAG ACCAGGGGAA AACTGTTTTA TTTGCATTG
1301 AAGAAGCTAT TGGATACATG TGCTGCCCTT TTGTTCTGGA CAAAGATGGA
1351 GTCAGTGCCG CTGTCATAAG TGCAGAGTTG GCTAGCTTCC TAGCAACCAA
1401 GAATTTGTCT TTGCTCAGC AACTAAAGGC CATTTATGTG GAGTATGGCT
1451 ACCATATTAC TAAAGCTTCC TATTTTATCT GCCATGATCA AGAAACCATT
1501 AAGAAATTAT TTGAAAACCT CAGAAACTAC GATGGAAAAA ATAATTATCC
1551 AAAAGCTTGT GGCATAATTG AAATTTCTGC CATTAGGGAC CTTACAACCTG
1601 GCTATGATGA TAGCCAACCT GATAAAAAAG CTGTTCTTCC CACTAGTAAA
1651 AGCAGCCAAA TGATCACCTT CACCTTTGCT AATGGAGGCG TGGCCACCAT
1701 CGCACCAGT GGGACAGAGC CCAAAATCAA GTACTATGCA GAGCTGTGTG
1751 CCCCACTGG GAACAGTGAT CCTGAGCAGC TGAAGAAGGA ACTGAATGAA
1801 CTGGTCAGTG CTATTGAAGA ACATTTTTTC CAGCCACAGA AGTACAATCT
1851 GCAGCCAAAA GCAGACTAAA ATAGTCCAGC CTGGGTATA CTTGCATTTA
1901 CCAACAACCT AGCTGGGTTT AACTTGTTAA GCAATATTTT TAAGGGCCAA
1951 ATGATTCAAA ACATCACAGG TATTTATGTG TTTTACAAAG ACCTACATTC
2001 CTCATTGTTT CATGTTTGAC CTTTAAAGTG AAAAAAGAAA ATGGCCAAAC
2051 CCAACAACCT AACATTCTTA CTAAGAGTTT GAGCTTGGAC ATATTTTGAA
2101 TTTTGTAAAG TGAAGATTTT TAACTGACT AACTTAAAAA AATAGATTGT
2151 AATTGATGTG CCTTAATTTG CATAAATCAT AAATGTAATA AAAAAAATAA
2201 AAAA

```

BLAST Results

Entry HS705145 from database EMBL:

PS00005	314->317	PKC_PHOSPHO_SITE	PDOC00005
PS00006	28->32	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00006	276->280	CK2_PHOSPHO_SITE	PDOC00006
PS00007	231->240	TYR_PHOSPHO_SITE	PDOC00007
PS00008	297->303	MYRISTYL	PDOC00008

(No Pfam data available for DKF2phfkd2_24a15.3)

ORF from 219 bp to 1187 bp; peptide length: 323
 Category: similarity to unknown protein

```

1  MGNNLLKVLTR EIIENYPHFFL DFENAOPTG EREIWNQISA VLQDSESILA
51 DLQAYKGAGP EIRDAIQNP DIQLQEKAWN AVCPLVVRK RFYEFSIRLE
101 KALQSLLSL TCPPYTPTQH LEREQALAKE FAEILHFTLR FDELKMRNPA
151 IQNDFSYYRR TISRNRINNM HLDIENEVNN EMANRMSLFY AEATPMLKTL
201 SNATMHFVSE NKTLPIENTT DCLSTMTSVC KVMLETPEYR SRFTSEETLM
251 FCMRVMVGVI ILYDHVHPVG AFCKTSKIDM KGCIVLKEQ APDSVEGLLN
301 ALRFTTKHLN DESTSKQIRA MLQ
  
```

BLASTP hits

Entry CER07G3_7 from database TREMBL:
 gene: "R07G3.8"; *Caenorhabditis elegans* cosmid R07G3.
 Score = 544, P = 1.4e-52, identities = 119/323, positives = 186/323

Alert BLASTP hits for DKFZphfkd2_24a15, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_24a15, frame 3

Report for DKFZphfkd2_24a15.3

[LENGTH] 323
 [MW] 37313.06
 [pI] 5.71
 [HOMOL] TREMBL:CER07G3_7 gene: "R07G3.8"; *Caenorhabditis elegans* cosmid R07G3. 4e-54

[PROSITE] MYRISTYL 1
 [PROSITE] CK2_PHOSPHO_SITE 4
 [PROSITE] TYR_PHOSPHO_SITE 1
 [PROSITE] PKC_PHOSPHO_SITE 5
 [PROSITE] ASN_GLYCOSYLATION 3
 [KW] TRANSMEMBRANE 1

```

SEQ  MGNNLLKVLTR EIIENYPHFFL DFENAOPTG EREIWNQISA VLQDSESILA DLQAYKGAGP
PRD  cccccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  EIRDAIQNPNDIOLOEKAWNVCPLVVRKRFYEFSIRLEKALQSLLSLTCPPYTPTQH
PRD  hhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  LEREQALAKEFAEILHFTLR FDELKMRNPAIQNDFSYYRR TISRNRINNM HLDIENEVNN
PRD  hhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  EMANRMSLFYAEATPMLKTL SNATMHFVSENKTLPIENTT DCLSTMTSVC KVMLETPEYR
PRD  hhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  SRFTSEETLMFCMRVMVGVI ILYDHVHPVG AFCKTSKIDM KGCIVLKEQ APDSVEGLLN
PRD  cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ  ALRFTTKHLN DESTSKQIRA MLQ
PRD  hhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....
  
```

Prosites for DKFZphfkd2_24a15.3

PS00001	202->206	ASN_GLYCOSYLATION	PDOC00001
PS00001	211->215	ASN_GLYCOSYLATION	PDOC00001
PS00001	218->222	ASN_GLYCOSYLATION	PDOC00001
PS00005	96->99	PKC_PHOSPHO_SITE	PDOC00005
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00005	275->278	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005

DKF2phfkd2_24a15

group: transmembrane protein

DKF2phfkd2_24a15 encodes a novel amino acid protein with similarity to C. elegans cosmid R07G3.

The novel protein contains 1 transmembrane region.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes and as a new marker for kidney cells.

similarity to C. elegans R07G3.8

membrane regions: 1

Summary DKF2phfkd2_24a15 encodes a novel 323 amino acid protein, with similarity to C. elegans R07G3.8.

similarity to C. elegans R07G3.8

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1513 bp

Poly A stretch at pos. 1494, no polyadenylation signal found

```
1 GGGGTACTCG GCGGCGGCGG AGCGGGCGGC AGAGCAGGGC GGCGGCGACT
51 CGCAGGGTAC CACCATCTTA AGGACAGAAA AGCTACAGGA CTCTAGGAGG
101 CCACCGTCCT GATTTGGGAA GTCCAACCTTA CTTTGGCCAG ACAGCAGCTA
151 AGCTGGTTCA TCCCATCAGC CTGGATTGGT GAAACTGAAT CACAGGAGAT
201 ATTTCCAGGT TTGCTGGGAT GGGAAACCTG CTCAAAGTCC TTACCAGGGA
251 AATTGAAAAC TATCCACACT TTTTCTGGA TTTTGAATAA GCTCAGCCTA
301 CAGAAGGAGA GAGAGAAATC TGGAACCAGA TCAGCGCCGT CCTTCAGGAT
351 TCTGAGAGCA TCCTTGCAGA CCTGCAGGCT TACAAAGGCG CAGGCCCAGA
401 GATCCGAGAT GCAATTCAAA ATCCCAATGA CATTAGCTT CAAGAAAAAG
451 CTTGGAATGC GGTGTGCCCT CTGTGTGTA GGCTAAAGAG ATTTTACGAG
501 TTTTCCATTA GACTAGAAAA AGCTCTTCAG AGTTTATTGG AATCTCTGAC
551 TTGTCCACCC TACACACCAA CCAACACCTT GGAAAGGGAA CAGGCCCTGG
601 CAAAGGAGTT TGCCGAAATT TTACATTTTA CCCTTCGATT CGATGAGCTG
651 AAGATGAGGA ACCCGGCTAT TCAGAATGAC TTCAGCTACT ACAGAAGAAC
701 AATCAGTCCG AACCCGATCA ACAACATGCA CCTAGACATT GAGAATGAAG
751 TCAATAATGA GATGGCCAAT CGAATGTCCC TCTTCTATGC AGAAGCCACG
801 CCAATGCTGA AAACCTTAG CAATGCCACA ATGCACTTTG TCTCTGAAAA
851 CAAAACCTCT CCAATAGAGA ACACCACAGA CTGCCTCAGC ACAATGACAA
901 GTGTC7GTAA AGTCATGCTG GAAACTCCGG AGTACAGAAG TAGGTTTACG
951 AGTGAAGAGA CCCTGATGTT CTGCATGAGG GTGATGGTGG GAGTCATCAT
1001 CCTCTATGAC CATGTCCACC CTGTGGGAGC TTTCTGCAAG ACATCCAAGA
1051 TCGATATGAA AGGCTGCATA AAAGTTTGA AGGAGCAGGC CCCAGACAGT
1101 GTGGAGGGGC TGCTAAATGC CCTCAGGTTT ACTACAAAGC ACTTGAACGA
1151 TGAATCAACT TCCAAACAGA TTCGAGCAAT GCTTCAGTAG AGCTCTGCTC
1201 AAAGAAGAGG ATCTATGTGC TGACCTCAGA AGATGTATAT GTTTACATAA
1251 TTTAATACAG ATTGATGTTA ATACTTGTGT ATTTACATAA CCGTTTCCTT
1301 CTTGTCACTG AAATATATGG ACCTTAATTT GTATCCTGAC TGACTCAACC
1351 CAGCAGAGCA TAAATTGACT TGAGAGCCTT ACCTTTGATG TCTGAAATGA
1401 AACCCCTTTC TCCAAAGGCA AAATTCGGAG ACTTTGATCT TTGCTACTGG
1451 AGTCCTTTAA CAACATCTAT AACGATAAAA AATTCCTAAT TGTCAAAAAA
1501 AAAAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

[KW] Alpha_Beta

```
SEQ  MSYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSYQIFFDPSDFDRCKLKDR
PRD  cccccccccchhhhhhhhhhhccccccccccccccccccccccccccccchhhhhhhc

SEQ  LPSIVVEPTEGEVESGELRWPPEEFLVQEDEQDNCEETAKENKEQ
PRD  cccccccccccccccccccccccccccccccccccccchhhhhhhhhccc
```

(No Prosite data available for DKFZphfkd2_1j9.3)

(No Pfam data available for DKFZphfkd2_1j9.3)

```

2701 TGGCTGAGCT CCTATCTGGC CTCCTCTTTT TTTTTTTTTT CAAGTAATTT
2751 GTGTGTATTT CTAACGTATT GTATTGAAAA AATTCCTAGT ATTTCAGTAA
2801 AAATGCCTGT TGTGAGATGA ACCTCCTGTA ACTTCTATCT GTTCTTTTTT
2851 GAGGCTCAGG GAGAAACTAG CATTTTTTTT TTICCAAAC ACTTTTTGTC
2901 ACTGTGACAG TTGTAAATAA AGTTTGAAAA TGCTCAAAAA AAAAAAAAAA
2951 AAAAC

```

BLAST Results

Entry HSG19750 from database EMBL:

human STS A001X24.

Score = 1050, P = 1.9e-39, identities = 212/213

Entry HSG20267 from database EMBL:

human STS A005C12.

Score = 610, P = 4.1e-19, identities = 122/122

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 213 bp to 527 bp; peptide length: 105

Category: strong similarity to known protein

Classification: unset

```

1 MSYFPIHCP DYLRSAKMTE VMMNTQPMEE IGLSPRKDGL SYQIFPDPSD
51 FDRRCKLKDR LPSIVVEPTE GEVESGELRW PEEFLVQED EQDNCEETAK
101 ENKEQ

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_lj9, frame 3

PIR:S52241 XLCL2 protein - African clawed frog, N = 1, Score = 443, P = 8e-42

PIR:S52241 XLCL2 protein - African clawed frog, N = 1, Score = 443, P = 8.2e-42

>PIR:S52241 XLCL2 protein - African clawed frog
Length = 102

HSPs:

Score = 443 (66.5 bits), Expect = 8.0e-42, P = 8.0e-42

Identities = 80/104 (76%), Positives = 95/104 (91%)

```

Query:      1 MSYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSYQIFPDPSDFDRRCKLKDR 60
             MS+++PIHC DYLRSA+NTEV+MNTQ M+EIGLSPRKD SYQIFPDPSDF+R CKLKDR
Sbjct:      1 MSVFYPIHCTDYLRSAENTEVIMNTQSMDEIGLSPRKD--SYQIFPDPSDFERCCKLKDR 58

Query:      61 LPSIVVEPTEGEVESGELRWPPPEEFLVQEDEQDNCEETAKENKE 104
             LPSIVVEPTEG+VESGELRWPPPEEF+V ED++ C++T KEN++
Sbjct:      59 LPSIVVEPTEGDVESGELRWPPPEEFVVDKEDKEGTCQTKKENEQ 102

```

Pedant information for DKFZphfkd2_lj9, frame 3

Report for DKFZphfkd2_lj9.3

```

[LENGTH]      105
[MW]           12269.78
[pI]           4.40
[HOMOL]        PIR:S52241 XLCL2 protein - African clawed frog 5e-44

```

DKF2phfkd2_lj9

group: kidney derived

DKF2phfkd2_lj9.3 encodes a novel 105 amino acid protein with high similarity to *Xenopus laevis* XLCL2 protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

strong similarity to XLCL2 protein, African clawed frog

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: unknown

Insert length: 2955 bp

Poly A stretch at pos. 2935, polyadenylation signal at pos. 2915

```
1  GGGGGGGGCT GAGTGCTCAG TGGAGAGCGG GGAGTTGTGT CCACCTTGCC
51  GACGTGCTTA GCCGTGGGGC TGTCCTGGGA AGGCGGACGG CGAGCGCCCG
101 GTGTCCGCAC TCGGCCGCCT GCCGTGCCCG TCTGCGCCCG TGTCATCCTC
151 ACTCGGGACG CAGGGACCGT TTTTAAATCA CAGGGGCGTG TGTCAGCCTG
201 CCCTAGGACT TCATGTCTAT ATATTCCCC ATTCACTGCC CCGACTATCT
251 GAGATCGGCC AAGATGACTG AGGTGATGAT GAACACCCAG CCCATGGAGG
301 AGATCGGCCT CAGCCCCCGC AAGGATGGCC TTTCCTACCA GATCTTCCCA
351 GACCCGTCAG ATTTTGACCG CCGCTGCAAA CTGAAGGACC GTCTGCCCTC
401 CATAGTGGTG GAACCCACAG AAGGGGAGGT GGAGAGCGGG GAGCTCCGGT
451 GGCCCCCTGA GGAGTTCTCT GTCCAGGAGG ATGAGCAAGA TAACTGCGAA
501 GAGACAGCGA AAGAAAATAA AGAGCAGTAG AGTCCCTGTG GACTCCCATG
551 GGTCAATACCA GCCAGCATCT GTTCCTGAAC TGTGTTTTTC CCATCATGAC
601 GGAAGAAGAG AGTGAGCCGC AATTGTTCTG AAAATGTCAA ACGAGGCTTC
651 TGTTTTGCAC CTGCAGATCA CCGAGTTGGT TTTCTTTTCT TTTCTTGCCCT
701 TTTTTTTTTT TTTGAAATTT GCCGAGCAGT GGAGCCCTCT GACAATTTGC
751 AAGGCCCTCT GAGAAAGGAA GCTGCTTAGA GCCAGGGGGT TAGTGGGTGA
801 GGGGAGCGAG TGCTGTTTTT GAGATCATTG TCTGAACTCA GGCAGCCTAG
851 TAGAGGAGCT GGTGGGATTC CAATGGGTCT TGGTGGGTGG GAGGTGGGGC
901 ATGTGCAAG CAAGCAAGGA ACATTGGGG TAAGAAAACA AACATGAGGC
951 AAAAGAAAAA ATACATGTTT TTAAGAAAAC ATTGAGCAGA GAACTGCAGC
1001 CAGGATGCGC TCAGCAGACA TTCACCTGCG CCGCTGGGAC ATCAGAAAAC
1051 AAAGTCTTCA TCTCTCTCTC CAGTTTCACC CACCCACCCC TTTGCTTTCA
1101 TTTCAAGGTG GTTGGTCTAT ATGACAGGGA GGAGAGTAAA GGAGAGCAGG
1151 AGCAATTGGC TGCCTGCAAA GCCAGCTGGA GGTGAAGTGC AGGAAAGGAA
1201 AGGTCACCCC ATTCTACTCC ATGGCCTCTC TGCTCCAGC TGTTGGTAGC
1251 TCACATAGCC AGTGATGATC GTTTTAAAGA GGCAGTGCTT TTCAGCTTTT
1301 CTCCCTGATA TATCCATTTT GCTTCCCAGC ACTTTTATAG AGTAGTGAGA
1351 GCACTTCCCT CCCTTGTGGG AAGCCCCAGG GTGGACACTC AGCACGAAGG
1401 TCTCTCCCTT AACTGCTGCC CTTCCAAGAC TTGCTCCCGA GATGGAGTGG
1451 CCGTGGTCTT CCAGGCTGGC CCTTCCTTCT CCTCACCGCC ACCTTCCCTG
1501 CCCCAGCCCC AGCAGCCATG GGTACATGGG TCCCCAGCTC ACCTATGGAT
1551 TCCCGCCAGT CTGCCAGCT GCAGTACTCA CGCCCCATGG GGGATCTTGG
1601 TCTGTTTTTC TTGTGGGAGC CTAGTGGAGA GCAGACGTGG CTTTTTATGT
1651 GTCTTGTTGG GGAGGTGACT TGCATGGTGG GGACAAGGCT GTCGTGGCAA
1701 CCTTGGGATC GAGTTTGAGA CTAAAGCATG TCATGAGATC CCTGGCTTCT
1751 CCCCATGTTG TTCCCGGACA AGGGCAGAAG GGAGGCATGG CAAGGGACCT
1801 CTGCTGTCCT TACTCAACAG TGGTCCTCAT CCCTCCCCAC CTCCCACTGC
1851 TTCTGCAAG GGCACCAAGT GTATGAGAAA GTTGGCCTTT GGAATTAGGA
1901 TTTCTTATTG TAGCTAAGAG CCATCTGAAG CAGCAGGTTG CAGGACAAAT
1951 GCTTCAAGTC GCCGAGAGCA GTACCGTGTG GCCAAGAGGT GGACTCAGAG
2001 CCTTCTTGA GCTAAACTCG GCCAACCAGG GCACGCAGCA TGTCCCCCA
2051 GGTCTCCAGT CAGTCCAGGT TGACCCCTCAG TTCTGGACGT GTGTATATAG
2101 CTGTATTTAA TACCTCAAGG TCATTGTGGC TCTGGGGATG CCAGGGCAGG
2151 AGGACGAGGG TCGCTGTGGG ACACAGCAGT CCGCGGAATT CCGTTCTGGG
2201 AAGCCAATGG TCGCCGGCAC CCCTTGCTTC CTCCCTCTGT TGTCTGCCTG
2251 TGTGACACAC ATCAATGGCA ATAACTTCTT CCAACTCTCT GCAGAAGTGG
2301 GAGAGGCCG3 CAGCCTGCAC CGAGAGGGGG TTTCCTCTCT CTGTCTCCCC
2351 GCTTCGTCTT GTTTTGGCTG CAGAGAGTGG TTCATCCATA CTCTCATTCC
2401 CTGCGCTCCC CTTGTGGACG GGGGTCTTGC CTTTTCAATT CCTGTGTTTT
2451 GGTGTCTTCC CTTATCTGCT ACCCTGAATC ACCTGTCTCT GTCTTGCTGT
2501 GTGATGGGAA CATGCTTGTG AACTGCGTAA CAAATCTACT TTGTGTATGT
2551 GTCTGTTTAT GGGGCTGGTT TATTATTTTT GCTGCTCCCT AGACCACTTT
2601 GTATGACCGT TTGCAGTCTG AGCAGGCCAG GGGCTGCAGC CTAATGTCAG
2651 GACCCTCAGC GGTGGAGCCT GCTGGGGGGA CCCAGCTGCT CTGGACAAG
```

PS00006	142->146	CK2_PHOSPHO_SITE	PDOC00006
PS00006	234->238	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00006	341->345	CK2_PHOSPHO_SITE	PDOC00006
PS00006	419->423	CK2_PHOSPHO_SITE	PDOC00006
PS00007	106->115	TYR_PHOSPHO_SITE	PDOC00007
PS00008	56->62	MYRISTYL	PDOC00008
PS00008	212->218	MYRISTYL	PDOC00008
PS00008	232->238	MYRISTYL	PDOC00008
PS00008	272->278	MYRISTYL	PDOC00008
PS00008	277->283	MYRISTYL	PDOC00008
PS00008	279->285	MYRISTYL	PDOC00008
PS00008	361->367	MYRISTYL	PDOC00008
PS00008	476->482	MYRISTYL	PDOC00008
PS00008	509->515	MYRISTYL	PDOC00008
PS00008	574->580	MYRISTYL	PDOC00008
PS00008	590->596	MYRISTYL	PDOC00008
PS00008	640->646	MYRISTYL	PDOC00008
PS00009	122->126	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_82m6.3)

SEQ	MNGHLEAEQQQDQRPDQELTGSWGHGPRSTLVRAKAMAPPPPLAASTLLHGEFGSYPA
SEGXXXXXXXXXXXXX.....
PRD	ccchhhhhhhccccceeeccccccceehhhhhccccceeeceeecccccccc
SEQ	RGPRFALTITSQALHIQRLRPKEARPRGGLVPLAEVSGCCTLRSRSPSDSAAYFCIYTY
SEG
PRD	ccccceehhhhhhhhhhhhhccccccccccccceeeeeeceeeeeeccccccccceeeeee
SEQ	PRGRRGARRRATRTFRADGAATYEENRAEAQRWATALTCLLRGLPLPGDGEITPDLLRP
SEG	.XXXXXXXXXXXXXXXXXXXXX.....XXXXX
PRD	ccccchhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhcccccccccccccccccc
SEQ	PRLLLLVNPFGGRGLAWQWCKNHVLPmiseaglsfnliqterqnharelvqglslsewdg
SEG	xxxxxxx.....
PRD	ceeeeeeccccchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhccccce
SEQ	IVTVSGDGLLHEVLNGLDRPDWEEAVKMPVGILPCGSGNALAGAVNQHGGFEPALGLDL
SEGXXXXX
PRD	eeeeccccceeeccccccccchhhhhccccceeeccccccccccccccccccccchhhhhh
SEQ	LLNCSLLCRGGGHPDLLSVTLASGSRCSFSLSVAWGFVSDVDIQSERFRALGSARFTL
SEG	XXXXXXXXXXXXXXXXX.....
PRD	hhhhhhccccccccccccceeeeeeccccceeeeeeccccceeeehhhhhhhhhhhhhhhc
SEQ	GTVLGLATLHTYGRGLSYLPATVEPASPTPAHSLPRAKSELTLPDPAPPMASPLHRSV
SEG
PRD	hhhhhhhhhhhhcc
SEQ	SDLPLPLPQPALASPGSPPEPLPILSLNGGPELAGDWGAGDAPLSPDPLSSPPGSPKA
SEG	.XXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD	ccccccccccccccccccccceeeeeeccccccccccccccccccccccccccccccccce
SEQ	ALHSPVSEGAPlVPSSGLPLPTDARVGASTCGPPDHLLPPLGTPLPPDWVTLEGDFVL
SEG	xx.....XXXXXXXXXXXXXXXXX.....
PRD	eeccce
SEQ	MLAISPSHLGADLVAAPHARFDDGLVHLCWVRSGISRALLRFLAMERGHFSLGCPQL
SEG
PRD	eeeeccccccccccccccccccccceeeeeeccccchhhhhhhhhhhhhhhccccceeeccccch
SEQ	GYAAARAFRLEPLTPRGVLTVOGEQVEYGPLQAQMPHGIGTLLTGPPGCPGREP
SEGXXXXXXXXXXXXXXXXX.....
PRD	hhhhhhhhhhccccccccceeeccccceccccccccccccccccceeecccccccccc

PS000001	303->307	ASN_GLYCOSYLATION	PDOC000001
PS000002	245->249	GLYCOSAMINOGLYCAN	PDOC000002
PS000004	129->133	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	102->105	PKC_PHOSPHO_SITE	PDOC000005
PS000005	134->137	PKC_PHOSPHO_SITE	PDOC000005
PS000005	220->223	PKC_PHOSPHO_SITE	PDOC000005
PS000005	347->350	PKC_PHOSPHO_SITE	PDOC000005
PS000005	355->358	PKC_PHOSPHO_SITE	PDOC000005
PS000005	371->374	PKC_PHOSPHO_SITE	PDOC000005
PS000005	477->480	PKC_PHOSPHO_SITE	PDOC000005
PS000005	614->617	PKC_PHOSPHO_SITE	PDOC000005
PS000006	107->111	CK2_PHOSPHO_SITE	PDOC000006

Score = 253, P = 2.0e-25, identities = 70/234, positives = 116/234

Entry S51398 from database PIR:

hypothetical protein YLR260w - yeast (*Saccharomyces cerevisiae*)

>TREMBL:SCL8479_4 gene: "YLR260W"; product: "Ylr260wp"; *Saccharomyces cerevisiae* chromosome XII cosmid 8479.

Score = 251, P = 1.0e-24, identities = 62/198, positives = 103/198

Alert BLASTP hits for DKFZphfbr2_82m6, frame 3

TREMBL:AF068749_1 gene: "SPHK1b"; product: "sphingosine kinase"; *Mus musculus* sphingosine kinase (SPHK1b) mRNA, complete cds., N = 2, Score = 615, P = 1.2e-92

TREMBL:AF068748_1 gene: "SPHK1a"; product: "sphingosine kinase"; *Mus musculus* sphingosine kinase (SPHK1a) mRNA, partial cds., N = 2, Score = 616, P = 2e-92

TREMBL:ATF18E5_16 gene: "F18E5.160"; product: "putative protein"; *Arabidopsis thaliana* DNA chromosome 4, BAC clone F18E5 (ESSAII project), N = 2, Score = 370, P = 6.8e-33

>TREMBL:AF068748_1 gene: "SPHK1a"; product: "sphingosine kinase"; *Mus musculus* sphingosine kinase (SPHK1a) mRNA, partial cds.
Length = 504

HSPs:

Score = 616 (92.4 bits), Expect = 2.0e-92, Sum P(2) = 2.0e-92
Identities = 128/260 (49%), Positives = 173/260 (66%)

```
Query: 154 ATALTCLLRGLPLPGDGEITPDLLPRPPRLLLVNPFGGRGLAWQCKNHVLP MISEAGL 213
      A   C   L   +   E   LLPRP R+L+L+NP GG+G A Q ++ V P + EA +
Sbjct: 110 APVAPCQREPRDLAMEFECPRGLLP RCRVLVLLNPQGKGKALQLFQSRVQPFLEEAEI 169

Query: 214 SFNLIQTERQNHARELVQGLSLSEWDGIVTVSGDGLLHEVLNGLLDRPDWEEAVKMPVGI 273
      +F LI TER+NHARELV L WD + +SGDGL+HEV+NGL++RPDWE A++ P+
Sbjct: 170 TFKLILTERKNHARELVCAEELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCS 229

Query: 274 LPCGSGNALAGAVNQHGGEFEPALGLDLLNCSLLLCRGGGHPDLLSVTLASGSRCSFSL 333
      LP GSGNALA +VN + G+E DLL+NC+LLCR P++LLS+ ASG R +S L
Sbjct: 230 LPGGSGNALAASVNHAYAGYEQVTNEDLLINCTLLLCRRRLSPMNLSSLHTASGLRLYSVL 289

Query: 334 SVAWGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYGRRLSYLPA-TVEPASPTPAH 392
      S++WGFV+DVD++SE++R LG RFT+GT LA+L Y+G+L+YLP TV AS PA
Sbjct: 290 SLSWGFVADVDLESEKYRRLGEIRFTVCTFFRLASLRIYQQQLAYLPVCTV--ASKRPAS 347

Query: 393 SL-PRAKSELTLPDPAPPMMAH 413
      +L + + L P P +H
Sbjct: 348 TLVQKGPVDTHLVPLEEPVPSH 369
```

Score = 324 (48.6 bits), Expect = 2.0e-92, Sum P(2) = 2.0e-92
Identities = 72/160 (45%), Positives = 100/160 (62%)

```
Query: 499 LPLPTPDARVGASTC---GPPDHLLPPLGTPLPPDWVTL-EGDFVLM LAISPSHLGADLV 554
      LP+ T ++ AST GP D L PL P+P W + E DF+L+L + +HL ++L
Sbjct: 335 LPVGTVASKRPASTLVQKGPVDTHLVPLEEPVPSHWTVVPEQDFLLVLVLLHTHLSSELF 394

Query: 555 AAPHARFDDGLVHLCWVRSGISRAALLRLFLAMERGSIHFSLGCPQLGYAAARFRLEPLT 614
      AAP R + G++HL +VR+G+SRAALLRLFLAM++G H L CP L + AFRLEP +
Sbjct: 395 AAPMGRCEAGVMHLFVVRAGVSRAALLRLFLAMQKGMELDCPYLVHVPVVAFRLEPRS 454

Query: 615 PRGVLTVNDEQVEYGPLQAQMHPGIGTLLTGPPGCP-GRE 653
      RGV +VDGE + +Q Q+HP ++ G P GR+
Sbjct: 455 QRGVFSVDGELMVCEAVQGQVHPNYLWMVCGSRDAPSGRD 494
```

Score = 37 (5.6 bits), Expect = 3.6e-62, Sum P(2) = 3.6e-62
Identities = 8/20 (40%), Positives = 9/20 (45%)

```
Query: 459 GAGDAPLSPDPLLSSPPGSP 478
      G+ DAP D PP P
Sbjct: 485 GSRDAPSGRDSRRGPPPEEP 504
```

Pedant information for DKFZphfbr2_82m6, frame 3

Report for DKFZphfbr2_82m6.3

```

2351 CTCAGGATTG CGCTCGCTTT CATGGGACCA GACGTGATGC TGAAGGTGG
2401 GCGTCGTAC GGTAAAGAG AAATGGGCTC GTCCCGAGGG TAGTGCCTGA
2451 TCAATGAGGG CGGGGCCTGG CGTCTGATCT GGGGCCGCC TTACGGGGCA
2501 GGGCTCAGTC CTGACGCTTG CCACCTGCTC CTACCCGCC AGGATGGCTG
2551 AGGGCGGAGT CTATTTTACG CGTCGCCCAA TGACAGGACC TGAATGTAC
2601 TGGCTGGGGT AGGCCTCAGT GAGTCGCCCG GTCAGGCCCC GCAGCCTCGC
2651 CCCATCCACT CCGGTGCCTC CATTTAGCTG GCCAATCAGC CCAGGAGGGG
2701 CAGGTTCCCC GGGGCCGGCG CTAGGATTTG CACTAATGTT CCTCTCCCG
2751 CGGGTGGGGG CGGGGAAATT CATATCCCT GTTCGTCTCA TGGCGCTCCT
2801 CCGTCCCAA TCTAAAAAGC AATTGAAAAG GTCTATGCAA TAAAGGCAGT
2851 CGCTTCATT CTCTCAAAA AAAAA

```

BLAST Results

No BLAST result

Medline entries

99045661:
Tumor necrosis factor-alpha induces adhesion molecule expression through the sphingosine kinase pathway.

98395082:
Molecular cloning and functional characterization of murine sphingosine kinase.

98241633:
Purification and characterization of rat kidney sphingosine kinase.

99178622:
Sphingosine 1-phosphate: a prototype of a new class of second messengers.

Peptide information for frame 3

```

1 MNGHLEAEEQ QDQRPDQELT GSWGHPGRST LVRKAMAPP PPPLAASTSL
51 LHGEFGSYPA RGPREFALT LT SQALHIQRLR PKPEARPRGG LVPLAEVSGC
101 CTLRSRSPSD SAAFYCIYTY PRGRRGARRR ATRTRADGA ATYEENRAEA
151 QRWATALTCL LRGLPLPGDG EITPDLLPRP PRLLLLVNPF GGRGLAWQWC
201 KHVLPMPSE AGLSFNLIQT ERQNHARELV QGLSLSEWDG IVTVSGDGLL
251 HEVLNGLDR PDWEEAVKMP VGILPCGSGN ALAGAVNQHG GFEPALGLDL
301 LLNCSLLLCR GGGHPLDLLS VTLASGSRCE SFLSVWGFV SDVDIQSERF
351 RALGSARFTL GTVLGLATLH TYRGRLSYLP ATVEPASPTP AHSPLPRAKSE
401 LTLTPDPAPP MAHSPLHRSV SDLPLPLPQP ALASPGSPEP LPILSLNGGG
451 PELAGDWGGA GDAPLSPDPL LSSPPGSPKA ALHSPVSEGA PVIPPSSGLP
501 LPTPDARVGA STCGPPDHLL PPLGTPLPPD WVTLEGDFVL MLAISSPHLG
551 ADLVAAPHAR FDDGLVHLCW VRSGISRAAL LRLFLAMERG SHFSLGCPQL
601 GYAAARAERL EPLTPRGVLT VDGEQVEYGP LQAQNHGPGIC TLLTGPPGCP
651 GREP

```

ORF from 270 bp to 2231 bp; peptide length: 654
Category: similarity to known protein

BLASTP hits

Entry SPAC4A8_7 from database TREMBL:
gene: "SPAC4A8.07c"; product: "hypothetical protein"; S.pombe chromosome I cosmid c4A8.
Score = 301, P = 7.9e-32, identities = 68/190, positives = 109/190

Entry CEC34C6_3 from database TREMBLNEW:
product: "C34C6.5"; Caenorhabditis elegans cosmid C34C6.
>TREMBL:CEC34C6_3 product: "C34C6.5"; Caenorhabditis elegans cosmid C34C6
Score = 273, P = 9.0e-29, identities = 78/265, positives = 142/265

Entry S67059 from database PIR:
hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae)
>TREMBL:SC55021.9 gene: "O3615"; product: "O3615p"; Saccharomyces cerevisiae cosmid pUO1258 from chromosome 15R. >TREMBL:SCYOR170W_2
S.cerevisiae chromosome XV reading frame ORF YOR170W

DKFZphfbr2_82m6

group: signal transduction

DKFZphfbr2_82m6.3 encodes a novel 654 amino acid protein with similarity to murine sphingosine kinase.

Sphingosine kinase is a new type of lipid kinase, which is regulated by growth factors. The enzyme phosphorylates sphingosine, which subsequently exerts intracellular and extracellular actions. Intracellularly, sphingosine 1-phosphate (SPP) promotes proliferation and inhibits apoptosis. In yeast, survival of cells exposed to heat shock indicates is dependent on SPP. Extracellularly, SPP inhibits cell motility and influences cell morphology, effects that appear to be mediated by the G protein-coupled receptor EDG1.

The new protein can find application in modulating/blocking the shingosine kinase intracellular signal transmission pathway.

strong similarity to mouse "sphingosine kinase"

complete cDNA, complete cds, EST hits,
YLR260w/YOR171c Lcb5p/Lcb4p = long chain base kinases,
involved in biosynthesis of sphingolipids

Sequenced by DKFZ

Locus: unknown

Insert length: 2875 bp

Poly A stretch at pos. 2865, polyadenylation signal at pos. 2838

```
1 AGTGTGAG GTGAGGAGG GGGGCTGGCA GGGCTAGTCG GGGCATCTGG
51 AAATTTCCGA CCCCACGCTT CGGGCGTTTC CTTATCAGGT TCACCGCTCC
101 CTGATCTCGC GCTGCACTTC GTAGGCGCAG CCGCTGCTTG GGAAGTCCTA
151 CTTAAGAGCT GAAGGTCAGG CCAGGACAGT GAGACCTGAC TCCTTGCTCC
201 TACCAGCCTA CTATGGCTTA AGACCCAGGG CCAGGGTCCC GTTGATGTAA
251 CAGAGCAGAG GACCAGCAGA TGAATGGACA CCTTGAAGCA GAGGAGCAGC
301 AGGACCAGAG GCCAGACCAG GAGCTGACCG GGAGCTGGGG CCACGGGCCT
351 AGGAGCACCC TGGTCAGGGC TAAGGCCATG GCGCCGCCCC CACCGCCACT
401 GGCTGCCAGC ACCTCGCTCC TCCATGGCGA GTTGGCTCC TACCCAGCCC
451 GAGGCCACAG CTTTGCCCTC ACCCTTACAT CGCAGGCCCT GCACATACAG
501 CGGCTGCGCC CCAAACCTGA AGCCAGGCCC CGGGGTGGCC TGGTCCCGTT
551 GGCCGAGGTC TCAGGCTGCT GCACCCGCGC AAGCCGCGAG CCCTCAGACT
601 CAGCGGCCAT CTTCTGCATC TACACCTACC CTCGGGGCCG GCGCGGGGCC
651 CGGCGCAGAG CACTCGCAC CTCCGGGCA GATGGGGCCG CCACCTACGA
701 AGAGAACCGT GCCGAGGCCC AGCGCTGGGC CACTGCCCTC ACCTGTCTGC
751 TCCGAGGACT GCCACTGCCC GGGGATGGGG AGATCACCCC TGACCTGCTA
801 CCTCGGCCCG CCGGTTGCT TCTATTGGTC AATCCCTTTG GGGGTGCGGG
851 CCTGGCCTGG CAGTGGTGTA AGAACCACGT GCTTCCCATG ATCTCTGAAG
901 CTGGGCTGTC CTTCAACCTC ATCCAGACAG AACGACAGAA CCACGCCCGG
951 GAGCTGGTCC AGGGGCTGAG CCTGAGTGAG TGGGATGGCA TCGTCACGGT
1001 CTCGGGAGAC GGGCTGCTCC ATGAGGTGCT GAACGGGCTC CTAGATCGCC
1051 CTGACTGGGA GGAAGCTGTG AAGATGCCTG TGGGCATCCT CCCCTGCGGC
1101 TCGGGCAACG CGCTGGCCGG AGCAGTGAAC CAGCACGGGG GATTTGAGCC
1151 AGCCCTGGGC CTCGACCTGT TGCTCAACTG CTCACTGTTG CTGTGCCGGG
1201 GTGGTGGCCA CCCACTGGAC CTGCTCTCCG TGACGCTGGC CTCGGGCTCC
1251 CGCTGTTCTT CTTTCTGTC TGTGGCCTGG GGCTTCTGT CAGATGTGGA
1301 TATCCAGAGC GAGCGCTTCA GGGCCTTGGG CAGTGCCCGC TTCACACTGG
1351 GCACGGTGCT GGGCCTCGCC ACACTGCACA CCTACCGCGG ACGCCTCTCC
1401 TACCTCCCCG CCACTGTGGA ACCTGCCTCG CCCACCCCTG CCCATAGCCT
1451 GCCTCGTGCC AAGTCGGAGC TGACCCTAAC CCCAGACCCA GCGCCGCCCA
1501 TGGCCCACTC ACCCTGTCAT CGTTCTGTGT CTGACCTGCC TCTTCCCTG
1551 CCCCAGCCTG CCCTGGCCTC TCCTGGCTCG CCAGAACCCC TGCCCATCCT
1601 GTCCCTCAAC GGTGGGGGCC CAGAGCTGGC TGGGGACTGG GGTGGGGCTG
1651 GGGATGCTCC GCTGTCCCCG GACCCACTGC TGTCTTACC TCCTGGCTCT
1701 CCAAAGGCAG CTCTACACTC ACCCGTCTCC GAAGGGGCCC CGGTAATTCC
1751 CCCATCTCTT GGGCTCCAC TTTCCACCCC TGATGCCGGG GTAGGGGCCT
1801 CCACCTGCGG CCGGCCGAC CACCTGCTGC CTCCGCTAGG CACCCGCTG
1851 CCCCAGACT GGGTGACGCT GGAGGGGGAC TTTGTGCTCA TGTGGCCAT
1901 CTCGCCCAGC CACTAGGCG CTGACCTGGT GGCAGCTCCG CATGCGCGCT
1951 TCGACGACGG CTTGGTGAC CTGTGCTGGG TCGGTAGCGG CATCTCGCGG
2001 GCTGCGCTGC TGCGCCTTTT CTTGGCCATG GAGCGTGGTA GCCACTTCAG
2051 CCTGGGCTGT CCGCAGCTGG GCTACGCCGC GGCCCGTGCC TTCCGCCTAG
2101 AGCCGCTGAC ACCACGCGGC GTGCTCACAG TGGACGGGGA CGAGGTGGAG
2151 TATGGGCCCG TACAGGCACA GATGCACCCT GGCATCGGTA CACTGCTCAC
2201 TGGCCCTCTT CGCTGCCCGG GCGGGGAGCC CTGAAACTAA ACAAGCTTGG
2251 TACCCGCGCG GCGCGGGGCC TACATTCCAA TGGGGCGGAG CCTGAGCTAG
2301 GGGGTGTGCC CTGGTGCTTA GACTTGTGGT GGCAGGGGCC CTGGCCCCGT
```

Report for DKFZphfbr2_82m16.3

```

[LENGTH]      289
[MW]           32308.36
[pI]           8.76
[HOMOL]        PIR:T00268 hypothetical protein KIAA0597 - human (fragment) 9e-14
[FUNCAT]       04.99 other transcription activities [S. cerevisiae, YIL030c] 4e-09
[PIRKW]        transmembrane protein 9e-08
[PROSITE]      MYRISTYL 1
[PROSITE]      CK2_PHOSPHO_SITE 4
[PROSITE]      TYR_PHOSPHO_SITE 1
[PROSITE]      PKC_PHOSPHO_SITE 3
[PROSITE]      ASN_GLYCOSYLATION 3
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY 6.57 %

```

```

SEQ      MLGWCEAIARNPHRI PNNTRTPEISGLADASQTSTLNEKSPGRSASRSSNISKASSPTT
SEG      .....xxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      cccchhhhhhhccccccccccccccccccccchhhhhhhhhcccccccccccccccccccccc

SEQ      GTAPRSQSRLSVC PSTQDICRICHCEGDEESPLITPCRCTGTLRFVHQSLHQWIKSSDT
SEG      .....
PRD      cccccccccccccccccceeeeeecccccccccccccccccceeeehhhhhhhhhcccccc

SEQ      RCCELCKYDFIMETKLKPLRKWEKLQMTTSERRKIFCSVT FHVIAITCVVWSLYVLIDRT
SEG      .....
PRD      ceeeeeeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccc

SEQ      AEEIKQGN DNGVLEWPFWTKLVVVAIGFTGGLVFMVYVQCKVYVQLWRR LKAYNRVIFVQN
SEG      .....
PRD      ccccccccccccehhhhheccceeeecccccceeeehhhhhhhhhhhhhhhhhheeeeeee

SEQ      CPDTAKKLEKNFSCNVNTDIKDAVVVPVPQTGANS LPSAEGGPPEVVSV
SEG      .....
PRD      cccchhhhhhhcccccccccccccccccccccccccccccccccccccccccccccc

```

Prosites for DKFZphfbr2 82m16.3

PS00001	17->21	ASN_GLYCOSYLATION	PDOC00001
PS00001	51->55	ASN_GLYCOSYLATION	PDOC00001
PS00001	251->255	ASN_GLYCOSYLATION	PDOC00001
PS00005	102->105	PKC_PHOSPHO_SITE	PDOC00005
PS00005	150->153	PKC_PHOSPHO_SITE	PDOC00005
PS00005	244->247	PKC_PHOSPHO_SITE	PDOC00005
PS00006	36->40	CK2_PHOSPHO_SITE	PDOC00006
PS00006	75->79	CK2_PHOSPHO_SITE	PDOC00006
PS00006	148->152	CK2_PHOSPHO_SITE	PDOC00006
PS00006	180->184	CK2_PHOSPHO_SITE	PDOC00006
PS00007	121->129	TYR_PHOSPHO_SITE	PDOC00007
PS00008	187->193	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_82m16.3) .

2601 TGCTGTCCAA TAGAAACACA ACAGCCACAA ATGCAGGCCA CAGATGCAAA
 2651 TATTTAACTT CCCAGTAGCC CTATTTTAAA AAGTAAAAAT AAATGTTTGT
 2701 TTGTTAAAAA AAAA

BLAST Results

Entry G37457 from database EMBLNEW:
 SHGC-57357 Human Homo sapiens STS genomic.
 Length = 458
 Plus Strand HSPs:
 Score = 2116 (317.5 bits), Expect = 4.3e-91, P = 4.3e-91
 Identities = 444/456 (97%)

Medline entries

No Medline entry

Peptide information for frame 3

1 MLGWCEAIAR NPHRIPNNTR TPEISGDLAD ASQTSTLNEK SPGRSASRSS
 51 NISKASSPTT GTAPRSQSRL SVCSTQDQC RICHCEGDEE SPLITPCRCT
 101 GTLRFVHQSCLHQWIKSSDT RCCELCKYDF IMETKLKPLR KWEKLMQTTT
 151 ERRKIFCSVT FHVIAITCVV WSLYVLIDRT AEEIKQGNND GVLEWPFWTK
 201 LVVVAIGFTG GLVFMVYQCK VYVQLWRRLK AYNRVIFVQN CPDTAKKLEK
 251 NFSCNVNTDI KDAVVVPVPQ TGANSLPSAE GGPPEVVS

ORF from 978 bp to 1844 bp; peptide length: 289
 Category: similarity to unknown protein

BLASTP hits

Entry AB011169.1 from database TREMBL:
 gene: "KIAA0597"; product: "KIAA0597 protein"; Homo sapiens mRNA for
 KIAA0597 protein, partial cds.
 Score = 188, P = 6.0e-12, identities = 30/54, positives = 38/54

Entry SPBC14F5.7 from database TREMBL:
 gene: "SPBC14F5.07"; product: "hypothetical protein"; S.pombe
 chromosome II cosmid c14F5.
 Score = 185, P = 1.9e-11, identities = 29/53, positives = 38/53

Entry CEY57A10B.1 from database TREMBL:
 gene: "Y57A10B.1"; Caenorhabditis elegans cosmid Y57A10B
 Score = 171, P = 2.6e-10, identities = 40/107, positives = 58/107

Alert BLASTP hits for DKFZphfbr2_82m16, frame 3

TREMBL:ATF28A23_14 gene: "F28A23.140"; product: "putative protein";
 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII
 project), N = 1, Score = 198, P = 3.4e-13

>TREMBL:ATF28A23_14 gene: "F28A23.140"; product: "putative protein";
 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)
 Length = 1,051

HSPs:

Score = 198 (29.7 bits), Expect = 3.4e-13, P = 3.4e-13
 Identities = 38/103 (36%), Positives = 61/103 (59%)

Query: 28 LADASQTSTLNEKSPGRSASRS-SNISKASSPTTGTAPRSQSRLSVCSTQDQC RICHCE 86
 +++ S +S+ + SP +++ SN+ A S TG+ +D+CRIC
 Sbjct: 20 VSEPSVSSSSSPNQASPNPFSNMDDPAVSTATGSRYVDDDE-----DEEDVCRICRNP 74

Query: 87 GDEESPLITPCRCTGTLRFVHQSCLHQWIKSSDTRCCCELCKYDF 130
 GD +++PL PC C+G+++FVHQ CL QW+ S+ R CE+CK+ F
 Sbjct: 75 GDADNPLRYPCACSGSIKFVHQDCLLQWLNHSNARQCCEVCKHPF 118

DKFZphfbr2_82m16

group: brain derived

DKFZphfbr2_82m16 encodes a novel 289 amino acid protein with very weak similarity to A.thaliana F28A23.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to A.thaliana F28A23.140

complete cDNA, complete cds, few EST hits
many ATGs in front of the ORF
TRANSMEMBRANE 1

Sequenced by DKFZ

Locus: /map="4"

Insert length: 2715 bp

Poly A stretch at pos. 2705, polyadenylation signal at pos. 2687

```
1 AGAGGAGGGG AGAGGACTGG GGAGCCGAGC CAGAGCCGGG CTGCCTGCCA
51 CCCGGCTGCT CGTCCGCTAG CTGGGGAGGA GCGCTCCACC CGCAACTGAC
101 AAAGGATGGG AGAATGCCCG CGCCCCGGGA TGCCGGCCGC ACGCAGCCTG
151 GCGGCCGCCT GAGCTACTTC ACCCTCCGCC GGTAAGTGAC TGCAAACATC
201 ATTCAATCAA TCAGCCTCAC TGGGAGCCCC TTCTCTCCGG CTGGTAGTCC
251 TGGGCGGCTT GTCCTGATC CCGAGCGGGG CTTGGCACAG CATCAGCCCT
301 GGAGGGCAGG CAGCAGGTGC CTTGCTTGG TGGGTCCACT GGGGAGCGTG
351 GCTGGGGTTC GCGGCGGGTG CTGCCACCCA ACCTGCGGGC GCGGGGCTCG
401 CCCAGTAGGC GCCTCTCTGG TGACAGGAGG CCGCTCCAGC CCGCATCCTG
451 GGGTAGTTGC TACTATTGGC CCCCAGCGCC CGCTCTGCGC GCGCGCCGTT
501 TCTGGCGGAT CCCAGTGC GCGCGCGCTG TTTACACCGG CGTGGTACTA
551 GTCACGGAGC CGCACCCCTC GGAAAGCGCG GAGTCGATGA CAGCCACTTC
601 ACAGGCTCAC GCGCTCCTAG TGTGGGCTTG AAGGGGACGG GGACCGATTA
651 CCAAAGGAGA GCGCTGAGTA CGGAAGACAC AGGGCAGCCT TTGTCTTGGG
701 TTTAGCGCTG ATGCGCTCAA CCTGAGTCG GGTTCAGTGC AACTGTTGTG
751 TCCGATTTCG GTTCCCTGCA ACCGCCCTCC TGGGCGAGAG ATGTCATTGT
801 GTTCTGCGG CAGCGGGGAC TGAGAGCTGG GACTTAAGAC GCCAGGAGGG
851 TCCGCGCTC ACGGGAAATG TACCCCAAAA GAACCTCTAG AGAATATACT
901 CAACTGTCTT GCTGTGATTA AACAAGACTG CTGTATTTTA ATTTAGAAA
951 TTGAAAAGGG ATAGGAGGAA GGGGAAAATG CTGGGCTGGT GTGAAGCGAT
1001 AGCCCCGTAAC CCTACAGAA TTCCAAACAA CACGCGAACA CCCGAGATCT
1051 CAGGGGATTT GGCTGACGCC TCACAAACCT CCACATTGAA TGAAAAATCC
1101 CCAGGGCGAT CTGCAAGTCG ATCAAGTAAC ATTTCAAAAG CAAGCAGCCC
1151 AACAAACAGG ACAGCTCCCA GGAGCCAGTC AAGGTTGTCT GTCTGTCCAT
1201 CCACTCAGGA CATCTGCAGA ATCTGTCACT GCGAAGGGGA TGAAGAGAGC
1251 CCCCTCATCA CACCCTGTG CTGCACTGGG ACACTGCGCT TTGTCCACCA
1301 GCTCTGCTTC CACCACTGGA TAAAGAGCTC AGATAACGCG TGCTGTGAGC
1351 TCTGCAAGTA TGACTTCATA ATGGAGACCA AGCTCAAACC CCTCCGGAAG
1401 TGGGAGAAAC TACAGATGAC CACAAGTGA AGGAGGAAAA TATTCTGCTC
1451 TGTCACATTC CACGTAATCG CGATCACCTG TGTGGTTTGG TCTTTGTATG
1501 TATTGATAGA CCGGACAGCG GAGGAAATCA AGCAAGGCAA TGACAATGGT
1551 GTCCTTGAAT GGCCATTTTG GACAAAACCT GTTGTGGTAG CCATTGGCTT
1601 CACAGGAGGT CTTGTCTTCA TGTACGTACA GTGTAAAGTC TATGTTCACT
1651 TGTGGCGCAG GCTGAAGGCC TACAACCGTG TGATCTTTGT AAAAAATTGC
1701 CCAGACACTG CCAAAAAACT GGAGAAGAAC TTCTCATGTA ATGTAAACAC
1751 AGACATCAAA GATGCTGTGG TAGTGCCTGT ACCACAAACA GGTGCAAATT
1801 CACTGCCATC TGCAGAGGGT GGCCCCCTG AAGTTGTATC AGTCTGATGG
1851 AACCTGTTGG GAGTTTCTTC ACCGAAGAAT ATCTTTCTAG CCTCAGCCA
1901 CTACAAATGA CAGAAGTGAC CTTGAATTAT TTAATCCCTT CAGCTCCTCC
1951 TTTCTCCTAC TGACACATTT TTCCTGACTT TGTTCAAAGA GGAAAGGAGA
2001 AAAACAAACA AACAGACCAA ATGCCAGGGA GCCCATGAAG TAATAGCGTA
2051 AAGTAAAGTA TGATATGGAA ATGTGAAGTT TGCAAGAGAA TGATTTCCAA
2101 GACAATTAAG AACTACTGGG GCAATGAATG CTTTATAGGA GTAATCAAAG
2151 ATTAATGGA CCAATGATAC TCTTCTTAC AGTAACAGGG GAAAGTTTCA
2201 AGAATACAGA CTTGAATTGC GATGTGTATT ACTTCTAGGG CCTTGTAAATG
2251 TTAATCTGCT CATCTGGAAA TAATAACTAA CATATTGGT TTTAAGCCTG
2301 AAATTGTTCT GATTATCCCT AAGTCACATT GGAAGTGAAC TTGGAGGATG
2351 CATATTTTGA TATGCTTTGA CAGCTAACAG ATTTGTATGG TTTAGTGGAG
2401 TCTGGTTATT TTGACAGATG CATGTTTTTT TTAAATAGAT GCAATATACA
2451 TTTGAAGACA TTGATATTTG GAATTAATTA TGTTTGTTTA AGTCACGCAA
2501 AAGATTTTCA GAAATGTTC GGATATAATT AGCTCTGTGA AATACCCACA
2551 GAACTGTTAT CAGTCTTAT ATTTATTTTC ATCTGGTTCC TCTAATACAG
```

```
Query      160 LELLVVDEADLLFSFGFEEELKSLCHLP--RIYQAFLEMSATFNEDVQAL  207
HMM          ARrFMRNPiRInIdMdElTtnEnIkQwYiyVerEMWKfdCLcrLle*
          + +++NP+ + + +++L + ++Q+ +++E E++KF +L+ L++
Query      208 KELILHNPVTLKLQESQLPGPDQLQQFQVVCETEEKFLLLYALLK  253

HMM_NAME      Helicases conserved C-terminal domain
HMM          *EilleeWLknlGirvmYIHGdMpQeERdeIMddFNnGEynVLicTDV...
          +L+ +L++ I+++++ G +P + R I+ +FN+G Y++ I+TD+
Query      272 YRLRLFLEQFSIPTCVLNGELPLRSRCHIISQFNQGFYDCVIATDAEVL  320
HMM          .....ggRGIDIPdVNHVINYDMPWNPEqYI
          +RGID+ V+ V N+D+P +PE YI
Query      321 GAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNFDLPPTPEAYI  370
HMM          QRIGRTgRIG*
          +R+GRT+R++
Query      371 HRAGRTARAN  380
```



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[SUPFAM]      WW repeat homology 1e-26
[SUPFAM]      DEAD/H box helicase homology 1e-107
[SUPFAM]      unassigned DEAD/H box helicases 1e-107
[SUPFAM]      ATP-dependent RNA helicase DBP1 3e-31
[SUPFAM]      ATP-dependent RNA helicase DHH1 2e-35
[SUPFAM]      translation initiation factor eIF-4A 2e-38
[SUPFAM]      tobacco ATP-dependent RNA helicase DB10 1e-26
[PROSITE]     ATP_GTP_A      1
[PROSITE]     LEUCINE_ZIPPER 1
[PFAM]        Helicases conserved C-terminal domain
[PFAM]        DEAD and DEAH box helicases
[KW]          Alpha_Beta
[KW]          LOW_COMPLEXITY      9.87 %

SEQ      MEDSEALGFHEMGLDPRLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSGKTAA
SEG      .....
PRD      cccccccccccccchhhhhhhhhcccccccccccccccccccccccccccccccccccccc

SEQ      YAIPMLQLLLHRKATGPVVEQAVRGLVLVPTKELARQAQSMIQLATYCARDVRVANVSA
SEG      .....
PRD      ehhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      AEDSVSQRVLMKPDVVVGTPSRILSHLQQDSLKLKRLDSLELLVVDEADLLFSFGFEEEL
SEG      .....
PRD      ccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      KSLCHLPRYQAFILMSATFNEDVQALKELILHNPVTLKLOESQLPGPDQLQQFQVVCET
SEG      .....
PRD      hhhhhhhccccchhhhhhhhhccccchhhhhhhhhcccccccccccccccccccccccccccc

SEQ      EEDKFLLLYALLKLSLIRGKSLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSRCHI
SEG      .....
PRD      hhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      ISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNF
SEG      .....
PRD      hhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      DLPPTPEAYIHRAGRTARANNPGIVLTFVLPTQFHLGKIEELLSGENRGPILLPYQFRM
SEG      .....
PRD      cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccch

SEQ      EEIEGFRYRCRDAMRSVTKQAIAREARLKEIKEELLHSEKLKTYFEDNPRDLQLLRHDLPL
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhccc

SEQ      HPAVVVKPHLGHPDYLVPALRGLVRPHKKRKLSSSCRKAKRAKSONPLRSFKHKGKKF
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      RPTAKPS
SEG      .....
PRD      ccccccc

```

Prosites for DKFZphfbr2_82i24.1

PS00017	51->59	ATP_GTP_A	PD000017
PS00029	149->171	LEUCINE_ZIPPER	PD000029

Pfam for DKFZphfbr2_82i24.1

HMM_NAME	DEAD and DEAH box helicases		
HMM	*gLPWILRnIyeMGFEkPTPIQQAIPiILEGRDVMACAOTGSGKTAAF		
Query	13	GLDPRLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSGKTAAY	61
HMM	LIPMLQHIDwdP...WpqpPQdPrALILAPTRELAMQIEEcRkFgkHMn		
Query	62	AIPMLQLLLHRKATGPVVEQA-VRGLVLVPTKELARQAQSMIQLATYCA	110
HMM	g.IRImcIYGGtnMRdQMRmLeRGpPHIVATPGRLLIDHIERgtldLDr.		
Query	111	RDVRVANVSAEDSVSQRVLMKPDVVVGTPSRILSHLQQDSLKLKRLDS	159
HMM	IeMLVMDEADRLDMGFIDQIRrIMrqIPmpwNRQTMFSATMPdeIqEL		
	+E LV DEAD +++ GF++++ ++ ++P + Q + SAT+ +++Q L		

Query: 9 FEHMGLOPRLQAVTDLGWSRPTLIQEKAIPALEGKOLLARARTGSGKTAAYAI PMLQL 68
 F + LD R+L+AV LGW +PTLIQ AIPL LEGKD++ RARTGSGKTA YA+P++Q
 Sbjct: 11 FHELELDQRILKAVAQLGWQQPTLIQSTAIPLLEGKDVVRARTGSGKTATYALPLIQK 70

Query: 69 LLHRKATGPVVEQAVRGLVLPVKELARQAQSMIQQLATYCARDVRVANVS-AAEDSVSQ 127
 +L+ K EQ V +VL PTKEL RQ++ +I+QL C + VRVA+++ ++ D+V+Q
 Sbjct: 71 ILNSKLNAS--EQVSAVVLAPTKELCRQSRKVIEQLVESCGKVVRVADIADSSNDTVTQ 128

Query: 128 RAVLMEKPDVVVGTPSRILSHLQQDSLKLRLDSLELLVVDDEADLLFSFGFEEELKSLCHL 187
 R L E PD+VV TP+ +L++ + S+ +E LVVDEADL+F++G+E++ K L+ HL
 Sbjct: 129 RHALSESPDIVVATPANLLAYAEAGSVVDLKHVETLVVDEADLVFAYGYEKDFKRLIKHL 188

Query: 188 PRIYQAFILMSATFNEDVQALKELILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFL 247
 P IYQA L+SAT +DV +K L L+NPVTLKL+E +L DQL +++ E E DK +
 Sbjct: 189 PPIYQAVLVSATLTDDVVRMKGCLNNPVTLKLEEPQLVPODQLSHQRI LAE-ENDKPAI 247

Query: 248 LYALLKLSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSRCHIISQFNQG 307
 LYALLKL LIRGKS++FVN+++R Y++RLFLEQF I CVLN ELP R H ISQFN+G
 Sbjct: 248 LYALLKLRLIRGKSIIFVNSIDRCYKVRFLFLEQFGIRACVLNSEL PANIRIHTISQFNKG 307

Query: 308 FYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNFDLPPTPE 367
 YD +IA+D + P G + K ++ D E+ +RGIDF V+ V+NFD P
 Sbjct: 308 TYDIIIASDEHHMEKP--GGKSATNRKSPRSGDMESSASRGIDFQCVNNVINFDPRDVT 365

Query: 368 AYIHRAGRTARANNPGIVLTFVLPTEQFHLGKIEELL----SGENRGPIILPYQFRMEEI 423
 +YIHRAGRTAR NN G VL+V E +E+ L + + I+ YQF+MEE+
 Sbjct: 366 SYIHRAGRTARGNNKGSVLSFVSMKESKVNDSVEKKLCCSFAAQEGEQI IKNYQFKMEEV 425

Query: 424 EGFYRCRDAMRSVTKQAIAREARLKEIKEELLHSEKLKTYFEDNPRDLQLLRHDPLHPA 483
 E FRYR +D R+ T+ A+ + R++EIK E+L+ EKLK +FE+N RDLQ LRHD PL
 Sbjct: 426 ESFRYRAQDCWRAATRVAVHDTRIIEIKIEILNCEKCLKAFFEENKRDLQALRHDKPLRAI 485

Query: 484 VVKPHLGHVPDYLVPPALRGLV 505
 V+ HL +P+Y+VP AL+ +V
 Sbjct: 486 KVQSHLSDMPEYIVPKALKRVV 507

Pedant information for DKFZphfbr2_82i24, frame 1

Report for DKFZphfbr2_82i24.1

[LENGTH] 547
 [MW] 61589.88
 [PI] 9.34
 [HOMOL] TREMBL:AF017777_10 gene: "hlc"; product: "helicase"; *Drosophila melanogaster* tweety (tty), flightless (fli), dodo (dod), penguin (pen), small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox (bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs) genes, complete cds. 1e-121
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YLR276c] 1e-109
 [FUNCAT] j mrna translation and ribosome biogenesis [H. influenzae, HI0231 RNA] 2e-42
 [FUNCAT] 04.01.04 rna processing [S. cerevisiae, YLL008w] 8e-40
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YLL008w] 8e-40
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YLL008w] 8e-40
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YKR059w] 3e-39
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YKR059w] 3e-39
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YDL160c] 3e-35
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPL119c] 3e-29
 [FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YMR290c] 4e-29
 [FUNCAT] 1 genome replication, transcription, recombination and repair [H. influenzae, HI0892] 1e-27
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YJL033w] 2e-27
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YDR194c] 4e-21
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL064c] 1e-05
 [BLOCKS] BL00039D DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039C DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039B DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039A DEAD-box subfamily ATP-dependent helicases proteins
 [PIRKW] nucleus 4e-34
 [PIRKW] RNA binding 7e-41
 [PIRKW] DEAD box 2e-38
 [PIRKW] transmembrane protein 9e-20
 [PIRKW] DNA binding 8e-23
 [PIRKW] ATP 1e-107
 [PIRKW] purine nucleotide binding 2e-38
 [PIRKW] P-loop 1e-107
 [PIRKW] hydrolase 2e-35
 [PIRKW] protein biosynthesis 2e-38
 [PIRKW] ATP binding 7e-43

Entry HSG05793 from database EMBL:

human STS WI-6581.

Length = 206

Minus Strand HSPs:

Score = 992 (148.8 bits), Expect = 6.0e-38, P = 6.0e-38

Identities = 204/208 (98%), Positives = 204/208 (98%), Strand = Minus /
P1

Entry AC004938 from database EMBL:

Homo sapiens clone DJ0971C03; HTGS phase 1, 18 unordered pieces.

Score = 1269, P = 6.5e-202, identities = 269/282

12 exons Bp ~87920-93706 (matching 1-1497)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 10 bp to 1650 bp; peptide length: 547

Category: strong similarity to known protein

Classification: Nucleic acid management

Prosite motifs: ATP_GTP_A (51-59)

LEUCINE_ZIPPER (149-171)

```

1 MEDSEALGFE HMGLDPRLLQ AVTDLGWSRP TLIQEKAIP L ALEGKDLLAR
51 ARTGSGKTA YAIPMLQLLL HRKATGPEVVE QAVRGLVLVP TKELARQAQS
101 MIQQLATYCA RDVRVANVSA AEDSVSQRV LMEKPDVVVG TPRSILSHLQ
151 QDSLKLRLDSL ELLVVDEADL LFSFGFEEEL KSL LCHLPRI YQAF LMSATF
201 NEDVQALKEL ILHNPVTLKL QESQLPGPDQ LQOFQVVCET EEDKFLLLYA
251 LLKLSLIRGK SLLEFNTLER SYRLRLFLEQ FSIPTCVLNG ELPLRSRCHI
301 ISQFNQGFYD CVIATDAEVL GAPVKGKRRG RGPKGDKASD PEAGVARGID
351 FHHVSAVLNF DLPPTPEAYI HRAGRTARAN NPGIVLTFVL PTEQFHLGKI
401 EELLSGENRG PILLPYQFRM EEIEGFYRYC RDAMRSVTKQ AIREARLKEI
451 KEELLHSEKL KTYFEDNPRD LQLLRHDLPL HPAVVKPHLG HVPDYLVPPA
501 LRGLVRPHKK RKKLSSSCRK AKRAKSNPL RSFKHKGKKF RPTAKPS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82i24, frame 1

TREMBL:AF017777_10 gene: "hlc"; product: "helicase"; *Drosophila melanogaster* tweety (tty), flightless (fli), dodo (dod), penguin (pen), small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox (bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs) genes, complete cds., N = 1, Score = 1230, P = 3.2e-125

TREMBL:SPCC1494_6 gene: "SPCC1494.06c"; product: "atp dependent helicase"; *S.pombe* chromosome 11 cosmid cl494., N = 2, Score = 753, P = 2.5e-113

PIR:S51412 hypothetical protein YLR276c - yeast (*Saccharomyces cerevisiae*), N = 2, Score = 711, P = 8.2e-117

TREMBL:AF025451_2 gene: "C24H12.4"; *Caenorhabditis elegans* cosmid C24H12., N = 2, Score = 564, P = 2.7e-99

>TREMBL:AF017777_10 gene: "hlc"; product: "helicase"; *Drosophila melanogaster* tweety (tty), flightless (fli), dodo (dod), penguin (pen), small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox (bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs) genes, complete cds.
Length = 560

HSPs:

Score = 1230 (184.5 bits), Expect = 3.2e-125, P = 3.2e-125
Identities = 251/497 (50%), Positives = 344/497 (69%)

DKFZphfbr2_82i24

group: nucleic acid management

DKFZphfbr2_82i24 encodes a novel 547 amino acid protein with similarity to DEAD-box superfamily ATP-dependent helicases.

RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis.

The novel protein contains a DEAD-box an ATP/GTP-binding site motif A (P-loop, interacting with one of the phosphate groups of the nucleotide) and a leucine zipper. Mutations in the closely related *Drosophila* Hlc gene result in lethality in homozygotes. Therefore the new protein seems to be critical involved in RNA processing in eukaryotic cells.

The new protein can find application in modulating RNA metabolism and gene expression.

strong similarity to DEAD-box subfamily ATP-dependent helicase

complete cDNA, complete cds, EST hits
potential start at Bp 9 matches Kozak consensus PyNNatgG,
[PFAM] Helicases conserved C-terminal domain
[PFAM] DEAD and DEAH box helicases

Sequenced by DKFZ

Locus: /map="720_A_3; 758_H_4; 772_E_3; 804_A_5; 175.5 cR from topFT of Chr7 linkage group"

Insert length: 1860 bp

Poly A stretch at pos. 1850, polyadenylation signal at pos. 1829

```
1 AGCAGCGCCA TGGAGGACTC TGAAGCACTG GGCTTCGAAC ACATGGGCCT
51 CGATCCCCGG CTCTTCAGG CTGTCACCGA TCTGGGCTGG TCGCGACCTA
101 CGCTGATCCA GGAGAAGGCC ATCCCACTGG CCCTAGAAGG GAAGGACCTC
151 CTGGCTCGGG CCCGCACGGG CTCGGGAAG ACGGCCGCTT ATGCTATTCC
201 GATGCTGCAG CTGTTGCTCC ATAGGAAGGC GACAGGTCCG GTGGTAGAAC
251 AGGCAGTGAG AGGCCTTGTT CTGTTCCTA CCAAGGAGCT GGCACGGCAA
301 GCACAGTCCA TGATTCAGCA GCTGGCTACC TACTGTGCTC GGGATGTCCG
351 AGTGGCCAAAT GTCTCAGCTG CTGAAGACTC AGTCTCTCAG AGAGCTGTGC
401 TGATGGAGAA GCCAGATGTG GTAGTAGGGA CCCCATCTCG CATATTAAGC
451 CACTTGCAAGC AAGACAGCCT GAAACTTCGT GACTCCCTGG ACCTTTTGGT
501 GGTGGACGAA GGTGACCTTC TTTTTCCTT TGGCTTTGAA GAAGAGCTCA
551 ASAGTCTCCT CTGTCACTTG CCCCAGATT ACCAGGCTTT TCTCATGTCA
601 GCTACTTTTA ACGAGGACCT ACAAGCACTC AAGGAGCTGA TATTACATAA
651 CCCGGTTACC CTAAAGTTAC AGGAGTCCCA GCTGCCTGGG CCAGACCAGT
701 TACAGCAGTT TCAGGTGGTC TGTGAGACTG AGGAAGACAA ATTCTCTCTG
751 CTGTATGCCC TGCTCAAGCT GTCATTGATT CGGGGCAAGT CTCTGCTCTT
801 TGTC AACACT CTAGAACGGA GTTACCGGCT ACGCCTGTTC TTGGAACAGT
851 TCAGCATCCC CACCTGTGTG CTCAATGGAG AGCTTCCACT GCGCTCCAGG
901 TGCCACATCA TCTCACAGTT CAACCAAGGC TTCTACGACT GTGTCATAGC
951 AACTGATGCT GAAGTCCTGG GGGCCCCAGT CAAGGGCAAG CGTCGGGGCC
1001 GAGGGCCCCA AGGGGACAAG GCCTCTGATC CGGAAGCAGG TGTGGCCCCG
1051 GGCATAGACT TCCACCATGT GTCTGCTGTG CTCAACTTTG ATCTTCCCCC
1101 AACCCCTGAG GCCTACATCC ATCGAGCTGG CAGGACAGCA CGCGCTAACA
1151 ACCCAGGCAT AGTCTTAACC TTTGTGCTTC CCACGGAGCA GTTCCACTTA
1201 GGCAAGATTG AGGAGCTTCT CAGTGGAGAG AACAGGGGCC CCATTCTGCT
1251 CCCCTACCAG TCCCGGATGG AGGAGATCGA GGGCTTCCGC TATCGCTGCA
1301 GGGATGCCAT GCGCTCAGTG ACTAAGCAGG CCATTGCGGA GGCAAGATTG
1351 AAGGAGATCA AGGAAGAGCT TCTGCATTCT GAGAAGCTTA AGACATACTT
1401 TGAAGACAAC CCTAGGGACC TCCAGCTGCT GCGGCATGAC CTACCTTTGC
1451 ACCCCGAGT GGTGAAGCCC CACCTGGGCC ATGTTCTCTG CTACCTGGTT
1501 CCTCTCTGTC TCCGTGGCCT GGTACGCCT CACAAGAAGC GGAAGAAGCT
1551 GTCTTCTCTT TGTAGGAAGG CCAAGAGAGC AAAGTCCAG AACCCACTGC
1601 GCAGCTTCAA GCACAAAGGA AAGAAATTCA GACCCACAGC CAAGCCCTCC
1651 TGAGGTTGTT GGGCCTCTCT GGAGCTGAGC ACATTGTGGA GCACAGGCTT
1701 ACACCCCTCG TGGACAGGCG AGGCTCTGGT GCTTACTGCA CAGCCTGAAC
1751 AGACAGTTCT GGGGCCGGCA GTGCTGGGCC CTTAGCTTCC TTGGCACTTC
1801 CAAGCTGGCA TCTTGCCCTT TGACAACAGA ATAAAAATTT TAGCTGCCCC
1851 AAAAAAAAAA
```

BLAST Results

```

[EC]          3.6.1.37 Na+/K+-exchanging ATPase 6e-08
[PIRKW]       transmembrane protein 1e-09
[PIRKW]       hydrolase 6e-08
[PROSITE]     ATP1G1_PLM_MAT8      1
[PROSITE]     MYRISTYL      1
[PROSITE]     CK2_PHOSPHO_SITE      1
[PROSITE]     TYR_PHOSPHO_SITE      1
[PROSITE]     PKC_PHOSPHO_SITE      2
[PROSITE]     ASN_GLYCOSYLATION      1
[KW]          Alpha_Beta
[KW]          SIGNAL_PEPTIDE 19

```

```

SEQ    MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSR
PRD    ccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccc

```

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SEQ    CKCSFNQKPRAPGDEEAQVENLITANATEPQKAEN
PRD    hhhccccccccccccchhhhhhhhhhhcccccccccc

```

Prosites for DKFZphfbr2_82i17.2

PS00001	86->90	ASN_GLYCOSYLATION	PDOC00001
PS00005	36->39	PKC_PHOSPHO_SITE	PDOC00005
PS00005	58->61	PKC_PHOSPHO_SITE	PDOC00005
PS00006	19->23	CK2_PHOSPHO_SITE	PDOC00006
PS00007	25->33	TYR_PHOSPHO_SITE	PDOC00007
PS00008	41->47	MYRISTYL	PDOC00008
PS01310	28->42	ATP1G1_PLM_MAT8	PDOC01014

(No Pfam data available for DKFZphfbr2_82i17.2)

Medline entries

91250422:

Purification and complete sequence determination of the major plasma membrane substrate for cAMP-dependent protein kinase and protein kinase C in myocardium.

95091702:

Protein kinase C and cyclic AMP-dependent protein kinase phosphorylate phospholemman, an insulin and adrenaline-regulated membrane phosphoprotein, at specific sites in the carboxy terminal domain.

95138184:

Mat-8, a novel phospholemman-like protein expressed in human breast tumors, induces a chloride conductance in *Xenopus* oocytes.

Peptide information for frame 2

1 MELVLVFLCS LLAPMVLASA AEKEKEMDPF HYDYQTLRIG GLVFAVVLFS
51 VGILLILSRR CKCSFNQKPR APGDEEAQVE NLITANATEP QKAEN

ORF from 32 bp to 316 bp; peptide length: 95
Category: strong similarity to known protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82i17, frame 2

SWISSPROT:PLM_HUMAN PHOSPHOLEMMAN PRECURSOR., N = 1, Score = 196, P = 1.2e-15

TREMBL:AF091390_1 product: "phospholemman precursor"; *Mus musculus* phospholemman precursor, gene, complete cds., N = 1, Score = 187, P = 1.1e-14

PIR:A40533 cAMP-dependent protein kinase major membrane substrate precursor - dog, N = 1, Score = 189, P = 6.5e-15

SWISSPROT:PLM_RAT PHOSPHOLEMMAN PRECURSOR., N = 1, Score = 185, P = 1.7e-14

>SWISSPROT:PLM_HUMAN PHOSPHOLEMMAN PRECURSOR.
Length = 92

HSPs:

Score = 196 (29.4 bits), Expect = 1.2e-15, P = 1.2e-15
Identities = 43/85 (50%), Positives = 56/85 (65%)

Query: 4 VLVLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKC 63
+LVF LL +AE KE DPF YDYQ+L+IGGLV A +LF +GIL++LSRRC+C
Sbjct: 7 ILVFCVGLT---MAKAESPKEHDPFTYDQSLQIGGLVIAGILFILGILIVLSRRRC 62

Query: 64 SFNQKPRA--PGDEEAQVENLITANAT 88
FNQ+ R P +EE + I +T
Sbjct: 63 KFNQQQRTGEPDEEEGTFRSSIRRLST 89

Pedant information for DKFZphfbr2_82i17, frame 2

Report for DKFZphfbr2_82i17.2

[LENGTH] 95
[MW] 10542.37
[pI] 5.05
[HOMOL] SWISSPROT:PLM_HUMAN PHOSPHOLEMMAN PRECURSOR. 3e-15
[BLOCKS] BL01310

DKFZphfbr2_82i17

group: signal transduction

DKFZphfbr2_82i17 encodes a novel 334 amino acid protein with similarity to the plasma membrane substrate for the cAMP-dependent protein kinase.

The novel protein is a transmembrane protein with strong similarity to the phospholemman protein, a membrane substrate for the cAMP-dependent protein kinase. It seems to serve as a chloride channel or as a chloride-channel regulator.

The new protein can find application in modulating/blocking cAMP-dependent protein kinase-dependent pathways.

similarity to plasma membrane substrate for cAMP-dependent protein kinase

complete cDNA, complete cds, EST hits
potential start at Bp 31 matches Kozak consensus PyNNatG
might be a SODIUM/POTASSIUM-TRANSPORTING ATPASE
TRANSMEMBRANE 1

Sequenced by DKFZ

Locus: /map="11; 920_E_12; 786_(A,H)_11; (797,802)_(E,H)_7"

Insert length: 1647 bp

Poly A stretch at pos. 1637, polyadenylation signal at pos. 1615

```

1 AGTCTCGGAG GGGACCGGCT GTGCAGACGC CATGGAGTTG GTGCTGGTCT
51 TCCTCTGCAG CCTGCTGGCC CCCATGGTCC TGGCCAGTGC AGCTGAAAAG
101 GAGAAGGAAA TGGACCTTT TCATTATGAT TACCAGACCC TGAGGATTGG
151 GGGACTGGTG TTCGCTGTGG TTCTCTTCTC GGTGGGATC CTCTTATCC
201 TAAGTCGCAG GTGCAAGTGC AGTTTCAATC AGAAGCCCGG GGGCCAGGA
251 GATGAGGAAG CCCAGGTGGA GAACCTCATC ACCGCCAATG CAACAGAGCC
301 CCAGAAAGCA GAGAACTGAA GTGCAGCCAT CAGGTGGAAG CCTCTGGAAC
351 CTGAGGCGGC TGCTTGAACC TTTGGATGCA AATGTCGATG CTTAAGAAAA
401 CCGGCCACTT CAGCAACAGC CCTTTCCCCA GGAGAAGCCA AGAACTTGTG
451 TGTCCCCCAG CCTATCCCTT CTAACACCAT TCCTCCACCT GATGATGCAA
501 CTAACACTTG CCTCCCCGCT GCAGCCTGTG GTCTGCCCCA CTTCCCGTGA
551 TGTGTGTGTG TGTGTGTGTG TGTGTGACTG TGTGTGTTTG CTAAGTGTGG
601 TCTTTGTGGC TACTTGTGTT TGGATGGTAT TGTGTTTGT AGTGAAGTGT
651 GGACTCGCTT TCCCAGGCAG GGGCTGAGCC ACACGGCCAT CTGCTCCTCC
701 CTGCCCCCGT GGCCCTCCAT CACCTTCTGC TCCTAGGAGG CTGCTTGTG
751 CCCGAGACCA GCCCCCTCCC CTGATTTAGG GATGCGTAGG GTAAGAGCAC
801 GCGCACTGGT CTTCACTCGT CTGGGACCT GCGAAGGTTT GCAGCACTTT
851 CTCATCATTC TTCATGGACT CCTTCACTC CTTAACAACA AACCTTGCTT
901 CTTTATCCCA CTGATCCCA GTCTGAAGGT CTCTTAGCAA CTGGAGATAC
951 AAAGCAAGGA GCTGGTGAGC CCAGCGTTGA CGTCAGGCAG GCTATGCCCT
1001 TCCGTGGTTA ATTTCTTCCC AGGGGCTTCC ACAGAGAGTC CCCATCTGCC
1051 CCGCCCCCTT ACAGAGCGCC CGGGGATTCC AGGCCAGGG CTCTACTCT
1101 GCCCCCTGGG AATGTGTCCC CTGCATATCT TCTCAGCAAT AACTCCATGG
1151 GCTCTGGGAC CTAACCCCTT CCAACCTTCC CTGCTTCTGA GACTTCAATC
1201 TACAGCCCAG CTCATCCAGA TGCAGACTAC AGTCCCTGCA ATTGGGTCTC
1251 TGGCAGGCAA TAGTTGAAGC ACTTCTGTT CCGTTGGGGC CAGCACACCG
1301 GGATGGATGG AGGGAGAGCA GAGGCCTTTG CTCTCTGCC TACGTCCCCT
1351 TAGATGGGCA GCAGAGGCAA CTCCCGCATC CTTTGTCTG CTTGTCACTG
1401 GTCAGAGCGG TGAGCGAGGT GGGTTGGAGA CTCAGCAGGC TCCGTGCAGC
1451 CCTTGGGAAC AGTGAGAGGT TGAAGGTCAT AACGAGAGTG GGAAGTCAAC
1501 CCAGATCCCG CCCCTCCTGT CCTCTGTGTT CCCGCGGAAA CCAACCAAAC
1551 CGTGGCGTGT GACCCATTGC TGTCTCTGT ATCGTGACCT ATCCTCAACA
1601 ACAACAGAAA AAAGGAATAA AATATCCTTT GTTCTCTAAA AAAAAAA

```

BLAST Results

Entry HS31455 from database EMBL:

human STS WI-2739.

Length = 103

Minus Strand HSPs:

Score = 487 (73.1 bits), Expect = 4.4e-14, P = 4.4e-14

Identities = 101/104 (97%), Positives = 101/104 (97%), Strand = Minus /

Plus

frame shift in primer binding site

BNSDOCID: <WO__0112659A2_I_>

Entry HS727347 from database EMBL:
 human STS WI-16589.
 Length = 275
 Plus Strand HSPs:
 Score = 1365 (204.8 bits), Expect = 3.0e-55, P = 3.0e-55
 Identities = 275/276 (99%), Positives = 275/276 (99%), Strand = Plus /
 Pl

Medline entries

No Medline entry

Peptide information for frame 3

1 MSSEPPPPYP GGPTAPLLEE KSGAPPTPGR SSPAVMQPPP GMPPLPPADIG
 51 PPPYEPPGHP MPQPGFIPPH MSADGTYMPP GFYPPPGPHP PMGYPPPGPY
 101 TPGPYPGPGG HTATVLVPSG AATTVTVLQG EIFEGAPVQT VCPHCQQAIA
 151 TKISYEIGLM NFVLGFFCCF MGCDLGCCLI PCLINDFKDV THTCPSCKAY
 201 IYTYKRLC

ORF from 177 bp to 800 bp; peptide length: 208
 Category: similarity to known protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phfbr2_82q14, frame 3

PIR:S57447 HPBRII-7 protein - human, N = 1, Score = 206, P = 8.4e-16

PIR:A47655 spliceosome-associated protein SAP 62 - human, N = 1, Score
 = 198, P = 4.3e-15

>PIR:S57447 HPBRII-7 protein - human
 Length = 551

HSPs:

Score = 206 (30.9 bits), Expect = 8.4e-16, P = 8.4e-16
 Identities = 57/115 (49%), Positives = 62/115 (53%)

Query: 5 PPPPYPGGPTAPLLEEKSGAPPTPGRSSPAVMQPPPGMPLPPADIGPP-----PYEP--- 56
 P P P P G T P G P P G P P P P G L P P G P P
 Sbjct: 226 P P P P P A G Q T P P R P L G P P G P P G P P P P P G Q V L P P P L A G P P N R G D R P P P P V L F 279

Query: 57 PGHPMPQP--GFIPPHMSADGTYMP--PGFYPPPGPHPPM-GYYPP-GPYTPGPYPGPGGH 111
 P G P Q P G + P P G P P G + P P P G P P G P P G P + P P P G P G
 Sbjct: 280 P G Q P F G Q P P L G P L P P G P P P P V P G Y G P P P P P P Q G P P P P P G P F P P R P - P G P L G P 333

Query: 112 TATVLVP 118

T+ P
 Sbjct: 334 PLTLAPP 340

Score = 177 (26.6 bits), Expect = 1.1e-12, P = 1.1e-12
 Identities = 55/120 (45%), Positives = 61/120 (50%)

Query: 5 PPPPYPGGPTAP--LLEEKSGAPPTPGRSSPAVM---QP---PPGMPLPPADIGPPPYE 55
 P P P P G P P + L P P G R P V + Q P P P P L P P G P P P
 Sbjct: 244 P G P P G P P P P P G Q V L P P P L A G P P N R G D R P P P P V L F P G Q P F G Q P P L G P L P P G P P P - P 299

Query: 56 PPGHPMPQPGFIPPHMSADGTYMPPGFYPP--PGP-HPPMGYYPPGPYTGPYPG---PG 109
 P G + P P G P P G P P G + P P P G P P + P P P + P G P P G P
 Sbjct: 300 V P G Y G - P P P G P P P P Q --- G P P P P P G P F P P R P P G P L G P P L T L A P P - P H L P G P P P G A P P P A 354

Query: 110 GHTATVLVP 118

H P
 Sbjct: 355 PHVNPAFFP 363

Score = 168 (25.2 bits), Expect = 1.1e-11, P = 1.1e-11
 Identities = 47/118 (39%), Positives = 51/118 (43%)

Query: 5 PPPPYPG-GPTAPLLEEKSGAPPTPGRSSPAVMQP--PPGMPLPPADI-GPPPYEPPGHP 60

DKF2phfbr2_82g14

group: transmembrane protein

DKF2phfbr2_82g14 encodes a novel 208 amino acid proline-rich protein without similarity to known proteins.

The protein contains one transmembrane domain.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

unknown prolin rich protein

membrane regions: 1

Summary DKF2phfbr2_82g14 encodes a novel 208 amino acid protein.

unknown prolin rich protein

complete cDNA, complete cds, EST hits

TRANSMEMBRANE 1

Sequenced by DKF2

Locus: /map="26.2 cR from top of Chr16 linkage group"

Insert length: 2059 bp

Poly A stretch at pos. 2049, polyadenylation signal at pos. 2024

```
1 AGAAGTGC GA CTGCCAGCTG CCGAGGCGTT CGGTCTCTGCT GTTGCGGGCCG
51 CTGCCCCAGG GCTGCGGGGA CGCTCCCGGA GCCCTGCCTG TCCCTGTGCC
101 ATCCAGGCCA GCAGCTGAAG GAGCCTCACC TGCCTCCCTT CTCTGAGTAG
151 CACGGATTTC AGGAGAAGCA GCGAAGATGT CCAGCGAGCC TCCCCCTCCT
201 TATCCTGGGG GCCCACAGC CCCACTTCTG GAAGAGAAAA GTGGAGCCCC
251 GCCCACCCCA GCGCGTTCCCT CCCAGCTGTG GATGCAGCCC CCTCCAGGCA
301 TGCCACTGCC CCTGCGGGAC ATTGGCCCCC CACCCTATGA GCCGCCGGGT
351 CACCCAATGC CCCAGCCTGG CTTTCATCCA CCACACATGA GTGCAGATGG
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651 TTGATGAATT TCGTGCTGGG TTTCTTCTGT TGCTTCATGG GATGTGATCT
701 GGGCTGCTGC CTGATCCCCT GCCTCATCAA TGACTTCAAG GATGTGACGC
751 ACACATGCCC CAGCTGCAAA GCCTACATCT ACACGTACAA GCGCCTGTGC
801 TAACGGAGCT GGAAGTCGGG ACTCCCCGCC CTGTCACTCT GGCCCCCTGT
851 GCTTTGCTCC CTGCGCTCAG TGGTCACTTT CCGCTCCCA CTGGGGGCTG
901 GGAGCCGTGC CACCATCCCC TAGAAGTCCT GTCTCTTCA CCCTGCCCTA
951 CCTGAGCCGC TGACTCTTCT GGCAAAAATT CTGTTGGGAT TTAAGGCCAA
1001 GGGTCAGTGG GTGGCAGGGG GCTGGCAATG AGCTGTGTG TTGTTGGTCT
1051 GCTTGGTGTG TGTGATCGGG AAGATAAGCT GGGAGGGGTC TCCTGCTGGG
1101 GTCCTGATGC CTCTGTTTCC AAACAAGGTA CAGGTTCACT CCAGACTCTT
1151 TCCCCCTGGG ACCAACAGCA GCCAGAGCAG TTAGCCAGTT AGTCCCCAGG
1201 CCTGTGGCCA CAGGCGTTTC TGACCTGCTG GGCCGAGAAT GGGTAAGTTG
1251 TCTGGAGTCA GGTGGGCCCCA CGTAGGACAG GGTACAAAAG CCTGGGTTTG
1301 TTTCTGGGTA CTTTGCGCCT CTGGGGTGCT AGAGGTGGGG CATGGTGGCT
1351 GGAAGTAAAA CTGCCAACTC TGGCCCTCAG AACTCTCAGG TATAGAAGCC
1401 CAGGATGTCT AATACCCTGT CCCAGTGCCC GAGAGCTGCC TGGTGTGAGG
1451 TAGAGAGGAC ACTGTACCTG GGTGAATGAT CAGACCCTGG TAGCTAAGAA
1501 GGAAGTTGTC CTTTGAGTC AGTGTGCAGA CCCCCTTTCA GGCCATGCCT
1551 CTGTGAACCC TGTATTGCTG GGGCCGGAAG GAGCCCCTGA GCCTAGCCCC
1601 TTCCCGTCTG CCCTGTGTCC TCACTGCGTG TGGGTATGAC CTCTGCCTGG
1651 TGGCTGGTGT ATCCCAACTG GGCAAGAGAT GGCAGAGGGT CCCCCTTGTG
1701 GGTGCGCTTG GATGTGCAGA GCCTTCTCCA TGGATTTTCT TCCCTGTAAG
1751 TGCCGGGGCC CCCACCCAGC CTGACAGGCT GTTGCTGTGC CTGCTCACAC
1801 CTGCTCCTGC AGGCACACTG GGCTAGGGAC GAGGAAGGAG CAGCCACAAG
1851 TGGTAGAACT GCCTTGGTGG ACACCAGCCT CGCCCTGTCT TTATTTCTCT
1901 AATGGTTTGT GAACTTGCTC ACCTGGACCA CTGTATCCTG CCACTGTCTT
1951 TCCTGGTCTC GCACTGCCAC TGCAATGGCTT CCTGTCACTG TGAATCGTGG
2001 CCCAGTCTCA GTTTGTAGTT TCTCATTAAA TTGGCCCTTT CACTCCCCCA
2051 AAAAAAAA
```

BLAST Results

```

SEQ   ATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPTTQS
SEG   .....
1a06- .....

SEQ   SAMLATKAAATPEPAMAQPDSTAPEGATGQAPPSSKGEEAAGYAQESQREEAS
SEG   .....
1a06- .....

```

Prosites for DKFZphfbr2_82e4.1

PS00005	21->24	PKC_PHOSPHO_SITE	PDOC00005
PS00005	46->49	PKC_PHOSPHO_SITE	PDOC00005
PS00005	51->54	PKC_PHOSPHO_SITE	PDOC00005
PS00005	91->94	PKC_PHOSPHO_SITE	PDOC00005
PS00005	103->106	PKC_PHOSPHO_SITE	PDOC00005
PS00005	118->121	PKC_PHOSPHO_SITE	PDOC00005
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00005	264->267	PKC_PHOSPHO_SITE	PDOC00005
PS00005	394->397	PKC_PHOSPHO_SITE	PDOC00005
PS00005	454->457	PKC_PHOSPHO_SITE	PDOC00005
PS00005	467->470	PKC_PHOSPHO_SITE	PDOC00005
PS00006	7->11	CK2_PHOSPHO_SITE	PDOC00006
PS00006	91->95	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	118->122	CK2_PHOSPHO_SITE	PDOC00006
PS00006	248->252	CK2_PHOSPHO_SITE	PDOC00006
PS00006	313->317	CK2_PHOSPHO_SITE	PDOC00006
PS00006	336->340	CK2_PHOSPHO_SITE	PDOC00006
PS00006	442->446	CK2_PHOSPHO_SITE	PDOC00006
PS00006	455->459	CK2_PHOSPHO_SITE	PDOC00006
PS00006	467->471	CK2_PHOSPHO_SITE	PDOC00006
PS00007	456->464	TYR_PHOSPHO_SITE	PDOC00007
PS00007	127->136	TYR_PHOSPHO_SITE	PDOC00007
PS00008	260->266	MYRISTYL	PDOC00008
PS00008	321->327	MYRISTYL	PDOC00008
PS00008	324->330	MYRISTYL	PDOC00008
PS00009	59->63	AMIDATION	PDOC00009

Pfam for DKFZphfbr2_82e4.1

HMM_NAME	Eukaryotic protein kinase domain		
HMM	*YeigRiIGeGsFGtVYkCiWr.TGeIVAIIkkrsms.....FlREIq		
Query	24	YDLGQVIKTEEFCEIFRAKDKTTGKLTCKKFKQRDGRKVRKAAKNEIG	72
HMM	IMRrLnHPNITRFYDwFedddDHIYMIMEYMeGGDLFDYIrrngpMsEwe		
Query	73	ILKMKVHKPNILQLVDVFEV-TRKEYFIFLELATGREVFDWILDQGYYSERD	121
HMM	IrfIMyQILrGMeYLHSMgIIHRDLKPENILIDeN...gqIKIcDFGLAR		
Query	122	TSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAK	171
HMM	qMnnYerMttfCGTPWY*		
Query	172	LEN--GLIKEPCGTPEY	186
HMM	*GepPFYd.....dnMemImrIqrfrrpfWpnCSeElyDFMr		
Query	188	GNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSFYWDDISQAADLVT	236
HMM	wCwnyDPekRPTFrQILnHPWF*		
Query	237	RLMEVEQDQRITAEAAISHEWI	258

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 [PIRKW] glycoprotein 4e-19
 [PIRKW] skeletal muscle 3e-28
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 [PIRKW] signal transduction 1e-21
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 [PIRKW] purine nucleotide binding 5e-25
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 [SUPFAM] immunoglobulin homology 7e-31
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 [SUPFAM] protein kinase SPK1 3e-20
 [SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 2e-36
 [SUPFAM] Ca2+/calmodulin-dependent protein kinase 3e-45
 [SUPFAM] calmodulin repeat homology 5e-29
 [SUPFAM] protein kinase DUN1 2e-24
 [SUPFAM] Dictyostelium cAMP-dependent protein kinase catalytic chain 1e-14
 [SUPFAM] death-associated protein kinase 2e-31
 [SUPFAM] myosin-light-chain kinase, nonmuscle 1e-29
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 [SUPFAM] ankyrin repeat homology 2e-31
 [SUPFAM] protein kinase homology 8e-66
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 [SUPFAM] twitchin 1e-18
 [SUPFAM] protein kinase C zinc-binding repeat homology 1e-16
 [SUPFAM] titin 4e-19
 [SUPFAM] protein kinase cdrl 2e-20
 [SUPFAM] kinase-related transforming protein 2e-38
 [SUPFAM] Ca2+/calmodulin-dependent protein kinase I 8e-66
 [SUPFAM] kinase interaction domain homology 2e-24
 [SUPFAM] protein kinase C mu 1e-16
 [PROSITE] AMIDATION 1
 [PROSITE] MYRISTYL 3
 [PROSITE] CK2_PHOSPHO_SITE 10
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 11
 [PFAM] Eukaryotic protein kinase domain
 [KW] All_Alpha
 [KW] 3D
 [KW] LOW_COMPLEXITY 7.40 %

SEQ MPFGCVTLGDKKNYNQPSVETDRYDLGQVIKTEEFCEIFRAKDKTGKLTCKKFQKROG
 SEG
 1a06-CEETTTGGGCCEEEEEEBCGGGGGEEEEETTTTCEEEEEEEEC---

 SEQ RKVRKAAKNEIGILKMVKHPNQLQVDFVTRKEYFIFLELATGREVFDWILDQGYYSER
 SEG
 1a06- -----HHHHHHHHHCCTTTBCEEEEEEEETEEEEEECCCCCEHHHHHHHTTTTBHH

 SEQ DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP
 SEG
 1a06- HHHHHHHHHHHHHHHHHHHHCCTTTTTEEECCCTTTTCEEECCCTTTTCHHHHHHCCC

 SEQ CGTPEYLGNNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSFYWDDISQAADLVTRLME
 SEG
 1a06- HHHHHHHHCCTTTT-----THHHHHHHHHCCCCCTTTTTCCHHHHHHHHHHCT

 SEQ VEQDQRITAEAEISHEWISGNAASDKNIKDGVCQAIEKNFARAKWKKAVRVTTLMKRLRA
 SEG
 1a06- TTGGGCCCHHHHHHTTTTTCCTCCCCBHHHHHHHHHHHHHCCTTTTBTBHHHHHHHC..

 SEQ PEQSSTAAAQASATDTATPGAAGGATAAAASGATSAPEGDAARAASDNVAPADRSATP
 SEG
 1a06-

[FUNCAT] 11.01 stress response [S. cerevisiae, YDR477w] 3e-19
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDR477w] 3e-19
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YPL141c] 1e-16
[FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YMR001c] 3e-16
[FUNCAT] 03.13 meiosis [S. cerevisiae, YOR351c] 1e-15
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YDR122w] 3e-14
[FUNCAT] 10.03.11 key kinases [S. cerevisiae, YCR073c] 6e-11
[FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YNR031c] 8e-11
[FUNCAT] 10.02.11 key kinases [S. cerevisiae, YJL095w] 2e-09
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR362w] 1e-08
[FUNCAT] 10.05.11 key kinases [S. cerevisiae, YLR362w] 1e-08
[FUNCAT] 10.04.11 key kinases [S. cerevisiae, YLR362w] 1e-08
[FUNCAT] 02.19 metabolism of energy reserves (glycogen, trehalose) [S. cerevisiae, YPL031c] 7e-08
[FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YPL031c] 7e-08
[FUNCAT] 01.04.04 regulation of phosphate utilization [S. cerevisiae, YPL031c] 7e-08
[FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YFL033c] 1e-07
[FUNCAT] 04.99 other transcription activities [S. cerevisiae, YFL033c] 1e-07
[FUNCAT] 10.05.09 regulation of g-protein activity [S. cerevisiae, YBL016w] 5e-07
[FUNCAT] 05.07 translational control [S. cerevisiae, YDR283c] 8e-07
[FUNCAT] 01.06.10 regulation of lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YHR079c] 5e-06
[FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YHR079c] 5e-06
[FUNCAT] 30.01 organization of cell wall [S. cerevisiae, YIR019c] 1e-05
[FUNCAT] 30.90 extracellular/secretion proteins [S. cerevisiae, YIR019c] 1e-05
[FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae, YIR019c] 1e-05
[FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YDL108w] 1e-05
[FUNCAT] 01.02.04 regulation of nitrogen and sulphur utilization [S. cerevisiae, YNL183c] 8e-05
[FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL183c] 8e-05
[FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDR523c] 2e-04
[FUNCAT] c energy conversion [M. genitalium, MG109] 3e-04
[BLOCKS] BL00107A Protein kinases ATP-binding region proteins
[BLOCKS] BL00939F
[SCOP] dlgol_ 5.1.1.1.9 MAP kinase Erk2 [rat Rattus norvegicus] 3e-62
[SCOP] dlwfc_ 5.1.1.1.8 MAP kinase p38 [human (Homo sapiens)] 5e-59
[SCOP] dlkoa_ 5.1.1.1.7 (1-350) Twitchin, kinase domain [Caenorhabditis] 1e-75
[SCOP] dlkoba_ 5.1.1.1.6 Twitchin, kinase domain [California sea hare] 1e-72
[SCOP] dlphk_ 5.1.1.1.5 gamma-subunit of glycogen phosphorylase kinase 4e-65
[SCOP] dlirk_ 5.1.1.2.4 insulin receptor [Human (Homo sapiens)] 2e-56
[SCOP] dlapme_ 5.1.1.1.4 cAMP-dependent PK, catalytic subunit [mouse (Mus musculus)] 4e-71
[SCOP] dlfgka_ 5.1.1.2.3 Fibroblast growth factor receptor 1 [human (Homo sapiens)] 1e-50
[SCOP] dlydre_ 5.1.1.1.3 cAMP-dependent PK, catalytic subunit [bovine (Bos taurus)] 3e-70
[SCOP] dlfmk_ 5.1.1.2.2 (168-437) c-src tyrosine kinase [human (Homo sapiens)] 5e-49
[SCOP] dlcdkb_ 5.1.1.1.2 cAMP-dependent PK, catalytic subunit [pig (Sus scrofa)] 2e-72
[SCOP] d2hcka_ 5.1.1.2.1 (167-437) Haemopoietic cell kinase Hck [human (Homo sapiens)] 5e-46
[SCOP] dlcsn_ 5.1.1.1.11 Casein kinase-1, CK1 [Schizosaccharomyces pombe] 9e-42
[SCOP] dljsua_ 5.1.1.1.1 Cyclin-dependent PK [Human (Homo sapiens)] 1e-56
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[PIRKW] transferase 8e-30
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[PIRKW] phorbol ester binding 1e-16
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[PIRKW] cell cycle control 2e-20
[PIRKW] serine/threonine-specific protein kinase 8e-66
[PIRKW] phospholipid binding 1e-16
[PIRKW] autophosphorylation 8e-66
[PIRKW] brain 1e-14
[PIRKW] heterotetramer 2e-16
[PIRKW] polymer 3e-29
[PIRKW] mitosis 2e-20
[PIRKW] magnesium 7e-22
[PIRKW] ATP 8e-66
[PIRKW] alternative initiators 1e-29

TREMBLNEW:FRU010348_3 product: "calmodulin binding protein kinase";
Fugu rubripes UBE1-like gene, PRGFR2 gene and gene encoding calmodulin
binding protein kinase, clone 168J21, N = 2, Score = 846, P = 2.6e-139

TREMBL:RNPRKI_1 product: "protein kinase I"; Rattus norvegicus
calcium/calmodulin-dependent protein kinase I mRNA, complete cds., N =
2, Score = 364, P = 5.1e-63

>PIR:I56542 calmodulin-binding protein - rat
Length = 504

HSPs:

Score = 1246 (186.9 bits), Expect = 4.0e-228, Sum P(2) = 4.0e-228
Identities = 255/289 (88%), Positives = 259/289 (89%)

Query: 188 GNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSFYWDDISQAAKDLVTRLMEVEQDQRI 247
GNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSFYWDDISQAAKDLVTRLMEVEQDQRI
Sbjct: 216 GNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSFYWDDISQAAKDLVTRLMEVEQDQRI 275

Query: 248 TAEAAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTA 307
TAEAAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQS TA
Sbjct: 276 TAEAAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSGTA 335

Query: 308 AAQSASATDTATPGAAGGATAAAASGATSAP-----GDAARAASDNVAPADRSAT 359
A +D ATPGAAGGA AAAA GA A GDA AAKSD++A ADRSAT
Sbjct: 336 AT-----SDAATPGAAGGAVAAAAGGAAPASGASATVGTGGDAGCAAKSDDMASADRSAT 390

Query: 360 PATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPTTQ 419
PATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVP Q
Sbjct: 391 PATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPAQ 450

Query: 420 SSAMLATKAAATPEPAMAQPDSTAPEGATGQAPPSSKGEEAAGYAQESQREEAS 473
SSA A KAAATPEPA+AQPDSTA EGATGQAPPSSKGEEA G AQESQR E S
Sbjct: 451 SSAAPAAKAAATPEPAVAQPDSTALEGATGQAPPSSKGEEATGCAQESQRVETS 504

Score = 978 (146.7 bits), Expect = 4.0e-228, Sum P(2) = 4.0e-228
Identities = 186/187 (99%), Positives = 187/187 (100%)

Query: 1 MPFGCVTLGDKKNYNQPSVETDRYDLGQVKTKEEFCEIFRAKDKTGKLHTCKKFQKRDG 60
MPFGCVTLGDKKNYNQPSVETDRYDLGQV+KTEEFCEIFRAKDKTGKLHTCKKFQKRDG
Sbjct: 1 MPFGCVTLGDKKNYNQPSVETDRYDLGQVVKTEEFCEIFRAKDKTGKLHTCKKFQKRDG 60

Query: 61 RKVRKAAKNEIGILKMVKHPNQLQVDFVTRKEYFIFLELATGREVFDWILDQGYYSER 120
RKVRKAAKNEIGILKMVKHPNQLQVDFVTRKEYFIFLELATGREVFDWILDQGYYSER
Sbjct: 61 RKVRKAAKNEIGILKMVKHPNQLQVDFVTRKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 121 DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP 180
DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP
Sbjct: 121 DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP 180

Query: 181 CGTPEYL 187
CGTPEYL
Sbjct: 181 CGTPEYL 187

Pedant information for DKFZphfbr2_82e4, frame 1

Report for DKFZphfbr2_82e4.1

[LENGTH] 473
[MW] 51208.89
[pI] 5.30
[HOMOL] PIR:I56542 calmodulin-binding protein - rat 0.0
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YFR014c] 4e-30
[FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YFR014c] 4e-30
[FUNCAT] 03.01 cell growth [S. cerevisiae, YFR014c] 4e-30
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKL101w] 2e-26
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YKL101w] 2e-26
[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision
repair) [S. cerevisiae, YDL101c] 8e-26
[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YCL024w] 5e-24
[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YDR507c] 7e-23
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YDR507c]
7e-23
[FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YPL153c] 1e-21
[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YPL153c] 1e-21

```

2251 TATTTGTGTT ATTCCTGCC TTTCCGAGTC CTGCAGTGGG CTGCCCTGTA
2301 CCCTGAACCT CATGAGCCTC TAAGGGAAAG GAGGAACAAT TAGGACGTGG
2351 CAATGAGACC TGGCAGGGCA GAGTACAAGC CCAGCACCCA GTGTCCCAGC
2401 CTTACTGGGT CTTTACCCTG GGCCAAACAG GGAGGGCTGA TACCTCCTTG
2451 CTCTTCCTAG ATGCCACCT CCTACAATCT CAGCCCACAA GTCCTCTCCA
2501 CCCTAGGGGG CTGCTGCAT GGCAATAACT CATAATCTGA TTTGGAGGTT
2551 TGCCCTTTAC AGGGGCAGAT TTTCTGCTCA GTTCAACAAT GAAATGAAGA
2601 GGAACCTCCT CTTTCTACAG CTCACTTCTA TCAGAGGCCC AGGTGCCTCA
2651 GAGCCACATT GAGTTGCTTT TTCTGGGATG AGGAAGTAGG GTTAAACTCC
2701 CCAGTTTCCT GAGGGAGGCT CCTGACAGGT GCCCTTGTC AGACCTTACC
2751 ACAGCCTGGA TAGGCAGCCA CATTGGTCCT CGCCCTTGCT CGGCACTCCG
2801 TGGTGGTCTC GCCCTTCTCC CTGCATGCC CTGGGTCTGC TCTGGTGTGT
2851 GAAGGTCGGT GGGTTAACTG TGTGCCTACT GAACCTGGCA AATAAACATC
2901 ACCCTGCAAA GCCAAAAAAA AAA

```

BLAST Results

Entry HS452352 from database EMBL:

human STS WI-15318.

Length = 350

Minus Strand HSPs:

Score = 1547. (232.1 bits), Expect = 5.2e-63, P = 5.2e-63

Identities = 331/348 (95%), Positives = 331/348 (95%), Strand = Minus / P1

Medline entries

94110847:

J Neurosci 1994 Jan;14(1):1-13

IG5: a calmodulin-binding, vesicle-associated, protein kinase-like protein enriched in forebrain neurites.

Godbout M, Erlander MG, Hasel KW, Danielson PE, Wong KK, Battenberg EL,

Foye PE,

Bloom FE, Sutcliffe JG

Peptide information for frame 1

```

1 MPFGCVTLGD KKNYNQPSSEV TDRYDLGQVI KTEEFCEIFR AKDKTTGKLM
51 TCKKFQKR DG RKVRKA AKNE IGILKMVKHP NILQLVDV FV TRKEYFIFLE
101 LATGREVF DW ILDQGYYSER DTSNVVRQVL EAVAYLHSLK IVHRNLKLEN
151 LVYYNRLK NS KIVISDFHLA KLENGLIKEP CGTPEYLGNP PFYEEVEEDD
201 YENHDKNL FR KILAGDYFFD SPYWDDISQA AKDLVTRLME VEQDQRITAE
251 EAISHEWIS G NAASDKNIKD GVCAQIEKNF ARAKWKKA VR VTTLMKRLFA
301 PEQSSTAA AQ SASATDTATP GAAGGATAAA ASGATSAPEG DAARAASDN
351 VAPADRSAT P ATDGSATPAT DGSVTPATDG SITPATDGSV TPATDRSATP
401 ATDGRATP AT EESTVPTTQS SAMLATKAAA TPEPAMAQPD STAPEGATGQ
451 APPSSKGEEA AGYAQESQRE EAS

```

ORF from 163 bp to 1581 bp; peptide length: 473

Category: strong similarity to known protein

BLASTP hits

Entry S50193 from database PIR:

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat

Length = 374

Score = 371 (130.6 bits), Expect = 2.2e-66, Sum P(2) = 2.2e-66

Identities = 74/176 (42%), Positives = 115/176 (65%)

Entry S57347 from database PIR:

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human

Length = 370

Score = 369 (129.9 bits), Expect = 4.6e-66, Sum P(2) = 4.6e-66

Identities = 74/176 (42%), Positives = 114/176 (64%)

Alert BLASTP hits for DKFZphfbr2_82e4, frame 1

PIR:I56542 calmodulin-binding protein - rat, N = 2, Score = 1246, P = 4e-228

DKF2phfbr2_82e4

group: signal transduction

DKF2phfbr2_82e4 encodes a novel 473 amino acid protein with strong similarity to the calmodulin-binding proteins.

The novel protein is similar to human and rat Ca²⁺/calmodulin-dependent protein kinase (EC 2.7.1.123), rat calmodulin-binding protein, calmodulin binding protein kinase of Fugu rupies and Rattus norvegicus calcium/calmodulin-dependent protein kinase I. Calmodulin is the archetype of the family of calcium-modulated proteins of which nearly 20 members have been found. Calmodulin is involved in regulation of growth and cell cycle as well as in signal transduction and the synthesis and release of neurotransmitters. The novel protein seems to be involved in calmodulin-mediated pathways in human neuronal cells.

The new protein can find clinical application in modulating/blocking calmodulin-mediated pathways in human neuronal cells.

strong similarity to calmodulin-binding proteins

complete cDNA, complete cds, EST hits
splice variant in comparison to rat I56542
ESTs HS2254543/HS1141907 define splice variant
see also DKF2phfbr2_82g20 unspliced form

Sequenced by DKFZ

Locus: /map="200.5 cR from top of Chr3 linkage group"

Insert length: 2923 bp

Poly A stretch at pos. 2913, polyadenylation signal at pos. 2890

```
1 ATGCTGGAGG TTCGCTAGCC GAAGCGGCTG CATCTGGCGC CGCGTCTGCC
51 CCGCGTGCTC GGAGCGGATT CTGCCCCGCG TCCCCGGAGC CCTCGGCGCC
101 CCGCTGAGCC CGCGATCACT TCCTCCCTGT GACCAACCGG CGCTGCAGGT
151 TAGAGCCTGG CAATGCCGTT TGGGTGTGTG ACTCTGGGTG ACAAGAAGAA
201 CTATAACCAG CCATCGGAGG TGA CTGACAG ATATGATTG GGACAGGTCA
251 TCAAGACTGA GGAGTTTGT GAAATCTTCC GGGCCAAGGA CAAGACGACA
301 GGCAAGCTGC ACACCTGCAA GAAGTTCCAG AAGCGGGACG GCCGCAAGGT
351 GCGGAAAGCT GCCAAGAACG AGATAGGCAT CCTCAAGATG GTGAAGCATC
401 CCAACATCCT ACAGCTGGTG GATGTGTTT TGACCCGCAA GGAGTACTTT
451 ATCTTCCCTG AGCTGGCCAC GGGGAGGGAG GTGTTTGACT GGATCCTGGA
501 CCAGGGCTAC TACTCGGAGC GAGACACAAG CAACGTGGTA CGGCAAGTCC
551 TGGAGGCCGT GGCCTATTTG CACTCACTCA AGATCGTGCA CAGGAATCTC
601 AAGCTGGAGA ACCTGGTTTA CTACAACCGG CTGAAGAAGT CGAAGATTGT
651 CATCAGTGAC TTCCATCTGG CTAAGCTAGA AAATGGCCTC ATCAAGGAGC
701 CCTGTGGGAC CCGGAGTAT CTGGGCAACC CACCTTTCTA TGAGGAGGTG
751 GAAGAAGATG ATTATGAGAA CCATGATAAG AATCTCTTCC GCAAGATCCT
801 GGCTGGTGAC TATGAGTTTG ACTCTCCATA TTGGGATGAT ATTTCCGAGG
851 CAGCCAAAGA CTTGGTCACA AGGCTGATGG AGGTGGAGCA AGACCAGCGG
901 ATCACTGCAG AAGAGGCCAT CTCCCATGAG TGGATTCTG GCAATGCTGC
951 TTCTGATAAG AACATCAAGG ATGGTGCTCG TGCCAGATT GAAAAGAACT
1001 TTGCCAGGGC CAAGTGAAG AAGGCTGTCC GAGTGACCAC CCTCATGAAA
1051 CGGCTCCGGG CACCAGAGCA GTCCAGCAGC GCTGCAGCCC ACTCGGCCCTC
1101 AGCCACAGAC ACTGCCACCC CCGGGGCTGC AGGTGGGGCC ACAGCTGCAG
1151 CTGCGAGTGG AGCTACCTCA GCCCCTGAGG GTGATGCTGC TCGTGCTGCA
1201 AAGAGTGATA ATGTGGCCCC CGCAGACCGT AGTGCCACCC CAGCCACAGA
1251 TGGAAGTGCC ACCCCAGCCA CTGATGGCAG TGTACCCCA CCCACCGATG
1301 GAAGCATCAC TCCAGCCACT GATGGGAGTG TCACCCAGC CACTGACAGG
1351 AGCGCTACTC CAGCCACTGA TGGGAGAGCC ACACCAGCCA CAGAAGAGAG
1401 CACTGTGCCC ACCACCCAAA GCAGTGCCAT GCTGGCCACC AAGGCAGCTG
1451 CCACCCCTGA GCCGGCTATG GCCCAGCCGG ACAGCACAGC CCCAGAGGGC
1501 GCCACAGGCC AGGCTCCACC CTCTAGTAAA GGGGAAGAGG CTGCTGGTTA
1551 TGCCCAGGAG TCTCAAAGGG AGGAGGCCAG CTGAGTAGGC AGCCTGGTGA
1601 GGGGGGGCAG GGGATGGGCA GGAGGGTGGG AGAGTGATG AGGGGCTTCT
1651 CACTGTACAT AGAGTCACTG GCATGATGCC CTCGCTCCCC CATGCCCCCA
1701 CATCCAGTGG GGGCATAACT AGGGGTCACG GGAGAGCAGT CTCGTCTCCT
1751 GTGTGTATGT GTGTGAGTGG TGGGAGGCC AGTGGCAGG CCGGCCCTGC
1801 CCCCTGCATG GATTCCTTGT GGCTTTTCTG TCTTTTGCTA GCTTCACCA
1851 TTTCTGTTCC TTGTGGGATG CTGCTCTAGG GATACTCAGG GGGCTCCTGC
1901 TCTCCTTCCC TTCCCTTCT TGCCTACCA TTCCCTAGG CAGGCCCTGC
1951 AGGTCCCACT CTCTCCAGG CCCTAAACTT GGGCGGCCCTT GCCCTGAGAG
2001 CTGGTCTCCT AGCGAGGCC TGTCAGCGGT CTTAGGCTCC TGCACATGAA
2051 GGTGTGTGCC TGTGGTGTGT GGGCTGCTCT AGGAGCAGAT ACAGGCTGGT
2101 ATAGAGGATG CAGAAAGGTA GGGCAGTATG TTAAAGTCCA GACTTGGCAC
2151 ATGGCTAGGG ATACTGCTCA CTAGCTGTGG AGGTCCTCAG GAGTGGAGAG
2201 AATGAGTAGG AGGGCAGAAG CTTCCATTTT TGTCTTCTCT AAGACCTGT
```


[PROSITE]	AMIDATION	1	
[PROSITE]	MYRISTYL	3	
[PROSITE]	CAMP_PHOSPHO_SITE	1	
[PROSITE]	CK2_PHOSPHO_SITE	3	
[PROSITE]	PKC_PHOSPHO_SITE	4	
[PROSITE]	ASN_GLYCOSYLATION	1	
[KW]	TRANSMEMBRANE	6	
[KW]	LOW_COMPLEXITY	7.72	%

```
SEQ      CYDLLVRKKRLIVLFSHWLLHAYGIIISIRVDKLEQDLPALLALVPTPALFYLFTAKFTEP
SEG      .....xxxxxxxxxxxxx.....
PRD      hhhhhhhhhhhhhhhhhhhhhhhcccceeechhhhhceeeeeccccceeeecccccc
MEM      mmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmm
```

```

SEQ      SRILSEGANGH
SEG      .....
PRD      ceeeeeccccc
MEM      MM.....

```

Prosite for DKFZphfbr2 82e17.1

PS00001	22->26	ASN_GLYCOSYLATION	PDOC00001
PS00004	82->86	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	80->83	PKC_PHOSPHO_SITE	PDOC00005
PS00005	119->122	PKC_PHOSPHO_SITE	PDOC00005
PS00005	186->189	PKC_PHOSPHO_SITE	PDOC00005
PS00005	294->297	PKC_PHOSPHO_SITE	PDOC00005
PS00006	234->238	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00006	269->273	CK2_PHOSPHO_SITE	PDOC00006
PS00008	11->17	MYRISTYL	PDOC00008
PS00008	37->43	MYRISTYL	PDOC00008
PS00008	182->188	MYRISTYL	PDOC00008
PS00009	80->84	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2 82e17.1)

Identities = 208/208 (100%), Positives = 208/208 (100%), Strand = Minus
/ Plus

Entry HSG20716 from database EMBL:

human STS A006D06.

Length = 195

Minus Strand HSPs:

Score = 975 (146.3 bits), Expect = 1.8e-37, P = 1.8e-37

Identities = 195/195 (100%), Positives = 195/195 (100%), Strand = Minus
/ Plus

Medline entries

No Medline entry

Peptide information for frame 1

```

1 MAVDIQPACL GLYCGKTLF KNGSTEIYGE CGVCPRGORT NAQKYCQPCT
51 ESPELYDWLY LGFMAMLPV LHWFFIEWYS GKKSSSALFQ HITALFECSM
101 AAIITLLVSD PVGVLYIRSC RVLMLSDWYT MLYNPSPDYV TTVHCTHEAV
151 YPLYTIVFIY YAFCLVLMML LRPLLVKKIA CGLGKSDRFK SIYAALYFFP
201 ILTVLQAVGG GLLYYAFPII ILVLSLVTLA VYMSASEIEN CYDLLVRKKR
251 LIVLFSHWLL HAYGIISISR VDKLEQDLPL LALVPTPALF YLFTAKETEP
301 SRILSEGANG H

```

ORF from 40 bp to 972 bp: peptide length: 311
Category: similarity to unknown protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82e17, frame 1

TREMBL:AF068718_5 gene: "R01B10.5"; Caenorhabditis elegans cosmid
R01B10., N = 1, Score = 399, P = 1.4e-36

>TREMBL:AF068718_5 gene: "R01B10.5"; Caenorhabditis elegans cosmid R01B10.
Length = 670

HSPs:

Score = 399 (59.9 bits), Expect = 1.4e-36, P = 1.4e-36
Identities = 95/280 (33%), Positives = 152/280 (54%)

```

Query:      2 AVDIQPACLGLYCGKTLFKN-----GSTEIYGE CGVCPRGORTNAQKYCQPC 49
            A IQP+CLG +CG+T+L N          GST +   CG C  G R NA  C+ C
Sbjct:    292 ASTIQPSCLG-FCGRTVLGVNGYSEDVEATTTAAGSTSL-SRCGPCSFGYRNNAMSICESC 349

Query:      50 TESPELYDWLYLGFMAMLPVLVHWWFFIEWYSGKKSSSALFQ---HITALFECSMAAIITL 106
            + YDW+YL F+A+LPL+LH F1 + K + ++ ++ + E +A +I +
Sbjct:    350 DTPLQPYDWMYLLFIALPLLLHMQFIR-IARKYCRTRYEVSEYLCVILENVIACVIAV 408

Query:     107 LVSDPVGVLVYIRSCRVLMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV 166
            L+ P ++ C + +WY YNP Y T+ CT+E V+PLY+I FI++ +
Sbjct:    409 LIYPPRFTFFLNGCSKTDIKEWYPACYNPRIGYTKTMRCTYEVVFLYSITFIHHLILIG 468

Query:     167 LMMLLRPLLVKKIAACGLGKSDRFKSIYAALYFFPIILTVLQAVGGGLLYYAFPIIILVLSL 226
            +++LR L + L K+ K YAA+ PIL V+ AV G+++Y FPYI+L+ SL
Sbjct:    469 SILVLRSTLYCVL---LYKTYNGKPFYAAIVSVPI LAVIHAVLSGVVFTFPYILLIGSL 525

Query:     227 VTLAVYMSASEIENCYDLLVR---KKRLIVLFSHWLLHAYGIISI 268
            + +++ ++VR LI L L+ ++G+I+I
Sbjct:    526 WAMCFHLALEGKRPLKEMIVRIATSPTHLIFLSITMLMLSFGVIAI 571

```

Pedant information for DKFZphfbr2_82e17, frame 1

Report for DKFZphfbr2_82e17.1

DKFZphfbr2_82e17

group: transmembrane protein

DKFZphfbr2_82e17 encodes a novel 311 amino acid protein with very weak similarity to C. elegans cosmid R01B10.

The novel protein contains 6 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to C.elegans "R01B10.5" ;
membrane regions: 6
Summary DKFZphfbr2_82e17 encodes a novel 311 amino acid protein with
similarity to a hypothetical C.elegans protein.

similarity to C.elegans "R01B10.5"

complete cDNA, EST HS763158 extends the sequence, complete cds, EST
hits
six potential transmembrane domains

Sequenced by DKFZ

Locus: /map="779_C_?; 818_A_1; 877_C_1; 734_C_12; 760_E_11; 171.7 cR from top of Chr14 linkage
group"

Insert length: 1618 bp
Poly A stretch at pos. 1608, polyadenylation signal at pos. 1588

```
1 CTGATCTAGT GCTTCTCGAA AAAACCTTC AGGCGGCCCA TGGCTGTCGA
51 TATTCAACCA GCATGCCTTG GACTTTATTG TGGGAAGACC CTATTATTTA
101 AAAATGGCTC AACTGAAATA TATGGAGAAT GTGGGGTATG CCCAAGAGGA
151 CAGAGAACGA ATGCACAGAA ATATTGTCAG CCTTGCACAG AATCTCCTGA
201 ACTTTATGAT TGGCTCTATC TTGGATTATG GGCAATGCTT CCTCTGGTTT
251 TACATTGGTT CTTCATTGAA TGGTACTCGG GGAAAAAGAG TTCCAGCGCA
301 CTTTTCACAC ACATCACTGC ATTATTGAA TGCAGCATGG CAGCTATTAT
351 CACCTTACTT GTGAGTGATC CAGTTGGTGT TCTTTATATT CGTTCATGTC
401 GAGTATTGAT GCTTTCTGAC TGGTACACGA TGCTTTACAA CCCAAGTCCA
451 GATTACGTTA CCACAGTACA CTGTACTCAT GAAGCCGTCT ACCCACTATA
501 TACCATTGTA TTTATCTATT ACGCATTCTG CTTGGTATTA ATGATGCTGC
551 TCCGACCTCT TCTGGTGAAG AAGATTGCAT GTGGGTTAGG GAAATCTGAT
601 CGATTAAAAA GTATTATGTC TGCACCTTAC TTCTTCCCAA TTTTAACCGT
651 GCTTCAGGCA GTTGGTGGAG GCCTTTTATA TTACGCCTTC CCATACATTA
701 TATTAGTGTT ATCTTTGGTT ACTCTGGCTG TGTACATGTC TGCTTCTGAA
751 ATAGAGAACT GCTATGATCT TCTGGTCAGA AAGAAAAGAC TTATTGTTCT
801 CTTACGCCAC TGGTTACTTC ATGCCATGGA AATAATCTCC ATTTCCAGAG
851 TGGATAAACT TGAGCAAGAT TTGCCCTTTT TGGCTTGGT ACCTACACCA
901 GCCCTTTTTT ACTTGTTTAC TGCAAAATTT ACCGAACCTT CAAGGATACT
951 CTCAGAAGGA GCCAATGGAC ACTGAGTGTA GACATGTGAA ATGCCAAAAA
1001 CCTGAGAAGT GCTCCTAATA AAAAAGTAAA TCAATCTTAA CAGTGTATGA
1051 GAACCTATTCT ATCATATATG GGAACAAGAT TGTCAGTATA TCTTAATGTT
1101 TGGGTTTGTC TTTGTTTGTG TTATGGTTAG ACTTACAGAC TTGGAAAAATG
1151 CAAAACCTCT TAATACTCTG TTACACAGGG TAATATTATC TGCTACACTG
1201 GAAGGCCGCT AGGAAGCCCT TGCTTCTCTC AACAGTTCAG CTGTTCTTTA
1251 GGGCAAAATC ATGTTTCTGT GTACCTAGCA ATGTGTTCCC ATTTTATTAA
1301 GAAAAGCTTT AACACGTGTA ATCTGCAGTC CTTAACAGTG GCGTAATTGT
1351 ACGTACCTGT TGTGTTTCAG TTTGTTTTTC ACCTATAATG AATTGTAAAA
1401 ACAAAACATAC TTGTGGGGTC TGATAGCAAA CATAGAAATG ATGTATATTG
1451 TTTTGTGTTA TCTATTATT TTCAATCAATA CAGTATTTTG ATGTATTGCA
1501 AAAATAGATA ATAATTTATA TAACAGGTTT TCTGTTTATA GATTGGTTCA
1551 AGATTGTGTT GGATTATTGT TCCTGTAAAG AAAACAATAA TAAAAAGCTT
1601 ACCTACATAA AAAAAAAA
```

BLAST Results

Entry HS981146 from database EMBL:
human STS WI-6253.
Length = 208
Minus Strand HSPs:
Score = 1040 (156.0 bits), Expect = 1.9e-40, P = 1.9e-40

SEQ ASPQRDLDHFRS
SEG
PRD ccchhhhhccccc
MEM

Prosites for DKFZphfbr2_82c20.2

PS00001	8->12	ASN_GLYCOSYLATION	PDOC00001
PS00002	47->51	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	212->216	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	316->320	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00005	147->150	PKC_PHOSPHO_SITE	PDOC00005
PS00005	241->244	PKC_PHOSPHO_SITE	PDOC00005
PS00005	245->248	PKC_PHOSPHO_SITE	PDOC00005
PS00005	443->446	PKC_PHOSPHO_SITE	PDOC00005
PS00006	241->245	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	342->346	CK2_PHOSPHO_SITE	PDOC00006
PS00008	21->27	MYRISTYL	PDOC00008
PS00008	24->30	MYRISTYL	PDOC00008
PS00008	28->34	MYRISTYL	PDOC00008
PS00008	48->54	MYRISTYL	PDOC00008
PS00008	231->237	MYRISTYL	PDOC00008
PS00009	2->6	AMIDATION	PDOC00009
PS00009	134->138	AMIDATION	PDOC00009
PS00029	168->190	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphfbr2_82c20.2)

Score = 146 (21.9 bits), Expect = 4.6e-29, Sum P(2) = 4.6e-29
Identities = 34/86 (39%), Positives = 50/86 (58%)

Query: 52 SSSPLATQTVPVPLQHCIPPELP-VQASILFELQLFFCQLIALFVHYINYKTVWWYPPSH 110
+S P A+ + + H P++ Q + FE LF ++ALF+ Y+NIYKT+WW P S+
Sbjct: 19 ASIPRASGVTLVS-HPIWPDQIQTQGELEFFECTLFLYSVLALFLQYLNLYKTLWWLPKSY 77

Query: 111 PPSHTSLNLFHLLIDFNLMVTTIVLGR 137
H SL FHLI+ L ++LG R
Sbjct: 78 --WHYSLKFHLINPYFLSCVGLLLGWR 102

Score = 39 (5.9 bits), Expect = 6.8e-18, Sum P(2) = 6.8e-18
Identities = 12/41 (29%), Positives = 20/41 (48%)

Query: 154 LFRSILLFLTRFTVLTATGWSLCRSLIHLFRTYSFLNLLFL 194
L+ + LFL ++ + T W L +S H + +N FL
Sbjct: 53 LYSVLALFL-QYLNLYKTLWWLPKSYWHYSLKFHLINPYFL 92

Pedant information for DKFZphfbr2_82c20, frame 2

Report for DKFZphfbr2_82c20.2

[LENGTH] 492
[MW] 56274.05
[pI] 9.51
[HOMOL] TREMBL:CEAF3151_8 gene: "D1007.5"; Caenorhabditis elegans cosmid D1007. 4e-31

[PROSITE] LEUCINE_ZIPPER 1
[PROSITE] AMIDATION 2
[PROSITE] MYRISTYL 5
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] CK2_PHOSPHO_SITE 3
[PROSITE] GLYCOSAMINOGLYCAN 1
[PROSITE] PKC_PHOSPHO_SITE 5
[PROSITE] ASN_GLYCOSYLATION 1
[KW] TRANSMEMBRANE 7
[KW] LOW_COMPLEXITY 8.74 %

SEQ MGGRRGPNRTSYCRNPLCEPGSSGGSSGSHTSASVTSVRSTRSSSGTGLSSPLATQT
SEG
PRD ccc
MEM

SEQ VVPLQHCIPPELPVQASILFELQLFFCQLIALFVHYINYKTVWWYPPSHPPSHTSLNLFH
SEG
PRD eeeeecc
MEMMM

SEQ LIDFNLLMVTTIVLGRFIGSIVKEASQRGKVSIFRSILLFLTRFTVLTATGWSLCRSLI
SEG
PRD eehhh
MEM MMM

SEQ HLFRTYSFLNLLFLCYPFGMYIPFLQNLCDLRKTSLFNHMASMGPREAVSGLAKSRDYL
SEG
PRD hhh
MEM

SEQ TLRETWKQHTRQLYGPDAMPTHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSMLSAYYV
SEG
PRD hhh
MEMMM

SEQ AFVPVWFVKNTHYDKRWSCEFLFLVSISTSVILMOHLLPASCYDLLHKAHAHLGCWQKV
SEG
PRD heeeeecc
MEM MMM

SEQ DPALCSNVLQHPWTEECMWPQGVLVKHSKNVYKAVGHYNVAIPSDVSHFRHFFFSKPLR
SEGxx
PRD ccc
MEMMM

SEQ ILNILLLEGAVIVYQLYSLMSSEKWHQTISLALILFSNYAFAFKLLRDRLVLGKAYSYS
SEG xxxxxxxx.....
PRD hhh
MEM MMM

Score = 1225, P = 1.3e-50, identities = 263/281

Medline entries

No Medline entry

Peptide information for frame 2

```

1  MGGRRGPNRT  SYCRNPLCEP  GSSGGSSGSH  TSSASVTSVR  SSTRSSSGTG
51 LSSPPLATQT  VVPLQHCKIP  ELPVQASILF  ELQLFFCQLI  ALFVHYINII
101 KTVWVYPPSH  PPSHTSLNFH  LIDFNLLMVT  TIVLGRRFIG  SIVKEASQRG
151 KVSFLRSILL  FLTRETDLTA  TGWSLCRSLI  HLFRTYSFLN  LLFLCYPFGM
201 YIPFLQLNCD  LRKTSLFNHM  ASMGPREAVS  GLAKSRDYLL  TLRETWKQHT
251 RQLYGPDAMP  THACCLSPSL  IRSEVEFLKM  DENWRMKEVL  VSSMLSAYYV
301 AFVPVWFVKV  THYYDKRWSC  ELFLVLSIST  SVILMOHLLP  ASYCDLLHKA
351 AAHLGCWQKV  DPALCSNVLQ  HPWTEECMWP  QGVLVKHSKN  VYKAVGHYNV
401 AIPSDVSHFR  FHFFFSKPLR  ILNILLLEGG  AVIVYQLYSL  MSSEKWHQTI
451 SLALILFSNY  YAFFKLLRDR  LVLGKAYSYS  ASPQRDLDR  FS

```

ORF from 128 bp to 1603 bp; peptide length: 492
 Category: similarity to unknown protein
 Prosite motifs: LEUCINE_ZIPPER (210-232)
 LEUCINE_ZIPPER (210-232)

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82c20, frame 2

TREMBL:CEAF3151_8 gene: "D1007.5"; Caenorhabditis elegans cosmid
 D1007., N = 2, Score = 247, P = 4.6e-29

>TREMBL:CEAF3151_8 gene: "D1007.5"; Caenorhabditis elegans cosmid D1007.
 Length = 512

HSPs:

Score = 247 (37.1 bits), Expect = 4.6e-29, Sum P(2) = 4.6e-29
 Identities = 58/204 (28%), Positives = 102/204 (50%)

Query: 291 VSSMLSAYYVAFVPVWFVKNTHTYYDKRWSCFLVLSISTSVILMOHLLPASVCDLLHKA 350
 +S ML +V F + ++ W C+L ++V ++ + + +L P +Y DLLH+A
 Sbjct: 299 LSIMLPCIFVPFKTSQGIPOKILINEVWECQLAIVVGLTAFSLYVAYLSPLNYDLLHRA 358

Query: 351 AAHLGCWQKVD-PAL----CSNVLQHPWTEECMWPQGVLVKHSKN-VYKAVGHYNV---- 400
 A HLG W +++ P + + PW+E C++ G V+ Y+A ++
 Sbjct: 359 AIHLGSHWHQIEGPRIGHTGSMSSAPTWSSEFCLYNDGETVQMPDGRCRYAKSSNSIRTV 418

Query: 401 AIPSDVSHFRFHFFFSKPLRILNILLLEGAVIVYQLYSLMSSEKWHQTIISLALILFSNY 460
 A P H F KP ++NI+ E +I Q + L+ + W ++ L++F+NY
 Sbjct: 419 AHPESSRHNTFFKVLKPNLNINIMCSFEFLIFIQFWMLVLTNDWQHIVTFVLLMFANY 478

Query: 451 YAFFKLLRDRDLVLGKAYSYSASPQRDL 487
 F KL +D+++L + Y S Q DL
 Sbjct: 479 LLFAKLFKDKIILSRIYEPS---QEDL 502

Score = 178 (26.7 bits), Expect = 4.3e-21, Sum P(2) = 4.3e-21
 Identities = 50/179 (27%), Positives = 90/179 (50%)

Query: 262 HACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSMLSAYYVAFVPVWFV--KNTHYYDKR-- 317
 H C SP+ IR E++ L D R+K+ + + + +A+ +P FV K + ++
 Sbjct: 262 HMCSDSPAQIREEQVLIDDLVLVKKSIAGVSTAFSLIMLPCIFVPFKTSQGIPOKIL 321

Query: 318 ----WSCEFLVLSISTSVILMOHLLPASVCDLLHKA--AAHLGCWQKVD-PAL----CSNV 368
 W C+L ++V ++ + + +L P +Y DLLH+AA HLG W +++ P + +
 Sbjct: 322 INEVWECQLAIVVGLTAFSLYVAYLSPLNYDLLHRAAHLGSHWHQIEGPRIGHTGSMSS 381

Query: 369 LQHPWTEECMWPQGVLVKHSKN-VYKAVGHYNV-AIPSDVSHFRFHFFFSKPLRILNILL 426
 PW+E C++ G V+ Y+A ++ + + R + FF K LR N L+
 Sbjct: 382 APTPWSEFCLYNDGETVQMPDGRCRYAKSSNSIRTVAAHPESSRHNTFF-KVLKPNLNLI 440

DKFZphfbr2_82c20

group: transmembrane protein

DKFZphfbr2_82c20 encodes a novel 492 amino acid protein with very weak similarity to C. elegans cosmid D1007.

The novel protein contains 7 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to C.elegans D1007.5 ;
membrane regions: 7
Summary DKFZphfbr2_82c20 encodes a novel 492 amino acid protein with
similarity to a hypothetical C.elegans protein.

similarity to C.elegans D1007.5

complete cDNA (Bp 1-100 GC ritch), complete cds,
potential start at Bp 128 matches Kozak consensus PyNnatgG,
EST hits, localisation? primer B of STS doesn't match perfect!
TRANSMEMBRANE 7

Sequenced by DKFZ

Locus: /map="109.9 cR from top of Chr1 linkage group"???

Insert length: 1804 bp
Poly A stretch at pos. 1794, no polyadenylation signal found

```
1 CGGCGGGAGC GCGCGGCTGA TACCCGGGAC TGGGCTGCGG CGGTTAGTCC
51 TCTCCCGGCC GCCGTCGCCT CCGACATATT GCTCGCAGGA GCTGCGGCGG
101 CGAAGCGGAG AGCACC GGAGGAGATG GGAGGACGAA GAGGTCCCAA
151 CAGGACATCT TACTGTGCGAA ATCCGCTCTG TGAGCCGGGA TCCTCGGGGG
201 GCTCTAGTGG AAGCCACACT TCCAGTGCAT CGGTGACCAG TGTTCGTTC
251 CGCACCAGGA CGAGTTCTGG AACAGGCCTC TCCAGCCCTC CTCTGGCCAC
301 CCAAACCTGT GTGCCTCTAC AGCACTGCAA GATCCCGGAG CTGCCAGTCC
351 AGGCCAGCAT TCTGTTTGAG TTGCAGCTCT TCTTCTGCCA GCTCATAGCA
401 CTCTTCGTCC ACTACATCAA CATCTACAAG ACAGTGTGGT GGTATCCACC
451 TTCCACCCCA CCTCCACACA CCTCCCTGAA CTTCCATCTG ATCGACTTCA
501 ACTTGCTGAT GGTGACCACC ATCGTTCTGG GCCGCGCTT CATTTGGTCC
551 ATCGTGAAGG AGGCCTCTCA GAGGGGGAAG GTCTCCCTCT TTCGCTCCAT
601 CCTGCTGTTC CTCACCTGCT TCACCGTTCT CACGGCAACA GGCTGGAGTC
651 TGTGCCGATC CCTCATCCAC CTCTTCAGGA CCTACTCCTT CCTGAACCTC
701 CTGTTCTCTT GCTATCCGTT TGGGATGTAC ATTCCGTTCC TGCAGCTGAA
751 TTGCGACCTC CGCAAGACAA GCCTCTTCAA CCACATGGCC TCCATGGGGC
801 CCCGGGAGGC GGTCACTGGC CTGGCAAAGA GCCGGGACTA CCTCCTGACA
851 CTGCGGGAGA CGTGAAGCA GCACACAAGA CAGCTGTATG GCCCGGACGC
901 CATGCCACC CATGCTGCT GCCTGTCACC CAGCCTCATC CGCAGTGAGG
951 TGGAGTTCCT CAAGATGGAC TTCAACTGGC GCATGAAGGA AGTGCTCGTC
1001 AGCTCCATGC TGAGCGCCTA CTATGTGGCC TTTGTGCTTG TCTGGTTCGT
1051 GAAGAACACA CATTACTATG ACAAGCGCTG GTCCTGTGAA CTCTTCTGTC
1101 TGGTGTCCAT CAGCACCTCC GTGATCCTCA TGCAGCACCT GCTGCCTGCC
1151 AGCTACTGTG ACCTGCTGCA CAAGGCCGCC GCCCATCTGG GCTGTGGCA
1201 GAAGGTGGAC CCAGCGCTGT GCTCCAACGT GCTGCAGCAC CCGTGGACTG
1251 AAGAATGCAT GTGGCCGAG GCGTGCTGG TGAAGCACAG CAAGAACGTC
1301 TACAAAGCCG TAGGCCACTA CAACGTGGCT ATCCCTCTG ACCTCTCCCA
1351 CTTCCGCTTC CATTCTTTT TCAGCAAACC TCTGCGGATC CTCAACATCC
1401 TCCTGCTGCT GGAGGGCGCT GTCATTGTCT ATCAGCTGTA CTCCTTAATG
1451 TCCTTGAAA AGTGGCACCA GACCATCTCG CTGGCCCTCA TCCTCTTCAG
1501 CAACTACTAT GCCTTCTTCA AGCTGCTCCG GGACCGCTTG GTATTGGGCA
1551 AGGCCTACTC ATACTCTGCT AGCCCCAGA GAGACCTGGA CCACCGTTTC
1601 TCCTGAGCCC TGGGGTCACC TCAGGGACAG CGTCCAGGCT TCAGCCAAGG
1651 GCTCCTGGC AAGGGGCTGT TGGGTAGAAG TGGTGGTGGG GGGGACAAAA
1701 GACAAAAAAA TCCACCAGAG CTTTGTATT TTGTTACGTA CTGTTTCTTT
1751 GATAATTGAT GTGATAAGGA AAAAAGTCT ATTTTATAC TCCCAAAAAA
1801 AAAA
```

BLAST Results

Entry HS285343 from database EMBL:
human STS WI-17488.

TREMBLNEW:PCP115C_1 product: "P115C"; Pneumocystis carinii mRNA for P115C, partial sequence., N = 1, Score = 109, P = 0.00024

HSPs:

```

Query:      14  CKN-YKAVCLELKPPTKTFDYKAVKQEGRFKA-GVTQDLKNELREVREELKEKMEEIK  71
           CK  K  C  ELK  +  K  VK+  TK  G  ++LK+++++  E  KE++E  K
Sbjct:      22  CKTELKKYCEELKEADGLKVNDK-VKEICDDTKRDGCKELKDKVVKKELETFKEELE--K  78

Query:      72  QIKDLMDKDFDKLHEFVEIMKEMQKDMDEKMDILINTQKNYKPLRRAPKEQQELRLMGK  131
           +KD+  D++  +K  E  +++E  D  D  K  +  +  +  YKL  +R  E  LR  +GK
Sbjct:      79  ALKDIKDENCEKYEEKCILLEETNHD-DVKKNCVKLREGCYKLKRKRVA-EDLLLRALGK  136

Query:      132  THREFQLRPKKMDGAS  147
           +  +  K  D  S
Sbjct:      137  DVKNGECEKKMKDVCS  152

```

Report for DKF2phfbr2 7j4.3

[LENGTH]	233	
[MW]	26533.95	
[pI]	9.18	
[PROSITE]	MYRISTYL	3
[PROSITE]	CK2_PHOSPHO_SITE	3
[PROSITE]	PKC_PHOSPHO_SITE	3
[KW]	All_Alpha	
[KW]	LOW_COMPLEXITY	14.59 %
[KW]	COILED_COIL	13.73 %

[illegible]

Prosites for DKFZphfbr2 7j4.3

PS000005	2->5	PKC_PHOSPHO_SITE	PDOC000005
PS000005	108->111	PKC_PHOSPHO_SITE	PDOC000005
PS000005	132->135	PKC_PHOSPHO_SITE	PDOC000005
PS000006	132->136	CK2_PHOSPHO_SITE	PDOC000006
PS000006	179->183	CK2_PHOSPHO_SITE	PDOC000006
PS000006	228->232	CK2_PHOSPHO_SITE	PDOC000006
PS000008	151->157	MYRISTYL	PDOC000008
PS000008	196->202	MYRISTYL	PDOC000008
PS000008	204->210	MYRISTYL	PDOC000008

(No Pfam data available for DKF2phfbr2 7j4.3)

DKFZphfbr2_7j4

group: brain derived

DKFZphfbr2_7j4 encodes a novel 233 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, 1 EST hit

Sequenced by GBF

Locus: unknown

Insert length: 1050 bp

Poly A stretch at pos. 1027, polyadenylation signal at pos. 1007

```

1 GGGGACACAA AGGGGTGGTC ACCCTGCCCT CACCTTGACC TGTAAGTTGC
51 CTAGGACAGT GGCCTGGTCC CAGGGGCTGT TGTGGGGAGT TGAAGAACAC
101 CCTGGCCTCC TCCATCATGT CGGCCAAGAG GGCAGAATTG AAGAAAACAC
151 ATCTGTGCAA GAACTACAAG GCAGTTTGCC TGGGAATTGAA GCCAGAGCCG
201 ACCAAAACAT TTGATTACAA AGCAGTTAAA CAAGAAGGGC GGTTTACCAA
251 AGCAGGAGTG ACACAGGACC TAAAGAATGA ACTCAGGGAA GTGAGAGAAG
301 AGCTCAAGGA GAAAATGGAG GAGATAAAAC AGATAAAGGA TCTAATGGAC
351 AAGGATTTTG ATAACTTCA CGAATTGTG GAAATTATGA AGGAAATGCA
401 GAAAGATATG GATGAGAAGA TGGACATTTT AATAAATACA CAGAAGAACT
451 ATAAGCTTCC CTTAGAAGA GCACCAAAGG AGCAGCAGGA ACTCAGGCTG
501 ATGGGAAAGA CTCACAGAGA ACCACAGCTC AGGCCCAAGA AAATGGATGG
551 AGCCAGTGGA GTCAATGGAG CACCCTGTGC TCTTCACAAG AAGACGATGG
601 CACCACAAAA AACAAAACAG GGCTCACTGG ATCCCTTCA TCACTGTGGG
651 ACCTGCTGCG AGAAATGTTT GTTGTGTGCT CTAAAGAACA ACTACAATCG
701 GGGGAACATT CCTTCAGAGG CCTCAGGCCT TTACAAAGGT GGAGAGGAGC
751 CAGTGACCAC CCAACCTTCT GTGGGCCACG CTGTGCCTGC CCCAAGTCC
801 CAGACTGAGG GAAGGTGAAG CTTAACTGCC AGCTTGAAAT GAGAGTAAAG
851 AAGATACACA GCAAACAGTG TTTCAGAAAC TGTCTGCCC TGGGTGTGAT
901 TCTTTGGCTT CAATTGAAG GAGGAGGAAT GATGGGATTT CATATTTTAT
951 TTCACACCAG TTCCTCCTTG TTTCATCTCT TTGCTAAGCT GGCTGCTTCT
1001 ACCATCTAAT AAATAATTGG CCAAGTTAAA AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 117 bp to 815 bp; peptide length: 233
 Category: putative protein

```

1 MSAKRAELKK THLCKNYKAV CLELKPEPTK TFDYKAVKQE GRFTKAGVTQ
51 DLKNELREVR EELKEKMEEI KQIKDLMDKD FDKLHEFVEI MKEMQKDMDE
101 KMDILINTQK NYKLPLRRAP KEQELRLMG KTHREPQLRP KKMDGASGVN
151 GAPCALHKKK MAPQKTQGS LDPLHHCCTC CEKCLLCALK NNYNRRGNIPS
201 EASGLYKGGE EPVTTQPSVG HAVPAPKSQT EGR

```

BLASTP hits

Entry JC2223 from database PIR:
 major surface glycoprotein 3 - *Pneumocystis carinii* (fragment)
 Score = 109, P = 3.5e-04, identities = 41/136, positives = 67/136

BNSDOCID: <WO 0112659A2 | >

```

2451 GAATTGAGAC TTGGAGGTGA CTTTTCATGT TTGGAGTATC ATCTCTGTCT
2501 GGGCTCTGGG CTGACAAATT AAAACCTAGA GTAGTGCTTA TGCTGAAATG
2551 ATACTTTTCA TTTTGTGGTT GATTTTTTTG CCTTCCCTTC AATTTTAAAC
2601 TGAAGCATTT TAATGTGGGT AGAAACTCTA CACCAAATAC ACTAAACATT
2651 TTGGTGCTTA GTGGATTCT TTTTAGGTAA CTGGTACTTA CTTCCAAAGA
2701 CTGAATACAA GCCACACTCC ATCATATCCC TTAAACTTCA TGA AAAAACA
2751 TTCAAGATCC CCTTGCTGCA AACTGTCTCT CTCTTCTCT ACTAAATTCT
2801 ATTTCCAAAA TTGGTAATAG AGCCAGAAGG ATCCCCAGTA CCCAGCCCTC
2851 TGCCTGGCAC AAAGTGGTAG CACAATTAAA TTCAGTATGG GTGGAGCATG
2901 GTACAGTCTT GGTGCCATAG AAGGAGTAGT TGCATAGTCA CACATCATT
2951 GATAAGTTGG ATGTTCCATT ACATAGAGGA ACACAAAATT CCAGGGTTTT
3001 TGGAGGAAGG GATTAGATAG CGACTAAGCC GCCAGAATTG AGGTGGCCAT
3051 TCCTTTTTGT ATAGGCTAAG AAACAGGTTA TCAGTGAAAA GTTAATTATG
3101 GCTTTGGCAC TAGAATAGCA CTGTTGCAAA GTATTTAAGC ACCCCCATC
3151 TCAGCCCTTT ATTTTATCTT TCATGTGGGC TAATGTGAGG ATAATCTTAC
3201 AGATATTATA GGAATTTCTT TTCTATCTTT ATGAAAACAA CGTATATAAA
3251 ATATATCTAG AAAACCTTTG TTTGAGACTC TTATTTAATG GGCTTTTGAT
3301 TCTAATGATA ATTGTACCTT TATCTTTCAA AAGCTGATAT TTCCTACCTA
3351 AGCATCTCCC GAGAAAAATA TCTCATTAAA AAGCCCATAA ATAATAGGGG
3401 AGAAGAAAGC CTTAGGTATC AATTCCAAAA CAGTGATTGA AATTCCCAA
3451 AATAATTATG GCTTCTGTCA TCTCCAGAGA TAATCTGGCT TGGTTTACCC
3501 CATAATCTAA TTTGAGAAAA GAAAGCTTTA TTTTAACACT CATCTGAATC
3551 AACATTAAAG CCTTTCTCT CAAAGCGTTT ATTGAGAAAC TCAATGAAT
3601 ATACTTTTTG AATTACTGTC ATCAAAAAGT TACGGCTTCC TGTGCTGCTT
3651 GTGTCAAATG GAACCTGCCC TCTAAAGCAC TTTCTTTTCT TTAAGTGGCT
3701 GGTTCATGT AAGCTGTGCT GTTTAGAAAC AACATCTCAG ACTTTACAAA
3751 GAAATGACAA AGAAGGCAAT TGCACCTTTT AAGGGATATC GACAAGCAGT
3801 TTCTGTTTTT TAAAGGACAA AATACAGAGT GTGTGTCATT TTTAATTAGA
3851 TTCTTTCCCC TGCTGAGTTG GAAATCCAG TGCAGCACTG ATTGACCACA
3901 GTTGCCAATC TAAAGGCACA AAGACAGAAG TAAAGCTTTA TGCTAATTTT
3951 ATTTCAATAT GATAGAAAAT TTATCTTGGT ATGTCCTTTT TTAGATAACT
4001 CCAGCAGGAA ACTGTAACCT CTATGTCTTT AGGAAAACGT AGAAGAAAGA
4051 ACATTATTAT TCTTTAATTC CTACAAGGTA CTTGAAAACC TTAAGTGAAA
4101 AAGATTTCTA TCTTTTTATC TTGGCGCATT TATGGAAAAA ATATTAAGT
4151 TCCTGAATAT TTTATAATT TGTAGGAAAA ATATGCATCT ATTTTCTCT
4201 GACTTCTTTT ATATAGTAAT AAAAGTTATT TTGGAAAAA AAAAAA
4251 AAAA

```

BLAST Results

Entry HSG20626 from database EMBL:
human STS A005227.
Score = 860, P = 3.0e-32, identities = 176/181

Medline entries

89030633:
The structure of cytochrome b561, a secretory vesicle-specific electron transport protein.

Peptide information for frame 2

ORF from 74 bp to 931 bp; peptide length: 286
Category: strong similarity to known protein
Classification: unset

```

1 MAMEGYRRFL ALLGSALLVG FLSVIFALVW VLHYREGLGW DGSALFNWH
51 PVLMTVGFEV IQGIAIIVYR LPWTWKCSKL LKMSIHAGLN AVAILAIIS
101 VVAVFENHNH NNIANMYS LH SWVGLIAVIC YLLQLLSGFS VFLLPWAPLS
151 LRAFLMPIHV YSGIVIFGTV IATLMGLTE KLIFSRLDPA YSTFPPEGVF
201 VNTLGLLILV FGALIFWIIV RPQWKRPKEP NSTILHPNGG TEQGARGSMP
251 AYSGNMMDKS DSELNNEVAA RKRNLALDEA GQRSTM

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_7e22, frame 2

SWISSPROT:C561_SHEEP CYTOCHROME B561 (CYTOCHROME B-561).., N = 1, Score

DKFZphfbr2_7e22

group: brain derived

DKFZphfbr2_7e22.2 encodes a novel 286 amino acid protein similar to b561 cytochromes

The new protein shows strong similarity to B561 cytochromes, but contains no heme binding site. In addition, a myc-type, helix-loop-helix dimerization domain is present. This helix-loop-helix domain mediates protein dimerization and has been found in proteins such as the myc family of cellular oncogenes, proteins involved in myogenesis and vertebrate proteins that bind specific DNA sequences in various immunoglobulin chains enhancers.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

strong similarity to cytochrome b561

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 4254 bp

Poly A stretch at pos. 4234, polyadenylation signal at pos. 4217

```
1 GGGGACTACC CAGAGGGCTG CCGCCGCTC TCCAAGTTCT TGTGGCCCCC
51 GCGGTGCGGA GTATGGGCGG CTGATGGCCA TGGAGGGCTA CCGGCGCTTC
101 CTGGCGCTGC TGGGGTCGGC ACTGCTCGTC GGCTTCTGT CCGGTGATCTT
151 CGCCCTCGTC TGGGTCCTCC ACTACCGAGA GGGGCTTGCC TGGGATGGGA
201 GCGCACTAGA GTTTAACTGG CACCCAGTGC TCATGGTCAC CGGCTTCGTC
251 TTATCCAGG GCATCGCCAT CATCGTCTAC AGACTGCCGT GGACCTGGAA
301 ATGCAGCAAG CTCCTGATGA AATCCATCCA TGCAGGGTTA AATGCAGTTG
351 CTGCCATTCT TGCAATTATC TCTGTGGTGG CCGTGTGTTA GAACCACAAT
401 GTTAACAATA TAGCCAATAT GTACAGTCTG CACAGCTGGG TTGGACTGAT
451 AGCTGTCATA TGCTATTTGT TACAGCTTCT TTCAGGTTTT TCAGTCTTTC
501 TGCTTCCATG GGCTCCGCTT TCTCTCCGAG CATTTCTCAT GCCCATACAT
551 GTTTATTCTG GAATTGTCAT CTTTGGAACT GTGATTGCAA CAGCACTTAT
601 GGGATTGACA GAGAAACTGA TTTTTCCTT GAGAGATCCT GCATACAGTA
651 CATTCCCGCC AGAAGGTGTT TTCGTAAATA CGCTTGGCCT TCTGATCCTG
701 GTGTTGGGGG CCCTCATTTT TTGGATAGTC ACCAGACCGC AATGGAACAG
751 TCCTAAGCAG CCAAAATCTA CCATTCTTCA TCCAAATGGA GGCAGTGAAC
801 AGGGAGCAAG AGGTTCATG CCAGCCTACT CTGGCAACAA CATGCACAAA
851 TCAGATTGAG AGTTAAACAA TGAAGTAGCA GCAAGGAAAA GAAACTTAGC
901 TCTGGATGAG TCTGGGCAGA GATCTACCAT GTAAAATGTT GTAGAGATAG
951 AGCCATATAA CGTCACGTTT CAAAACAGC TCTACAGTTT TGCTTCTCCT
1001 ATTAGCCATA TGATAATTGG GCTATGTAGT ATCAATATTT ACTTTAATCA
1051 CAAAGGATGG TTTCTTGAAA TAATTGTAT TGATTGAGGC CTATGAAGTG
1101 ACCTGAATTG GAAAGGATGT GATTAATATA AATAATAGCA GATATAAAT
1151 GTGGTTATGT TACCTTTATC TTGTTGAGGA CCACAACATT AGCACGGTGC
1201 CTTGTGACAG ATAGATACTC AATATGTGAA TATGTGTCTA CTAGTAGTTA
1251 ATTGGATAAA CTGGCAGCAT CCCTGGCCTG TTGTCATGCA GTCATTTCCT
1301 GTTAATTCTG GGAGACAATG ATTTCAACAC TAGAGGGAAG CAGTCTCTAA
1351 AGTTTAAAT CCGATAAGGA ATATCTGGGA CAGGGTTTAG ATCATGACTC
1401 TACACAGATA CCATGATGAG AGTATATTAA AGAAATTTAG GAAAGCACCT
1451 GGTTCCTTTC TCCCCTATGC TGCTTCTGCT TCCCTCCCCA GCTGGTTTGG
1501 GCTCAAATTG TCCCTGGAGA CTAGGGTTTA TGTTAGGTTA TTGATAGATT
1551 AGACCAAGTG GTTGAAGAGA TCTTCTCTGG TCAGACTTGG AAGAATTTCC
1601 AAAAGTGAAG TTAGCCCCAA GACTTCCCTA GGGTTGATGT ACTTTATGAT
1651 CCAGATGCTA AACTTCTTAG AATGAAAATA TGCTTCAACA CTTAAGTAGC
1701 ATACACTGCC CTACAAACCT CAGAGAGCAC TTTTCCCCAA GTTCTTGTTT
1751 TTATTTTGA AAGTACTCAC ACAGCACTTA CTATGCTCCA AACACTCCTC
1801 TAAGCACTTT ACACATATTA GCTCATTCAG TCCCAGACA GACGGGATGA
1851 AGTAGGTATT GTTACTGTTC CCATTTTACA GGTGAGAGAT TTGAAGCCTG
1901 GGGAGGCTAG TAACTCACCC CAAGTCACA CGGCTCATA ATGGTGGGAC
1951 TGAGACTCAG ATGCAGGCAG TCTGGCACCT CAGTCTGGAT TCTAACCATT
2001 TCACATAAGT ATTTTGTCT TGTACTACTT TGACCCACCC CTGAATAAAC
2051 CTCATTGCT GAGGTGGGT GTAGTTATTA AAGGATGCT TTTTACCTTT
2101 TGCTGTCTGC TGTGGCAGAT TCCCAGATA ACCAAGGAAA AGGGGCCACC
2151 CATACCTGGA AATAGGCCAT AGGGCCCCCTA CTACTGCCAA CAAGCCATGG
2201 CCTACCTTGA CACTTGTTT ATCTTAAAT TGTGTCTTGG TAACAAAAGA
2251 TTTGACAGG CATATCTGTA GCTTCAAGT TAATTAATTG CAATATTTTT
2301 TTCTTCAGGA TTTTAGCTGC TGAACAACCT TCAGTTTGA GCTAAAACAG
2351 ACCGTCTCTA TGGTCTGCCC TTCCCTGGGG CAATAGCTAG GGTCTTTCCT
2401 GATTTTTATG GAATTTTAGG GGATATTTTG AGCTTTGGGT TCTCAGTAGT
```

```

HMM          *CpeGtYtDWNHvpqClpCtrCePEMGQYmvqPCTwTQNTVC*
              C++++ + + +Q   C++ E+  ++++++ T   + ++
Query        49  CHDSEESMEVF-RQH--CQIAEE--YLEVKKEITLLEQRKK

```

Peptide information for frame 1

ORF from 289 bp to 714 bp; peptide length: 142
Category: similarity to known protein

1 MISTARVPAD KPVRIAFSLN DASDDTPPED SIPLVFPELD QQLQPLPPCH
51 DSEESMEVFR QHCQIAEEYL EVKKEITLLE QKKELIAKL DQAEEEKVDA
101 AELVREFEAL TEENRTLRLA QSQCVEQLEK LRIQYQKRQG SS

BLASTP hits

Entry U92030_1 from database TREMBL:
product: "TAK1"; Xenopus laevis TGF-beta-activated kinase TAK1 mRNA,
complete cds.
Score = 343, P = 1.3e-30, identities = 69/143, positives = 104/143

Entry AB009356_1 from database TREMBL:
product: "TGF-beta activated kinase 1a"; Homo sapiens mRNA for
TGF-beta activated kinase 1a, complete cds.
Score = 339, P = 2.6e-30, identities = 67/143, positives = 104/143

Entry MMPK_1 from database TREMBL:
product: "TAK1 (TGF-beta-activated kinase)"; Mouse mRNA for TAK1
(TGF-beta-activated kinase), complete cds.
Score = 339, P = 2.6e-30, identities = 67/143, positives = 104/143

Entry AB009357_1 from database TREMBL:
product: "TGF-beta activated kinase 1b"; Homo sapiens mRNA for
TGF-beta activated kinase 1b, complete cds.
Score = 339, P = 3.2e-30, identities = 67/143, positives = 104/143

Entry AB009358_1 from database TREMBL:
product: "TGF-beta activated kinase 1c"; Homo sapiens mRNA for
TGF-beta activated kinase 1c, complete cds.
Score = 144, P = 3.8e-09, identities = 30/67, positives = 47/67

Alert BLASTP hits for DKFZphfbr2_7a24, frame 1

PIR:JC5955 transforming growth factor-beta activated kinase (EC
-.-.-.-) 1a - Human, N = 1, Score = 339, P = 3e-30

>PIR:JC5955 transforming growth factor-beta activated kinase (EC -.-.-.-) 1a
- Human
Length = 579

HSPs:

Score = 339 (50.9 bits), Expect = 3.0e-30, P = 3.0e-30
Identities = 67/143 (46%), Positives = 104/143 (72%)

Query: 1 MISTARVPADKPVRI-AFSLNDASDDTPPEDSIPLVFPELDQQLQPLPPCHDSEESMEVF 59
MI+T+ ++KP R ++ +D++D ++SIP+ + LD QLQPL PC +S+ESM VF
Sbjct: 437 MITTSGPTSEKPTRSHPWTPDDSTDTNGSDNSIPMAYLTLDHQLQPLAPCPNSKESMAVF 496
Query: 60 RQHCQIAEEYLEVKKEITLLEQRKKELIAKLDQAEEEKVDAAELVREFEALTEENRTLRL 119
QHC++A+EY++V+ EI LL QRK+EL+A+LDQ E+++ + + LV+E + L +EN++L
Sbjct: 497 EQHCKMAQEYMKVQTEIALLLQRKQELVAELDQDEKQNTSRLVQEHKKLLDENKSLST 556
Query: 120 AQSQCVEQLEKLRIQYQKRQGSS 142
QC +QLE +R Q QKRQG+S
Sbjct: 557 YYQQCKKQLEVIRSQQQKRQGTS 579

Pedant information for DKFZphfbr2_7a24, frame 1

Report for DKFZphfbr2_7a24.1

[LENGTH] 142
[MW] 16377.53
[PI] 4.64
[HOMOL] TREMBL:U92030_1 product: "TAK1"; Xenopus laevis TGF-beta-activated kinase TAK1
mRNA, complete cds. 6e-26
[PROSITE] CK2_PHOSPHO_SITE 3

DKFZphfbr2_7a24

group: brain derived

DKFZphfbr2_7a24 encodes a novel 142 amino acid protein with similarity to the C-terminal part of transforming growth factor-beta activated kinases.

The novel protein shows only similarity to the C-terminus of such kinases; no kinase domain is present.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to C-terminus of TGF-beta-activated kinase

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1697 bp

No poly A stretch found, no polyadenylation signal found

```
1 GGGGAGAGAG GGGTTGTGAA GGAAGCGGA AGGAAGGGA AGGGAGGTCC
51 CGTGGGACGC TGGGGTCTGG GGTAGAGCAG GTAGCAGCGT GCTGCCCTGA
101 CAGCTGTCTC CGCTCCTCAG ATTGTCACTG GCTGCTATGC AGCAGGTGCA
151 GCCTGGTCTC TCACTGAGTC TCTACTCCAC AAAGGCAACG ACTGGCCAAG
201 GCAGTGGCTG GCTCTGGGTT ACACAAGTGC AGACACTCAA CTAAGTGAGC
251 TGGAGAGACC AGGAGAAGGC GGAGGCTCAG GTGCCACAT GATCAGCACA
301 GCCAGGGTAC CTGTGACAA GCCTGTACGC ATCGCCTTTA GCCTCAATGA
351 CGCCTCAGAT GATACACCCC CTGAAGACTC CATTCTTTG GTCTTTCCAG
401 AATTAGACCA GCAGCTACAG CCCCTGCCGC CTTGTCTATG CTCGAGGAA
451 TCCATGGAGG TGTTGAGACA GCACTGCCAA ATAGCAGAAG AATACCTTGA
501 GGTCAAAAAG GAAATCACCC TGCTTGAGCA AAGGAAGAAG GAGCTCATTG
551 CCAAGTTAGA TCAGGCAGAA GAGGAGAAGG TGGATGCTGC TGAGCTGGTT
601 CGGGAATTCG AGGCTCTGAC GGAGGAGAAT CGGACGTTGA GGTGGCCCCA
651 GTCTCAATGT GTGGAACAAC TGGAGAACT TCGAATACAG TATCAGAAGA
701 GGCAGGGCTC GTCCTAACTT TAAATTTTTC AGTGTGAGCA TACGAGGCTG
751 ATGACTGCCC TGTGCTGGCC AAAAGATTTT TATTTTAAAT GAATAGTGAG
801 TCAGATCTAT TGCTTCTCTG TATTACCCAC ATGACAACG TCTATAATGA
851 GTTACTGCTT TGCCAGCTTC TAGCTTGAGA GAAGGGATAT TTTAAATGAG
901 ATCATTAAAC TGAAACTATT ACTAGTATAT GTTTTGGAG ATCAGAATTC
951 TTTTCCAAAG ATATATGTTT TTTTCTTTTT TAGGAAGATA TGATCATGCT
1001 GTACAACAGG GTAGAAAATG GTAAAATAG ACTATTGACT GACCCAGCTA
1051 AGAATCGCGG GCTGAGCAGA GTTAAACCAT GGGACAAACC CATAACATGT
1101 TCAGCATAGT TTCACGTATG TGTATTTTTA AATTTCATGC CTTTAATATT
1151 TCAAATATGC TCAAATTTAA ACTGTCAGAA ACTTCTCTGC ATGTATTTAT
1201 ATTTGCCAGA GTATAAACTT TTATACTCTG ATTTTATCC TTCAATGATT
1251 GATTATACTA AGAATAAATG GTCACATATC CTAAAAGCTT CTTTATGAAA
1301 TTATTAGCAG AAACCATGTT TGAAACCAAA GCACATTTGC CAATGCTAAC
1351 TGGCTGTTGT AATAATAAAC AGATAAGGCT GCATTTGCTT CATGCCATGT
1401 GACCTCACAG TAAACATCTC TGCCTTTGCC TGTGTGTGTT CTGGGGGAGG
1451 GGGGACATGG AAAAATATTG TTTGGACATT ACTTGGGTGA GTGCCCATGA
1501 AGACATCAGT GAACTTGTA CTATTGTTT GTTTTGGATT TAAGGAGATG
1551 TTTTAGATCA GTAACAGCTA ATAGGAATAT GCGAGTAAAT TCAGAATTGA
1601 AACAATTTCT CCTTGTCTA CCTATCACC CAATTTCTCA AATTGAACCT
1651 TTTGTTATAT GTCCATTCTT ATTCATGTAA CTTCTTTTTC ATTAAAC
```

BLAST Results

No BLAST result

Medline entries

98130593:
Role of TAK1 and TAB1 in BMP signaling in early Xenopus development.

(No Prosite data available for DKFZphfbr2_78n23.2)

(No Pfam data available for DKFZphfbr2_78n23.2)


```

51 GEGEASADD GSLNTSGAGP KSWQVPPAP EVQIRTPRVN CPEKVIICLD
101 LSEEMSLPKL ESFNGSKTNA LNVSQMIEM FVRTKHKIDK SHEFALVVVN
151 DDTAWLSGLT SDPRELCSCL YDLETASCST FNLEGLFSLI QQKTELPVTE
201 NVQTIPPPYV VRTILVYSRP PCQPQFSLTE PMKKMFQCPY FFFDVVYIHN
251 GTEEKEEEMS WKDMFAFMGS LDTKGTSYKY EVALAGPALE LHNMAKLLA
301 HPLQRPCQSH ASYSLLEEED EAIEVEATV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78n23, frame 2

PIR:T05304 hypothetical protein F26P21.80 - Arabidopsis thaliana, N = 1, Score = 142, P = 1.5e-07

>PIR:T05304 hypothetical protein F26P21.80 - Arabidopsis thaliana
Length = 264

HSPs:

Score = 142 (21.3 bits), Expect = 1.5e-07, P = 1.5e-07
Identities = 56/216 (25%), Positives = 97/216 (44%)

```

Query:   93 EKVIICLDL-SEEMSLPKLESFNGSKTNALNVSQMIEMFVRTKHKIDKSHEFALVVVND 151
          E ++IC+D+ +E M K NG + ++ I +F+ K I+ H FA +
Sbjct:   26 EDILICIDVDAESMVEMKTTGTNGRPLIRMECVQAIILFIHNKLSINPDHRFAFATLAK 85

Query:   152 DTAWLSG-LTSDPRELCSCLYDLE-TASCSTFNLEGLFSLIQQKTELPVTENVQTIPPPY 209
          AWL TSD + L L S S +L LF Q+ ++ +N
Sbjct:   86 SAAWLKKEFTSDAESAVASLRGLSGNKSSSRADLTLLFRAAAQEAQVSRQN-----R 138

Query:   210 VVRTILVYSRPPCQPQFSLTEPMKKMFQCPYFFFDVVYIHNNGTEEKEEEMSWKDMF-AFM 268
          + R IL+Y R +P P+ + F DV+Y+H ++ + +D++ + +
Sbjct:   139 IFRVILIYCRSSMRPTHEW--PLNQKL----FTLDVMYLH---DKPSPDNCPQDVYDSL 189

Query:   269 GSLD--TKGTSYKYEVALAGPALELHNMAKLLAHPQRPCQ 308
          +++ ++ Y +E G A + M+ LL HP QR Q
Sbjct:   190 DAVEHVSEYEGYIFESG-QGLARSVFKPMSMLLTHPQQRCAQ 230

```

Pedant information for DKFZphfbr2_78n23, frame 2

Report for DKFZphfbr2_78n23.2

```

[LENGTH]      329
[MW]           36560.10
[pI]           4.60
[HOMOL]        PIR:T05304 hypothetical protein F26P21.80 - Arabidopsis thaliana 7e-07
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY      9.73 %

```

```

SEQ      MEVAEPSSPTEEEEEEHSAEPRPRTRSNPEGAEDRAVGAQASVGSRSERGEASADD
SEG      .XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD      cccccccccchhhhhhhhhhhcccccccccccccccccccccccccccccccccccccc

SEQ      GSLNTSGAGPKSWQVPPAPAEVQIRTPRVNCPKVIICLDLSEEMSLPKLESFNGSKTNA
SEG      .....
PRD      cccccccccccccccccccccccccccccccccccccccccccccccccccccccce

SEQ      LNVSQMIEMFVRTKHKIDKSHEFALVVVNDDTAWLSGLTSDPRELCSCLYDLETASCST
SEG      .....
PRD      ehhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccc

SEQ      FNLEGLFSLIQQKTELPVTENVQTIPPPYVVRTILVYSRPPCQPQFSLTEPMKKMFQCPY
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccccccccccchhhhhheee

SEQ      FFFDVVYIHNNGTEEKEEEMSWKDMFAFMGSLDTKGTSYKYEVALAGPALELHNMAKLLA
SEG      .....
PRD      eeeeeeeccccchhhhhhhhhhhhhhhhhhhccccccccccccccccccccccccchhhhhhhhhhh

SEQ      HPLQRPCQSHASYSLLEEDEAIEVEATV
SEG      .....XXXXXXXXXXXX
PRD      hccccccccchhhhhhhhhhhhhhhhhhhcc

```

DKFZphf5r2_78n23

group: brain derived

DKFZphf5r2_78n23 encodes a novel 329 amino acid protein with similarity to A.thaliana F26P21.80 protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to A.thaliana F26P21.80

Sequenced by MediGenomix

Locus: /map="89.1 cR from top of Chr19 linkage group"

Insert length: 1447 bp

Poly A stretch at pos. 1374, polyadenylation signal at pos. 1353

```
1 TACAACTTCC GGCTGTAAAG ATGGCGGCTT CCTAGTGAGT CGGCGGCTGA
51 CTTAGAAGGA GGTTTCAGGCT ACGGTGAGCC GAAGCCACAC AGGAGCCATG
101 GAAGTGGCAG AGCCCAGCAG CCCCACTGAA GAGGAGGAGG AGGAAGAGGA
151 GCACTCGGCA GAGCCTCGGC CCCGCACTCG CTCCAATCCT GAAGGGGCTG
201 AGGACCGGGC AGTAGGGGCA CAGGCCAGCG TGGGCAGCCG CAGCGAGGGT
251 GAGGGTGAGG CCGCCAGTGC TGATGATGGG AGCCTCAACA CTCAGGAGGC
301 CGGCCCTAAG TCCTGGCAGG TGCCCCCGCC AGCCCCTGAG GTCCAAATTC
351 GGACACCAAG GGTCAACTGT CCAGAGAAAG TGATTATCTG CCTGGACCTG
401 TCAGAGGAAA TGTCACCTGC AAAGCTGGAG TCGTTCAACG GCTCCAAAAC
451 CAACGCCCTC AATGTCTCTC AGAAGATGAT TGAGATGTTC GTGCGGACAA
501 AACACAAGAT CGACAAAAGC CACGAGTTTG CACTGGTGGT GGTGAACGAT
551 GACACGGCCT GGCTGTCTGG CCTGACCTCC GACCCCCGCG AGCTCTGTAG
601 CTGCCTCTAT GATCTGGAGA CGGCCTCCTG TTCCACCTTC AATCTGGAAG
651 GACTTTTCAG CCTCATCCAG CAGAAAACCTG AGCTTCCGCT CACAGAGAAC
701 GTGCAGACGA TTCCCCCGCC ATATGTGGTC CGCACCATCC TTGTCTACAG
751 CCGTCCACCT TGCCAGCCCC AGTTCTCCTT GACGGAGCCC ATGAAGAAAA
801 TGTTCCAGTG CCCATATTTC TTCTTTGACG TTGTTTACAT CCACAATGGC
851 ACTGAGGAGA AGGAGGAGGA GATGAGTTGG AAGGATATGT TTGCCTTCAT
901 GGGCAGCCTG GATACCAAGG GTACCAGCTA CAAGTATGAG GTGGCACTGG
951 CTGGGCCAGC CCTGGAGTTG CACAACCTGCA TGGCGAAACT GTTGGCCAC
1001 CCCCTGCAGC GGCCTTGCCA GAGCCATGCT TCCTACAGCC TGCTGGAGGA
1051 GGAGGATGAA GCCATTGAGG TTGAGGCCAC TGTCTGAACC ATCCCTGTAC
1101 ATCTGCACCT TCTTGTGCAA GGAAGTCCTT GGCCTAAAGC CTTGGTTCTC
1151 AAAGTGGGTT CCTTGGGACC TCCGGGGTGG GGGGGTTCCA GGAGGCACGT
1201 AGGGTACCTT CGAGGGTCTT AGGAGGGAAA CCCAGGATTC CAGGAGGGAT
1251 CCCAGGAACG GTGGGCACCC ATTTTCTGTG TCTCCAGCC CATTCCACT
1301 CCTAGTTTGT CATGGATAAT TTTTGTCTT CCCTGTGTGA TTTTGGCCAT
1351 CAAAATAAAA ATTTGAGACT CGTTAAAAAA AAAAAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAAAAAAAAA AAAAAAGAAA AAAAAAAAAA AAAAAAA
```

BLAST Results

Entry HS806352 from database EMBL:
human STS EST192543.
Score = 1285, P = 2.5e-51, identities = 263/266

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 98 bp to 1084 bp; peptide length: 329
Category: similarity to unknown protein
Classification: no clue

1 MEVAEPSSPT EEEEEEEHS AEPRPRTRSN PEGAEDRAVG AQASVGSRSE

TAYLLVY K
 Sbjct: 357 TAYLLVYTK 365

Pedant information for DKFZphfbr2_78k24, frame 1

Report for DKFZphfbr2_78k24.1

[LENGTH] 372
 [MW] 43011.12
 [pI] 8.05
 [HOMOL] TREMBLNEW:AF069502_1 product: "ubiquitin specific protease UBP43"; Mus musculus
 ubiquitin specific protease UBP43 mRNA, complete cds. 1e-151
 [FUNCAT] 06.13 proteolysis [S. cerevisiae, YMR304w] 3e-19
 [FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YJL197w] 3e-16
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation,
 palmitoylation, farnesylation and processing) [S. cerevisiae, YMR223w] 1e-15
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YNL186w] 6e-12
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDR069c] 9e-11
 [FUNCAT] 10.03.99 other osmosensing activities [S. cerevisiae, YDR069c] 9e-11
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YDR069c] 9e-11
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDR069c] 9e-11
 [FUNCAT] 09.25 vacuolar and lysosomal biogenesis [S. cerevisiae, YDR069c] 9e-11
 [BLOCKS] BL00582A Ribosomal protein L33 proteins
 [BLOCKS] BL00972E
 [BLOCKS] BL00972D
 [BLOCKS] BL00972A
 [EC] 2.4.2.29 Queuine tRNA-ribosyltransferase 1e-06
 [PIRKW] pentosyltransferase 1e-06
 [PIRKW] glycosyltransferase 1e-06
 [PIRKW] tRNA modification 1e-06
 [PIRKW] alternative splicing 7e-11
 [PIRKW] hydrolase 7e-06
 [SUPFAM] deubiquinating enzyme SSV7 2e-09
 [PROSITE] UCH_2_2_1
 [PFAM] Ubiquitin carboxyl-terminal hydrolases family 2
 [PFAM] Ubiquitin carboxyl-terminal hydrolases family 2
 [KW] Alpha_Beta

SEQ MSKAFGLLRQICQSILAESSQSPADLEEKKEEDSNMKREQPRERPAWDYPHGLVGLHNI
 PRD cccceeechhhhhhhccccccccchhhhhhhcccccccccccccccccccccccccccc
 SEQ GQTCLNSLIQVFMNVDFTRILKRITVPRGADEQRRSVPFQMLLLEKMQDSRQKAVRP
 PRD cceeehhhhhhhhccccchhhhhhhccccccccccccchhhhhhhhhhhhhhhhhhhhhcccc
 SEQ LELAYCLQKCNVPLFVQHDAAQLYLKLWNLIKQDITDVHLVERLQALYTIRVKDSLICVD
 PRD hhhhccccccccccccchheeeee
 SEQ CAMESSRNSSMLTLPISLFDVDSKPLKTLEDALHCFQPRELSSKSKFCENCCKKTRGK
 PRD cccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhcccccccccecccccccc
 SEQ QVLKLTHLPQTLTIIHLMRFSIRNSQTRKICHSLYFPQSLDFSQILPMKRESCDAEEQSGG
 PRD cceeeccccchhhhhhhhhhhccccchhhhhcccccccccccccccccccccccccccccccc
 SEQ QYELFAVIAHVGMAADSGHYCVYIRNAVDGKWFCFNDNSNICLVSWEDIQCTYGNPNYHWQE
 PRD eeeeeeeeeccccccccceeeccccccccceeeccccccccccccccccccccccccchh
 SEQ TAYLLVYMKMEC
 PRD hhhhhhhhhcccc

Prosite for DKFZphfbr2_78k24.1

PS00973 302->320 UCH_2_2 PDOC00750

Pfam for DKFZphfbr2_78k24.1

HMM_NAME Ubiquitin carboxyl-terminal hydrolases family 2
 HMM *GIqN1GNTCYMNSIIQCL*
 G+ N+G TC +NS+IQ+
 Query 56 GLHNIGQTCLNSLIQVF 73

Medline entries

99182491:

A novel ubiquitin-specific protease, UBP43, cloned from leukemia fusion protein AML1-ETO-expressing mice, functions in hematopoietic cell differentiation.

Peptide information for frame 1

ORF from 160 bp to 1275 bp; peptide length: 372
 Category: strong similarity to known protein
 Classification: Protein management
 Prosite motifs: UCH_2_2 (302-320)

```

1 MSKAFGLLRQ ICQSILAESS QSPADLEEKK EEDSNMKREQ PRERPAWDY
51 PHGLVGLHNI GQTCCNLNLI QVFVMNVDFTRILKRITVPR GADEQRRSVP
101 FQMLLLLEKM QDSRQKAVRP LELAYCLQKC NVPLFVQHDA AQLYLKLWNL
151 IKDQITDVHL VERLOALYTI RVKDSLICVD CAMESSRNSS MLTLPPLSLFD
201 VDSKPLKTL DALHCFQPR ELSSKSKCFC ENCGKKTRGK QVLKLTHLPQ
251 TLTIHLMRFS IRNSQTRKIC HSLYFPQSLD FSQILPMKRE SCDAAEQSGG
301 QYELFAVIAH VGMADSGHYC VYIRNAVDGK WFCFNDNIC LVSWEDIQCT
351 YGNPNYHWQE TAYLLVYMK EC

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78k24, frame 1

TREMBLNEW:AF069502_1 product: "ubiquitin specific protease UBP43"; Mus musculus ubiquitin specific protease UBP43 mRNA, complete cds., N = 1, Score = 1367, P = 1e-139

SWISSPROT:UBPE_DROME UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E) ., N = 2, Score = 248, P = 5.3e-33

>TREMBLNEW:AF069502_1 product: "ubiquitin specific protease UBP43"; Mus musculus ubiquitin specific protease UBP43 mRNA, complete cds.
 Length = 368

HSPs:

Score = 1367 (205.1 bits), Expect = 1.0e-139, P = 1.0e-139
 Identities = 262/369 (71%), Positives = 295/369 (79%)

```

Query:      1 MSKAFGLLRQICQSILAESSQSPADLEEKK EEDSNMKREQPRERPAWDYPHGLVGLHNI 60
            M K FGLLR+ CQS++AE Q A LEE E   KR  R+  AWD PHGLVGLHNI
Sbjct:      1 MGKGFGLLRKPCQSVVAEPQQYSA-LEE--ERTMKRKRVLRSRLCSAWDSPHGLVGLHNI 57

Query:      61 GQTCCNLNLIQVFVMNVDFTRILKRITVPRGADEQRRSVPFQMLLLLEKMQDSRQKAVRP 120
            GQTCCNLNLIQVF+MN+DF ILKRITVPR A+E+RSVPFQ+LLLLEKMQDSRQKA+ P
Sbjct:      58 GQTCCNLNLIQVFMMNMDFRMILKRITVPRSAEERKRVSVPFQLLLLLEKMQDSRQKALLP 117

Query:      121 LELAYCLQKCNVPLFVQHDAQAQLYLKLWNLIKDQITDVHLVERLOALYTI RVKDSLICVD 180
            EL CLQK NVPLFVQHDAQAQLYL+WNL KDQITD L ERLQ L+TI ++SLICV
Sbjct:      118 TELVQCLOKYNVPLFVQHDAQAQLYLTIWNLTKDQITDITDLTERLQGLFTIWTQESLICVG 177

Query:      181 CAMESSRNSSMLTLPPLSLFDVDSKPLKTLEDALHCFQPRELSSKSKCFCENCGKKTRGK 240
            C ESSR S +LTL L LFD D+KPLKTLEDAL CF QP+EL+S  C CE CG+KT K
Sbjct:      178 CTAESSRRSKLLTSLPLFORDAKPLKTLEDALRCFVQPKELASSDMC-CETCGEKTPNWK 236

Query:      241 QVLKLTHLPQTLTIHLMRFSIRNSQTRKICHSLYFPQSLDFSQILPMKRESQDAEEQSGG 300
            QVLKLTHLPQTLTIHLMRFS RNS+T KICH+ FPQSLDFSQ+LP + + D +EQS
Sbjct:      237 QVLKLTHLPQTLTIHLMRFSARNRTEKICHSVNFPQSLDFSQVLPTEEDLGDTKEQSEI 296

Query:      301 QYELFAVIAHVGMADSGHYCVYIRNAVDGKWFCFNDNICLVSWEDIQCTYGNPNYHWQE 360
            YELFAVIAHVGMAD GHYC YIRN VDGKWFCFND+ +C V+W+D+QCTYGN Y W+E
Sbjct:      297 HYELFAVIAHVGMADFGHYCAYIRNPVDGKWFCFNDSHVCWVTWKDVQCTYGNHRYRWRE 356

Query:      361 TAYLLVYMK 369

```

DKFZphfbr2_78k24

group: metabolism

DKFZphfbr2_78k24 encodes a novel 372 amino acid protein with similarity to *Mus musculus* ubiquitin specific protease UBP43.

The novel protein contains a Prosite ubiquitin carboxyl-terminal hydrolases family 2 signature 2. Ubiquitin carboxyl-terminal hydrolases (EC 3.1.2.15) (UCH) (deubiquitinating enzymes) are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins.

The new protein can find application in modulation of protein stability/degradation in cells.

Ubiquitin carboxyl-terminal hydrolases family 2 signature 2.

strong similarity to mouse ubiquitin specific protease UBP43

Sequenced by MediGenomix

Locus: unknown

Insert length: 1874 bp

Poly A stretch at pos. 1852, polyadenylation signal at pos. 1836

```
1 AGTCCCGACG TGGAACTCAG CAGCGGAGGC TGGACGCTTG CATGGCGCTT
51 GAGAGATTCC ATCGTGCCTG GCTCACATAA GCGCTTCCTG GAAGTGAAGT
101 CGTGCTGTCC TGAACGCGGG CCAGGCAGCT GCGGCCTGGG GGTTTTGGAG
151 TGATCACGAA TGAGCAAGGC GTTTGGGCTC CTGAGGCAAA TCTGTCAGTC
201 CATCCTGGCT GAGTCCTCGC AGTCCCCGGC AGATCTTGAA GAAAAGGAAG
251 AAGAAGACAG CAACATGAAG AGAGAGCAGC CCAGAGAGCG TCCCAGGGCC
301 TGGGACTACC CTCATGGCCT GGTGGTTTCA CACAACATTG GACAGACCTG
351 CTGCCCTTAA TCCTTGATTC AGGTGTTTCT AATGAATGTG GACTTCACCA
401 GGATATTGAA GAGGATCACG GTGCCAGGGG GAGCTGACGA GCAGAGGAGA
451 AGCGTCCCTT TCCAGATGCT TCTGCTGCTG GAGAAGATGC AGGACAGCCG
501 GCAGAAAGCA GTGCGGCCCC TGGAGCTGGC CTACTGCCTG CAGAAGTGCA
551 ACGTGCCCTT GTTTGTCCAA CATGATGCTG CCCAACTGTA CCTCAAATC
601 TGGAACTGA TTAAGGACCA GATCACTGAT GTGCACTTGG TGGAGAGACT
651 GCAGGCCCTG TATACGATCC GGGTGAAGGA CTCCTTGATT TGCCTTGACT
701 GTGCCATGGA GAGTAGCAGA AACAGCAGCA TGCTCACCTT CCCACTTTCT
751 CTTTTTGATG TGGACTCAAA GCCCCTGAAG ACACCTGGAGG ACGCCCTGCA
801 CTGCTTCTTC CAGCCCAGGG AGTTATCAAG CAAAAGCAAG TGCTTCTGTG
851 AGAACTGTGG GAAGAAGACC CGTGGGAAAC AGGTCTTGAA GCTGACCCAT
901 TTGCCCCAGA CCTGACAAT CCACCTCATG CGATTCTCCA TCAGGAATTC
951 ACAGACGAGA AAGATCTGCC ACTCCCTGTA CTTCCCCCAG AGCTTGGATT
1001 TCAGCCAGAT CCTTCCAATG AAGCGAGAGT CTTGTGATGC TGAGGAGCAG
1051 TCTGGAGGGC AGTATGAGCT TTTTGCTGTG ATTGCGCAGC TGGGAATGGC
1101 AGACTCCGGT CATTACTGTG TCTACATCCG GAATGCTGTG GATGGAAAAT
1151 GGTCTGCTT CAATGACTCC AATATTTGCT TGGTGTCTG GGAAGACATC
1201 CAGTGATACCT ACGGAAATCC TAACTACCAC TGGCAGGAAA CTGCATATCT
1251 TCTGGTTTAC ATGAAGATGG AGTGCTAATG GAAATGCCCA AAACCTTCAG
1301 AGATTGACAC GCTGTCATT TCCATTTCCG TTCCTGGATC TACGGAGTCT
1351 TCTAAGAGAT TTTGCAATGA GGAGAAGCAT TGTTTTCAAA CTATATAACT
1401 GAGCCTTAT TATAATTAGG GATATTATCA AAATATGTAA CCATGAGGCC
1451 CCTCAGGTCC TGATCAGTCA GAATGGATGC TTTCAACAGC AGACCCGGCC
1501 ATGTGGCTGC TCGTCTCTGG GTGCTCGCTG CTGTGCAAGA CATTAGCCCT
1551 TTAGTTATGA GCCTGTGGGA ACTTCAGGGG TTCCCAGTGG GGAGAGCAGT
1601 GCGACTGGGA GGCATCTGGG GGCCAAAGCT CAGTGGCAGG GGGTATTTCA
1651 GTATTATACA ACTGCTGTGA CCAGACTTGT ATACTGGCTG AATATCAGTG
1701 CTGTTTGTA TTTTCACTT TGAGAACCBA CATTAATTCC ATATGAATCA
1751 AGTGTTTGT AACTGCTATT CATTATTCCA GCAAATATT ATTGATCATC
1801 TCTTCTCCAT AAGATAGTGT GATAAACACA GTCATGAATA AAGTTATTTT
1851 CCACAAAAAA AAAAAAAAAA AAAA
```

BLAST Results

Entry AC005500 from database EMBL:

, complete sequence.

Score = 859, P = 5.7e-143, identities = 175/179

8 exons matching Bp 317-1230

(No Pfam data available for DKFZphfbr2 78d13.2)

No Medline entry

Peptide information for frame 2

ORF from 125 bp to 901 bp; peptide length: 259
Category: similarity to unknown protein
Classification: no clue

```

1 MAACRALKAV LVDLSGTLHI EDAAVPGAQE ALKRLRGASV IIRFVTNTTK
51 ESKQDLLERL RKLEFDISED EIFTSLTAAR SLERKQVRP MLLVDDRALP
101 DFKGIQTS DP NAVVMGLAPE HFHYQILNQA FRLLLDGAPL IAIHKARYYK
151 RKDGLALGPG PFVTALEYAT DTKATVVGKP EKTFFLEALR GTGCEPEEAV
201 MIGDDCRDDV GGAQDVGM LG ILVKTGKYRA SDEEKINPPP YLTCESEFPA
251 VDHILQHLL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78d13, frame 2

TREMBL:CEUK08B12_1 gene: "K08B12.3"; Caenorhabditis elegans cosmid K08B12., N = 1, Score = 609, P = 2.2e-59

TREMBL:CEC13C4_5 gene: "C13C4.4"; Caenorhabditis elegans cosmid C13C4, N = 1, Score = 408, P = 4.4e-38

>TREMBL:CEUK08B12_1 gene: "K08B12.3"; Caenorhabditis elegans cosmid K08B12.

Length = 257

HSPs:

Score = 609 (91.4 bits), Expect = 2.2e-59, P = 2.2e-59
Identities = 132/251 (52%), Positives = 172/251 (68%)

```

Query:      7 LKAVLVDSGLTHIEDAAVPGAQEALKRLRGASV IIRFVTNTTKESKQDLLERLRKLEFD 66
             + +VL+DLSGT+HIE+ A+PGAQ AL+ LR + + +FVTNTTKESK+ L +RL F
Sbjct:      4 ISSVLIDLSGTIHIEEFAIPGAQTALQLLRQHAKV-KFVTNTTKESKRLHQLRLINCQFK 62

Query:     67 ISEDEIFTSLTAARSLERKQVRPMLLVDDRALPDFKGIQTS DPNAVVMGLAPEHFHYQI 126
             + ++EIFTSLTAAR L+ + Q RP +VDDRA+ DF+GI T DPNAV+GLAPE F+
Sbjct:     63 VEKEEIFTSLTAARDLIVKNQYRPF FIVDDRAMDEFEGISTDDPNAV+VIGLAPEKFNDDT 122

Query:    127 LNAQFRLLLDG-APLIAIHKARYYKRKDGALGPGPFVTALEYATDTKATVVGKPEKTEFF 185
             LN AFRL+ + A LIAI+K RY++ GL LGPG +V LEY+ +AT+VGKP K FF
Sbjct:    123 LTHAFRLIKEKKASLIAINKGRYHQTNAGLCLGPGTYVAGLEYSAGVEATIVGKPNKLF 182

Query:    186 LEALRGTG--CEPEEAVMIGDDCRDDVGGGAQDVGM LGILVKTGKYRASDEEKINPPPYLT 243
             AL+ + AVMIGDD DD GA +GM ILVKTGK+R DE K+
Sbjct:    183 ESALQSLNENVDFSSAVMIGDDVNDALGAIKIGMRAILVKTGKFRDGDDELKVKN---V 238

Query:    244 CESFPHAVDHILQH 257
             SF AV+ I+++
Sbjct:    239 ANSFVDVNMIIEN 252

```

Pedant information for DKFZphfbr2_78d13, frame 2

Report for DKFZphfbr2_78d13.2

```

[LENGTH]      259
[MW]           28536.04
[pI]           5.84
[HOMOL]        TREMBL:CEUK08B12_1 gene: "K08B12.3"; Caenorhabditis elegans cosmid K08B12. 3e-
62
[FUNCAT]       r general function prediction [M. jannaschii, MJ1437] 3e-05
[SUPFAM]       nagD protein 4e-18
[KW]           Alpha_Beta

```


DKF2phfbr2_78d13

group: brain derived

DKF2phfbr2_78d13 encodes a novel 259 amino acid protein with similarity to *C. elegans* putative protein from cosmid K08B12.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to *C.elegans* K08B12.3

Sequenced by MediGenomix

Locus: /map="338.4 cR from top of Chr18 linkage group"

Insert length: 2195 bp

Poly A stretch at pos. 2175, polyadenylation signal at pos. 2156

```
1 CGTCCGTCGG GCAGCAGCGG GGCTGTCTAT CCCGGCTGAG GACCCGCGGC
51 CAGTGGCGGT GGCTGGCTTT GCCATTAGCG GGGGCCTTTC CTGAGGACGG
101 CGTACGGAGT GTGGGGAATG AAGGATGGCA GCATGCCGTG CATTAAAAGC
151 TGTTTTGGTA GATCTCAGTG GCACACTTCA CATTGAAGAT GCAGCTGTGC
201 CAGGCGCACA GGAAGCTCTT AAAAGGTTAC GTGGTGCTTC TGTAATCATT
251 AGGTTTGTGA CCAATACAAC CAAAGAGAGC AAGCAAGACC TGTTAGAAAG
301 GTTGAGAAAA TTGGAATTTG ATATCTCTGA AGATGAAATA TTCACATCTC
351 TGACTGCAGC CAGAAGTTTA CTAGAGCGGA AACAAAGTCAG ACCCATGCTG
401 CTAGTTGATG ATCGGGCACT ACCTGATTTC AAAGGAATAC AAACAAGTGA
451 TCCTAATGCT GTGGTCATGG GATTGGCACC AGAACATTTT CATTATCAAA
501 TTCTGAATCA AGCATTCCGG TTACTCCTGG ATGGAGCACC TCTGATAGCA
551 ATCCACAAAG CCAGGTATTA CAAGAGGAAA GATGGCTTAG CCCTGGGGCC
601 TGGACCATTT GTGACTGCTT TAGAGTATGC CACAGATACC AAAGCCACAG
651 TCGTGGGGAA ACCAGAGAAG ACGTTCTTTT TGGGAAGCATT GCGGGGCACT
701 GGCTGTGAAC CTGAGGAGGC TGTCAATGTA GGAGATGATT GCAGGGATGA
751 TGTGGTGGG CCTCAAGATG TCGGCATGCT GGCATCTTA GTAAAGACTG
801 GGAATATCG AGCATCAGAT GAAGAAAAAA TTAATCCACC TCCTTACTTA
851 ACTTGTGAGA GTTCCCTCA TGCTGTGGAC CACATTCTGC AGCACCTATT
901 GTGAAGCAAT GTGTGCATCT GAAGCAACTT GAAATGCAGC TTCTTATTGT
951 CTGGAATGAA TCCCTTACCA ACTCAGTGCC AGCATCGGTA GACACCAGTC
1001 AGTGCTGATC CCTTTTAAAC CCTCTTTTGT TGTGCATTAA TTAGAAAGAA
1051 AGGTATTGAA TTGGCGCTAG CCAGTAAGCC TTGCTAATCT CTTTTATTTT
1101 GTAAGTGAAG ATGAGACCCA AAGAAAGGGA AAGCTGAGAT TTTGTGCCAT
1151 TCCTTTTAAA ATATTCATCA GCTTAGGTGC GCCTGTGGGG GAAAAGCTAC
1201 TACAGGGAAG AGTGTTCTCT GCTGTCTCTT CACTGGAATA CAGGGAGGGG
1251 GGATTTTCTA CTGTGAAGAA AGTTGAATGG TGGTTTTTAA ATTATAAAGT
1301 AATGTATTAA AAGGTGCATT AGGCTGTAGT TCTAATATTG AGTTCAACTG
1351 TGAATCCCAT CAGATGTGCC AAATGGAGAA GACAGAAAGC AACAAAGTGA
1401 ATTGTTCTTT AGCCCAAGTG GTACAGTGAA TTTGCTTTAA CAGATGTTGA
1451 AAATAAATTT TTCTACTGTA TTCCAGCAC GGGTGACTTC TTTTCTCTT
1501 CATTAGCCAG AGATGACTAA TTTAAATTTA GAACCAAGAT TTAATTTTAA
1551 TTAATATTTT CTAATAAAC CTACTCATTG CAGATACCTA TTACTACTGT
1601 TAACAGTTGT TTTGGAAATT TTATGTAAAA TTAAACTAT CAGTATTTTA
1651 CAGATGTTTT AATTAGACAT TGTATTAAAC AGGAACAGTG CAGAAACTAG
1701 AATCAAGCCT TATAATATCT TATAGACCAT GCATTTTGA AGTTAGTGTC
1751 CACTAGGGTC CTATTAAGTG TACATTTGCA AGATTTTATT ATTTTGCCT
1801 CTGACACTAT GGGAAAAATT TTTTAGAAGC TATGGGACA GATTCAAGCT
1851 TTTATGCACT TGGTTACTAC AGCTGTAAAA TGAATCTCG TCTGTAGCA
1901 TGGATTATTC TTCTCATGTT AAACCCACCA AAATAAAGGG GACTAAATAG
1951 GTAATGATT TCCTAGTGCA TTTGCATACT GTGATAATCC TGGGCCTTGC
2001 AATAGTTCTA CAGGGCTCTT GGGCATTGAA TTATTAGGAT GTAATTGTAC
2051 ATCATTGTAG TGTTACCTT ATTGAAGCTC ACTCTGATGT TAATGAGCTT
2101 CGGGTTTTGA TGCTTGTTTA GAGATCAGCA GTCTGGATG GGAGGGAACA
2151 AAGCTAAATA AATGTTAGTT TGGTAAAAA AAAAAAAAAA AAAAA
```

BLAST Results

Entry H5599355 from database EMBL:
human STS WI-13484.
Score = 1262, P = 3.6e-52, identities = 274/289

Medline entries

```

MEM .....
SEQ  SNSKTKTSLGGIKVNGPCLESLVLTYYINAIISRGDLPCMENAVLALAQIENSAAVQKAI AH
SEG  .....
PRD  cccceeeccccccccccccchhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhhh
COILS .....
MEM  .....

SEQ  YDQQMGGKQVQLPAETLQELLDLHRVSEEREATEVYMKNSFKDVDHFLQKKLAAQLDKKRDD
SEG  .....
PRD  hhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhh
COILS .....
MEM  .....

SEQ  FCKQNEASSDRCSALLQVIFSPLEEEVKAGIYSKPGGYCLFIQKLQDLEKKYYEPRKG
SEG  .....
PRD  hhhhhhhchhhhhhhhhhhhhhhhhhhhhhhccccccccceehhhhhhhhhhhhhhhhhhhhh
COILS .....
MEM  .....

SEQ  IQAEIILQTYLKSKEVTDAILQTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQ
SEG  .....xxxxxxxxxxxxx.....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS .....
MEM  .....

SEQ  QMEEKEKSYQEHVKQLTEKMERERAQLLEEQKTLTSKLQEQARVLKERCQGESTQLQN
SEG  .....xxxxxxxxxxxxx.....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
MEM  .....

SEQ  EIQLQKTLKKKTKRYMSHKLKI
SEG  ..xxxxxxxxxxxxx.....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS CCCCCC.....
MEM  .....

```

Prosites for DKFZphfbr2_78c24.3

PS00016	272->275	RGD	PDOC00016
PS00017	45->53	ATP_GTP_A	PDOC00017

(No Pfam data available for DKFZphfbr2_78c24.3)

Score = 1012 (151.8 bits), Expect = 4.9e-238, Sum P(2) = 4.9e-238
Identities = 194/211 (91%), Positives = 200/211 (94%)

Query:	1	MAPEIHMTGPMCLIENGTNGELVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG	60
		MA EIHMTGPMCLIENGTNG L+ANPEALKILSAITQP+VVVVAIVGLYRTGKSYLMNKLKAG	
Sbjct:	1	MASEIHMTGPMCLIENGTNGRLMANPEALKILSAITQPMVVVVAIVGLYRTGKSYLMNKLKAG	60
Query:	61	KNKGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDVKKGNQNDSWIFTLAV	120
		K KGFSLGSTV+SHTKGIWMWCVPHPKK H LVLLDTEGLGDV+KGNQNDSWIF LAV	
Sbjct:	61	KKKGFSLGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGNQNDSWIFALAV	120
Query:	121	LLSSTLVYNSMGITNQAMQQLYYVTELTTHRIRSKSSPDENENE--DSADFVSFFPDFVW	178
		LLSST VYNS+GTINQAMQQLYYVTELTTHRIRSKSSPDENENE DSADFVSFFPDFVW	
Sbjct:	121	LLSSTFVYNSIGITNQAMQQLYYVTELTTHRIRSKSSPDENENEVEDSADFVSFFPDFVW	180
Query:	179	TLRDFSLDLEADGQPLTPDEYLEYSKLKTQG	209
		TLRDFSLDLEADGQPLTPDEYL YSIKL +G	
Sbjct:	181	TLRDFSLDLEADGQPLTPDEYLTYSKLKKG	211

Pedant information for DKFZphfbr2_78c24, frame 3

Report for DKFZphfbr2_78c24.3

```

[LENGTH]      563
[MW]           64127.72
[pI]          5.45
[HOMOL]        PIR:A41268 guanine nucleotide-binding protein 1 - human 0.0
[SUPFAM]       guanine nucleotide-binding protein 1 0.0
[PROSITE]      ATP_GTP_A      1
[PROSITE]      RGD      1
[KW]           TRANSMEMBRANE  1
[KW]           LOW_COMPLEXITY      6.75 %
[KW]           COILED COIL      10.48 %

```

```

SEQ      MAPEIHMTGPMCLIENTNGELVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG
SEG      .....
PRD      cccccccccceeeeccccchhhhhhhhhhhhhhhccceeeeeecccccchhhhhhhh
COILS    .....
MEM      .....MMMMMMMMMMMMMMMMMM.....

```

```

SEQ      KNKGFSLGSTVKSHKGIWMWCVHPHKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAV
SEG      .....
PRD      cccccccccccccccccceeeeeccccccccceeeeeccccccccccccccccchhhhhhhh
COILS    .....
MEM      .....

```

```

SEQ      LLSSLVYNSMGITINQQAMDQLYYVTELTHRIKSSPDENENEDSADFVSFFPDFVWTL
SEC      .....
PRD      hhhhhheeeccccchhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccceeeccceeeh
COILS    .....
MEM      .....

```

SEQ RDFS L D L E A D G Q P L T P D E Y L E Y S L K L T Q G N R K L A Q L E K L Q D E L D P E F V Q Q V A D F C S Y I F
SEG
PRD hhhhhhhhccccccccchhhhhhhhhcccchhhhhhhhhhhcccccchhhhhhhhhhhhhc
COILS

```

2551 GTTGACCCCTG AATTAAATAG TCACATGGTA ACAATTATGC ACTGTGTAAT
2601 TTTAGTAATG TATAACATGC AATGATGCAC TTTAACTGAA GATAGAGACT
2651 ATGTTAGAAA ATTGAACATA TTTAATTATT TGATTGTTTT AATCCTAAAG
2701 CATAAGTTAG TCTTTTCCTG ATTCTTAAAG GTCATACTTG AAATCCTGCC
2751 AATTTTCCCC AAAGGGAATA TGGAAATTTT TTTGACTTTC TTTTGAGCAA
2801 TAAAATAATT GTCTTGCCAT TACTTAGTAT ATGTAGACTT CATCCCAATT
2851 GTCAAACATC CTAGGTAAGT GGTGACATT TCTTACAGCA ATTACAGATT
2901 ATTTTGAAC TAGAATAAAA CTAAACTAGA AACAAAAAAA AAAAAAAAAA
2951 AA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 201 bp to 1889 bp; peptide length: 563
 Category: strong similarity to known protein
 Classification: Cell signaling/communication
 Prosite motifs: RGD (272-275)
 ATP_GTP_A (45-53)

```

1 MAPEIHMTGP MCLIENNGE LVANPEALKI LSAITQPVVV VAIVGLYRTG
51 KSYLMNKLKAG KNGGFSLGST VKSHTKGIWM WCVPHPKKPE HTLVLLDTEG
101 LGDVKKGDNQ NDSWIFTLAV LLSSTLVYNS MGTINQOAMD QLYYVTELTH
151 RIRSKSSPDE NENEDSADFV SFFPDFVWTL RDFSLEAD QPLTPDEYL
201 EYSLKLTQGN RKLAQLEKLQ DEELDPEFVQ QVADFCYIF SNSKTKTLTG
251 GIKVNGPCLE SLVLTYYINAI SRGDLPCMEN AVLALAQIEN SAAVOKAIAH
301 YDOOMGQKQV LPAETLQELL DLHRVSEREA TEVYMKNSEK DVDHLEFQKKL
351 AAQLDKKRDD FCKQNEASS DRCSALLQVI FSPLEEEVKA GIYSKPGGYC
401 LFIQKLQDLE KKYEEPRKG IQAEEILQTY LKSKESVTDI ILQTDQILTE
451 KEKEIEVECV KAESAQASAK MVEEMQIKYO QMMEEEKSY QENVKQLTEK
501 MERERAQLE EQEKTLSKL QEQARVLKER CQGESTQLQN EIQLKQTLK
551 KKTKRYMSHK LKI

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphbr2_78c24, frame 3

PIR:A41268 guanine nucleotide-binding protein 1 - human, N = 2, Score = 1306, P = 4.9e-238

PIR:A46459 macrophage-activation gene-1 protein mag-1 - mouse, N = 2, Score = 942, P = 8.9e-184

PIR:S70524 guanine nucleotide-binding protein 2 - human, N = 2, Score = 1131, P = 4.1e-210

TREMBL:AF077007_1 gene: "Gbp2"; product: "interferon-induced guanylate binding protein GBP-2"; Mus musculus interferon-induced guanylate binding protein GBP-2 (Gbp2) mRNA, complete cds., N = 2, Score = 904, P = 1.2e-179

>PIR:A41268 guanine nucleotide-binding protein 1 - human
 Length = 592

HSPs:

Score = 1306 (195.9 bits), Expect = 4.9e-238, Sum P(2) = 4.9e-238
 Identities = 264/332 (79%), Positives = 288/332 (86%)

Query: 211 RKLAQLEKLQDEELDPEFVQVADFCYIFSNKTKTLSSGGIKVNGPCLESVLTYINAI 270
 RKLAQLEKLQDEELDPEFVQVADFCYIFSNKTKTLSSGGI+VNGP LESVLTY+NAI
 Sbjct: 245 RKLAQLEKLQDEELDPEFVQVADFCYIFSNKTKTLSSGGIQVNGPRLESVLTYVNAI 304

DKFZphfbr2_78c24

group: signal transduction

DKFZphfbr2_78c24 encodes a novel 563 amino acid protein with strong similarity to guanylate-binding proteins (GBPs).

GBPs were originally described as proteins that are strongly induced by interferons and are capable of binding to agarose-immobilized guanine nucleotides. hGBP1, the first of two members of this protein family in humans, represents a novel type of GTPase. The novel protein contains an ATP/GTP-binding site motif A (P-loop) and a RGD cell attachment site. It seems to be a new member of the GBP-family and shows a splicing pattern not described previously.

The new protein can find application in modulating/blocking the response of cells to interferons.

strong similarity to guanine nucleotide-binding protein 1/2
but different "splice variant" aa 211-245 of GBP1/2 missing

Sequenced by MediGenomix

Locus: unknown

Insert length: 2952 bp

Poly A stretch at pos. 2927, polyadenylation signal at pos. 2914

```

1  CAGTTTCATT AGGCTCTGAA GCCATTACAA AGGTGCTTA ACTTCTAATT
51  ATTTGATCAC TGAGGAAAAAT CCAGAAAGCT ACACAACACT GAAGGGGTGA
101 AATAAAAGTC CAGCGATCCA GCGAAAGAAA AGAGAAGTGA CAGAAACAAC
151 TTTACCTGGA CTGAAGATAA AAGCACAGAC AAGAGAACAA TGCCCTGGAC
201 ATGGCTCCAG AGATCCACAT GACAGGCCCA ATGTGCCTCA TTGAGAACAC
251 TAATGGGGAA CTGGTGGCGA ATCCAGAAGC TCTGAAAATC CTGTCTGCCA
301 TTACACAGCC TGTGGTGGTG GTGGCAATTG TGGGCCTCTA CCGCACAGGA
351 AAATCCTACC TGATGAACAA GCTAGCTGGG AAGAATAAGG GCTTCTCTCT
401 GGGTCCACAC GTGAAATCTC ACACCAAAGG AATCTGGATG TGGTGTGTGC
451 CTCACCCCAA AAAGCCAGAA CACACCTTAG TCCTGCTTGA CACTGAGGGC
501 CTGGGAGATG TAAAGAAGGG TGACAACCAG AATGACTCCT GGATCTTCAC
551 CCTGGCCGTC CCCTGAGCA GCACTCTCGT GTACAATAGC ATGGGAACCA
601 TCAACCCAGCA GGTATGGAC CACTGTACT ATGTGACAGA GCTGACACAT
651 CGAATCCGAT CAAAATCCTC ACCTGATGAG AATGAGAATG AGGATTCAGC
701 TGACTTTGTG AGCTTCTTCC CAGATTTTGT GTGGACACTG AGAGATTTCT
751 CCCTGGAGTT GGAAGCAGAT GGACAACCCC TCACACCAGA TGAGTACCTG
801 GAGTATTCCT TGAAGCTAAC GCAAGGTAAC AGGAAGCTTG CCCAGCTTGA
851 GAAACTACAA GATGAAGAGC TGGACCCTGA ATTTGTGCAA CAAGTAGCAG
901 ACTTCTGTTC CTACATCTTT AGCAATTCCA AACTATAAAC TCTTTCAGGA
951 GGCATCAAGG TCAATGGGCC TTGTCTAGAG AGCCTAGTGC TGACCTATAT
1001 CAATGCTATC AGCAGAGGGG ATCTGCCCTG CATGGAGAAC GCAGTCTCTG
1051 CCTTGGCCCA GATAGAGAAC TCAGCCGCGC TGCAAAAAGG TATTGCCACG
1101 TATGACCAGC AGATGGGCCA GAAGGTGCAG CTGCCCGCAG AAACCTTCCA
1151 GGAGCTGCTG GACCTGCACA GGGTTAGTGA GAGGGAGGCC ACTGAAGTCT
1201 ATGTGAAGAA CTCTTTCAAG GATGTGGACC ATCTGTTTCA AAAGAAATTA
1251 GCGGCCACAG TAGACAAAAA GCGGGATGAC TTTTGTAAAC AGAATCAAGA
1301 AGCATCATCA GATCGTTGCT CAGCTTTACT TCAGTCTATT TTCAGTCTCT
1351 TAGAAGAAGA AGTGAAGGCG GGAATTTATT CGAAACCAGG GGGCTATTGT
1401 CTCTTTATTC AGAAGCTACA AGACCTGGAG AAAAAGTACT ATGAGGAACC
1451 AAGGAAGGGG ATACAGGCTG AAGAGATTCT GCAGACATAC TTGAAATCCA
1501 AGGAGTCTGT GACCGATGCA ATTCTACAGA CAGACCAGAT TCTCACAGAA
1551 AAGGAAAAGG AGATTGAAGT GGAATGTGTA AAAGCTGAAT CTGCACAGGC
1601 TTCAGCAAAA ATGGTGGAGG AAATGCAAAAT AAAGTATCAG CAGATGATGG
1651 AAGAGAAAAG GAAGAGTTAT CAAGAACATG TGAACAATT GACTGAGAAG
1701 ATGGAGAGGG AGAGGCCCA GTTGTGGGAA GAGCAAGAGA AGACCTCAC
1751 TAGTAAACTT CAGGAACAGG CCCGAGTACT AAAGGAGAGA TGCCAAGGTG
1801 AAAGTACCCA ACTTCAAAAT GAGATACAAA AGCTACAGAA GACCCTGAAA
1851 AAAAAAACC AAGATATAT GTCGCATAAG CTAAAGATCT AAACAACAGA
1901 GCTTTCTGTG ATCCTTAACC CAAGGCATAA CTGAAACAAT TTTAGAATTT
1951 GGAACAAGTG TCACTATATT TGATAATAAT TAGATCTTGC ATCATAACAC
2001 TAAAGTTTAA CAAGAACATG CAGTTCAATG ATCAAAATCA TGTTTTTTCC
2051 TTAAGAAAGT TGTAAATTGT GCAACAAAGA TGCATTTACC TCTGTACCAA
2101 CAGAGGAGGG ATCATGAGTT GCCACCACTC AGAAGTTTAT TCTCCAGAC
2151 GACCAGTGGT TACTGAGGAA AGTCTTAGGT AAAAATCTTG GGACATATTT
2201 GGGCACTGGT TTGGCCAAGT GTACAATAGG TCCCAATATC AGAAACAACC
2251 ATCTAGCTT CCTAGGGAAG ACAGTGATCA GTTCTCCATT ATATCAAGGC
2301 TACAAGGTCT ATGAGCAATA ATGTGATTTC TGGACATTGC CCATGGATAA
2351 TTCTCACTGT TGGATCTCAA GCTAAAGCAA ACCATCTTAT ACAGAGATCT
2401 AGAATCTTAT ATTTTCCATA GGAAGGTAAA GMAATCATTA GCAAGAGTAG
2451 GAATTGAATC ATAACAACAT TGGCTAATGA AGAAATCTTT TCTTTCTTGT
2501 TCAATTCATC TAGATTATAA CCTTAATGTG ACACCTGAGA CCTTTAGACA

```

[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YBL078c] 4e-36
[FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YBL078c] 4e-36
[FUNCAT] 06.13.04 lysosomal and vacuolar degradation [S. cerevisiae, YBL078c] 4e-36
[SUPFAM] hypothetical protein YBL078c 8e-35
[PROSITE] ASN_GLYCOSYLATION 1
[KW] Alpha_Beta

SEQ MKFQYKEDHPFEYRKKEGEKIRKKYPDRVPVIVEKAPKARVPDLDRKYLVPSDLTVGQF
PRD cccccccccchhhhhhhhhhhhhccccceeeccccccccccccceccccchhhh
SEQ YFLIRKRIHLRPEDALFFVNNITIPPTSATMGQLYEDNHEEDYFLYVAYSDESUYGK
PRD hhhhhhhhhccccceeeccccccccchhhhhhhhhccccceeecccccccc

Prosites for DKFZphfbr2_72n12.2

PS00001 81->85 ASN_GLYCOSYLATION PDOC00001

(No Pfam data available for DKFZphfbr2_72n12.2)

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 227 bp to 577 bp; peptide length: 117
Category: strong similarity to known protein

1 MKFQYKEDHP FEYRKKEGK IRKKYPDRVP VIVEKAPKAR VPDLDKRKYL
51 VPSDLTVGQF YFLIRKRIHL RPEDALFFV NNTIPPTSAT MGQLYEDNHE
101 EDYFLYVAYS DESVYGK

BLASTP hits

Entry YQD9_CAEEL from database SWISSPROT:
HYPOTHETICAL 14.8 KD PROTEIN C32D5.9 IN CHROMOSOME II.
Score = 496, P = 1.8e-47, identities = 91/116, positives = 105/116

Entry SYRP_LACBI from database SWISSPROT:
SYMBIOSIS-RELATED PROTEIN.
Score = 390, P = 3.1e-36, identities = 68/117, positives = 94/117

Entry LBU93506_1 from database TREMBL:
product: "symbiosis-related protein"; Laccaria bicolor
symbiosis-related protein mRNA, partial cds.
Score = 390, P = 3.1e-36, identities = 68/117, positives = 94/117

Entry GEF2_RAT from database SWISSPROT:
GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2).
Score = 373, P = 2.0e-34, identities = 71/116, positives = 88/116

Alert BLASTP hits for DKFZphfbr2_72n12, frame 2

TREMBLNEW:AF044671_1 product: "MM46"; Homo sapiens MM46 mRNA, complete
cds., N = 1, Score = 549, P = 4.7e-53

SWISSPROT:GEF2_HUMAN GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2)., N = 1,
Score = 373, P = 2.1e-34

>TREMBLNEW:AF044671_1 product: "MM46"; Homo sapiens MM46 mRNA, complete
cds.

Length = 117

HSPs:

Score = 549 (82.4 bits), Expect = 4.7e-53, P = 4.7e-53
Identities = 101/116 (87%), Positives = 110/116 (94%)

Query: 1 MKFQYKEDHPFEYRKKEGKIRKKYPDRVPVIVEKAPKARVPDLDKRKYLVPSDLTVGQF 60
MKF YKE+HPFE R+ EGKIRKKYPDRVPVIVEKAPKAR+ DLDK+KYLVPSDLTVGQF
Sbjct: 1 MKFVYKEEHPFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDKKKYLVPSDLTVGQF 60
Query: 61 YFLIRKRIHLRPEDALFFVNNNTIPPTSATMGQLYEDNHEEDYFLYVAYSDESVYG 116
YFLIRKRIHLR EDALFFVNN IPPTSATMGQLY+++HEED+FLY+AYSDESVYG
Sbjct: 61 YFLIRKRIHLRAEDALFFVNNVIPPTSATMGQLYQEHEEDFFLYIAYSDESVYG 116

Pedant information for DKFZphfbr2_72n12, frame 2

Report for DKFZphfbr2_72n12.2

{LENGTH} 117
{MW} 14044.07
{pI} 8.67
{HOMOL} TREMBL:AF044671_1 product: "MM46"; Homo sapiens MM46 mRNA, complete cds. 1e-56

DKFZphfbr2_72n12

group: brain derived

DKFZphfbr2_72n12 encodes a novel 117 amino acid protein with similarity to a protein with conserved sequence in bacteria and eukariota.

The novel protein is very similar to human MM46, human and rat ganglioside expression factor-2 (GEF2), C. elegans 14.8 kD protein C32D5.9 and Laccaria bicolor symbiosis-related protein LBU93506_1. The function of this highly conserved proteins is not known.

The new protein can find application in studying the expression profile of brain-specific genes.

strong similarity to rat GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2)

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="12"

Insert length: 1880 bp

Poly A stretch at pos. 1859, polyadenylation signal at pos. 1830

```
1 GGGGGCCGGT ATTTCTCCAT CTGGCTCTCC TCTACCTCCA GGCAGGCTCA
51 CCCGAGATCC CCGCCCCGAA CCCCCCTGCG ACCTCGGCC CAGCGCTGTT
101 CCCCCCGGAG CGGACGTTTC TGCAGCTATT CTGAGCACAC CTTGACGTCG
151 GCTGAGGGAG CGGGACAGGG TCAGCGGCGA AGGAGGCAGG CCCCgcgCGG
201 GGATCTCGGA AGCCTGCGG TGCATCATGA AGTTCCAGTA CAAGGAGGAC
251 CATCCCTTTG AGTATCGGAA AAAGGAAGGA GAAAAGATCC GGAAGAAATA
301 TCCGGACAGG GTCCCCGTGA TTGTAGAGAA GGCTCCAAAA GCCAGGGTGC
351 CTGATCTGGA CAAGAGGAAG TACCTAGTGC CCTCTGACCT TACTGTTGGC
401 CAGTCTTACT TCTTAATCCG GAAGAGAATC CACCTGAGAC CTGAGGACGC
451 CTTATTCTTC TTTGTCAACA ACACCATCCC TCCCACCACT GCTACCATGG
501 GCCAACTGTA TGAGGACAAT CATGAGGAAG ACTATTTTCT GTATGTGGCC
551 TACAGTGATG AGAGTGTCTA TGGGAAATGA GTGGTTGGAA GCCCAGCAGA
601 TGGGAGCACC TGGACTTGGG GGTAGGGGAG GGGTGTGTGT GCGCGACATG
651 GCGAAAGAGG GTGGCTCCCA CCGCAAGGAG ACAGAAGGTG AAGACATCTA
701 GAAACATTAC ACCACACACA CCGTCATCAC ATTTTCACAT GGTCAATTGA
751 TATTTTTCG TGCTTCCTCG GCCCAGGGAG AAGCATGTCT AGGACAGAGC
801 TGTGATTGAT GCTTTGATAG AGGAATGGGG ATGATGTAAG TTTACAGTAT
851 TCCTGGGGTT TAATTGTTGT GCAGTTTCAT AGATGGGTCA GGAGGTGGAC
901 AAGTTGGGCG CAGAGATGAT GGCAGTCCAG CAGCAACTCC CTGTGCTCCC
951 TTCTCTTTGG GCAGAGATTC TATTTTTCGAC ATTTGCACAA GACAGGTAGG
1001 GAAAGGGGAC TTGTGGTAGT GGACCATAAC TGGGGACCAA AAGAGACCCA
1051 CTGTAATTGA TGCAATTGTG CCCCTGATCT TCCCTGTCTC ACACCTCTTT
1101 TCTCCCATCC CGGTTGCAAT CTCACACAGA CATCACAGTA CCACCCAGG
1151 GGTGGCAGTA GACAACAACC CAGAAATTTA GACAGGGATC TCTTACCTTT
1201 GGAATAATAG GGTTAGGCAT GAAGGTGGTT GTGATTAAGA AGATGGTTTT
1251 GTTATTAAAT AGCATTAAAC TGAATTGAC AAGAGTGTG AGCATCCCTG
1301 TCTAACCTGC TCTTTCTCTT TGGTGCCCCC TATCTACCCC CTTCTTGGG
1351 ATTTAATAAG TCTCAGGCAT TTCCAATTGT AGACTAAAAC CACTCTTAGC
1401 ATCTCCTCTA GTATTTTCCA TGTATCAGGA AAGAGGTGTC TTATGTAGGG
1451 AGGGGGCAAG TATGAAGTAA GGTAAATATA TACTACTCTC ATTCAGGATT
1501 CTTGCTCCCA TGCTGCTGTC CCTCAGGCT CACATGCACA GGAATGCTAC
1551 ATGATGGCCA GCTGCTTCCC TCCTTGGTTA TCATCCACTG CAGCTGCTAG
1601 TTAGAAAGGT TTGGAGGCAT GACTTTTAGT AAATCATGGG GATTTTATTG
1651 ATTTATTTTC ACTTTTGGGA TTTTGTGGGG TGGGAGTGGG GAGCAGGAAT
1701 TGCACTCAGA CATGACATTT CAATTCATCT CTGCTAATGA AAAGGGTTCT
1751 TTCTCTTGGG GGAATGTGT GTGTCAATTC TGTCAGCTGC AAGTTCTTGT
1801 ATAAATGAAGT CAATGCCATC AGGCCAAGGA AATAAAATAA TTGCTTACCT
1851 TAAAAATCGA AAAAAAATAA AAAAAAATAC
```

BLAST Results

Entry HS418210 from database EMBL:

human STS SHGC-10496.

Score = 1916, P = 4.0e-80, identities = 394/400

Entry AC006514 from database EMBLNEW:

*** SEQUENCING IN PROGRESS *** Homo sapiens; HTGS phase 1, 68 unordered pieces.

Score = 610, P = 2.7e-16, identities = 128/134

4 exons


```

1 MATVMAATAA ERVLEEEFR WLLHDEVHAV LKQLQDILKE ASLRFTLPGS
51 GTEGPAKQEN FILSCGDTQ VKGVLTLQGD ALSQADVNLK MPRNNQLLHV
101 AFREDKQWKL QQIQDARNHV SQAIYLTLSR DQSYQFKTGA EVLKLMDAHV
151 LQLTRARNRL TTPATLTLPE IAASGLTRME APALPSDLLV NVYINLNKLC
201 LTVYQLHALQ PNSTKNFRPA GGAVLHSPGA MFEWGSQRLE VSHVHKVECV
251 IPWLNDALVY FTVSLQCLCQ LDKDISVFS YWSYRPF

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2 72ml6, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2 72ml6, frame 3

Report for DKFZphfbr2 72m16.3

```
[LENGTH]          287
[MW]              32254.40
[pI]              8.30
[HOMOL]           TREMBL:AF025459_2 gene: "H14A12.3"; Caenorhabditis elegans cosmid H14A12. 3e-14

[PROSITE]         MYRISTYL          1
[PROSITE]         CK2_PHOSPHO_SITE      6
[PROSITE]         PKC_PHOSPHO_SITE      5
[PROSITE]         ASN_GLYCOSYLATION     1
[KW]              Alpha_Beta
[KW]              LOW_COMPLEXITY         6.27 %
```

```

SEQ      MATVMAATAAERAVLEEEFRWLLHDEVHAVLKQLQDILKEASLRFTLPGSSTEGPAKQEN
SEG      xxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      ccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccchhhh

SEQ      FILGSCGTDQVKGVLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLOQIQDARNHV
SEG      .....
PRD      hhccccccccceeeeeeeccccchhhhhhhccccchhhhhhhhhchhhhhhhhhhhchhh

SEQ      SQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLTTPATLTLPEIAASGLTRMF
SEG      .....
PRD      hhhhhhhhccccceecchhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccc

SEQ      APALPSDLLNVVYINLNKLCCLTVYQLHALQPNSTKNFRPAGGAVLHSPGAMFEWGSORLE
SEG      .....
PRD      cccccccceeeehhhhhhhhhhhheeeccccccccccccccccceecccccccccccccccc

SEQ      VSHVHKVECVIPWLNDAVYFTVSLQCLQKDKISVFSSYWSYRPF
SEG      .....
PRD      eeeeeeeeeeeccccceeeehhhhhhhhhhhheeeeeeecccc

```

Prosites for DKFZphfbr2 72m16.3

PS000001	212->216	ASN_GLYCOSYLATION	PDOC000001
PS000005	42->45	PKC_PHOSPHO_SITE	PDOC000005
PS000005	128->131	PKC_PHOSPHO_SITE	PDOC000005
PS000005	213->216	PKC_PHOSPHO_SITE	PDOC000005
PS000005	236->239	PKC_PHOSPHO_SITE	PDOC000005
PS000005	283->286	PKC_PHOSPHO_SITE	PDOC000005
PS000006	8->12	CK2_PHOSPHO_SITE	PDOC000006
PS000006	50->54	CK2_PHOSPHO_SITE	PDOC000006
PS000006	83->87	CK2_PHOSPHO_SITE	PDOC000006
PS000006	128->132	CK2_PHOSPHO_SITE	PDOC000006
PS000006	138->142	CK2_PHOSPHO_SITE	PDOC000006
PS000006	167->171	CK2_PHOSPHO_SITE	PDOC000006
PS000008	64->70	MYRISTYL	PDOC000008

(No Pfam data available for DKFZphfbr2 72m16.3)

DKFZphfbr2_72m16

group: unknown

DKFZphfbr2_72m16 encodes a novel 287 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="26.2 cR from top of Chr16 linkage group"

Insert length: 1462 bp

Poly A stretch at pos. 1441, polyadenylation signal at pos. 1421

```

1 GGGGAGGACC GGAGGACCGA GGACAGAAAG ATTGGTGGAC AGGAGCAGCG
51 GCCCGTGGGG AGGGCGCTCG GCGGCGGCCT GCGGCCATGG CCACCGTGAT
101 GGCAGCGACG GCGGCGGAGC GGGCGGTGCT GGAGGAGGAG TTCCGCTGGC
151 TGCTGCACGA CGAGGTGCAC GCTGTGTTGA AGCAGCTGCA GGACATCCTC
201 AAGGAGGCCT CTCTGCGCTT CACTCTGCCG GGCTCCGGCA CTGAGGGGCC
251 CGCCAAGCAA GAGAACTTCA TCCTAGGCAG CTGTGGCACA GACCAGGTGA
301 AGGGTGTGCT GACTCTGCAG GGGGATGCCC TCAGCCAGGC GGATGTGAAC
351 CTGAAGATGC CCCGGAACAA CCAGCTGCTG CACTTCGCCT TCCGGGAGGA
401 CAAGCAGTGG AAGCTGCAGC AGATCCAGGA TGCCAGAAAC CATGTGAGCC
451 AAGCCATTTA CTTGCTTACC AGCCGGGACC AGAGCTACCA GTTCAAGACG
501 GGCGTGAGG TCCTCAAGCT GATGGACGCA GTGATGCTGC AGCTGACCAG
551 AGCCCCAAAC CGGCTACCA CCCCCGCCAC CCTCACCTC CCCGAGATCG
601 CCGCCAGCGG CTTACGCGG ATGTTGCGCC CTGCCCTGCC GTCCGACCTG
651 CTGGTCAACG TCTACATCAA CCTCAACAAG CTCTGCCTCA CGGTGTACCA
701 GCTGCATGCC CTGCAGCCCA ACTCCACCAA GAACTTCCGC CCAGCTGGGG
751 GCGCGGTGCT GCATAGCCCT GGGGCCATGT TCGAGTGGGG CTCTCAGCGC
801 CTGGAGGTGA GCCACCTGCA CAAAGTGGAG TGCCTGATCC CCTGGCTCAA
851 CGACGCCCTG GTCTACTTCA CCGTCTCCCT GCAGCTCTGC CAGCAGCTTA
901 AGGACAAGAT CTCCGTGTTT TCCAGCTACT GGAGCTACAG ACCCTTCTGA
951 TCACAGCACC CAGGAGCTTG TCTCCAGGAA GGCGGCCCCG TCCCCTACTC
1001 ATACCCACCA CAGAGCACCA GCCAGTGCCA ACGCCAGGCT GCTATTTATC
1051 TCCCTATCCC ACCCCCTACC CCACCTAACA CATTTGCACT GCCGGGAATG
1101 GACACTGGAA GTGCCAGGAG GAAGGAAGGC TGGTTTGGTG GGGTAGTGGG
1151 GAGGTCAGGG AGGCGGGGCC AAGGGTGTC CACATTCCCA ACACCGCCCT
1201 CTGATCACCA TGGGAATCTT TGGACTCAGG ACAGGGCCAG GCGCAGGGCT
1251 CTCCCTCCTC TCCCCTTCGC TGTCCTCTCC CCCTGGAGGG CATGGTGTGC
1301 GGGGGTGGCA CTGAGCTATG AGTCCCGGGG ATGGTGAGGA ACGCCACAGA
1351 CAGAGCCACC TAGGAGTGA GTATAGTGCT GGTGACTGTG TTTCATAGCC
1401 CCAGTCCAGG GCTGTCTAAG AAATAAAGAT CATCAGACTC CAAAAA
1451 AAAAAAAAAA AC

```

BLAST Results

Entry HS604351 from database EMBL:
human STS WI-18474.
Score = 1178, P = 1.5e-48, identities = 250/268

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 87 bp to 947 bp; peptide length: 287
Category: similarity to unknown protein


```

1 MDFLVLFIFY LASVLMGLVL ICVCSKTHSL KGLARGGAQI FSCIPECLQ
51 RAVHGLLHYL FHTRNHTFIV LHLVLQGMVY TEYTWEVFGY CQELELSLHY
101 LLLPYLLLG V NLEFFTLTCG TNPGIITKAN ELLFLHVYEF DEVMFPKNVR
151 CSTCDLRKPA RSKHCSVCNW CVHRFDHHC VVNNCIGAWN IRYFLIYVLT
201 LTASAATVAI VSTTFLVHLV VMSDLYQETY IDDLGHLHVM DTVILIQYLF
251 LTFPRIVFEM GFVVVLSFLL GGYLLSVLYL AATNQTNEW YRGVWAWCQR
301 CPLVAWPPSA EPQVHRNIHS HGLRSNLQEI FLPAFPCHER KKQE

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_72112, frame 3

TREMBL:SPBC13G1_7 gene: "SPBC13G1.07"; product: "hypothetical protein";
S.pombe chromosome II cosmid c13G1., N = 2, Score = 247, P = 1.4e-22

TREMBL:CED2021_3 gene: "D2021.2"; Caenorhabditis elegans cosmid
D2021., N = 1, Score = 209, P = 9e-17

TREMBL:CEC43H6_2 gene: "C43H6.7"; Caenorhabditis elegans cosmid
C43H6., N = 1, Score = 206, P = 5.2e-15

PIR:S52691 probable membrane protein YDR126w - yeast (Saccharomyces
cerevisiae), N = 1, Score = 207, P = 8.4e-15

PIR:E71607 metal binding protein (DHHC domain) PFB0725c - malaria
parasite (Plasmodium falciparum), N = 1, Score = 182, P = 1.1e-13

>TREMBL:SPBC13G1_7 gene: "SPBC13G1.07"; product: "hypothetical protein";
S.pombe chromosome II cosmid c13G1.
Length = 356

HSPs:

Score = 247 (37.1 bits), Expect = 1.4e-22, Sum P(2) = 1.4e-22
Identities = 55/148 (37%), Positives = 85/148 (57%)

Query: 52 AVHGLLHYLFHTRNH--TFIVLHLVLQGM---VYTEYTWEVFGYCQELELSLHYLLPY 105

A+ L +Y+ + N F+ L L+ G+ +Y + F + + L +LLPY

Sbjct: 64 AMRSLSNYVLYKNNPLVFLYLALITIGIASFFIYGSSLTQKFSIIDWISV-LTSVLLPY 122

Query: 106 LLLGVNLEFFTLTCGTNPGIITKANELLFLHVYEFDEVMFPKNVRVRCSTCDLRKPARSKH 164

+L+ + +NPG I N + +D + + FP +CSTC KPARSKH

Sbjct: 123 ----ISLY---IAAKSNPGKIDLKNWNEASRRFPYDYKIFFPN---KCSTCKFEKPARSKH 173

Query: 165 CSVCNWCVHRFDHHCVVNNCIGAWNIRYFLIYVL 199

C +CN CV +FDHHC+W+NNC+G N RYF +++L

Sbjct: 174 CRLCNICVEKFDHHCIVNNCIVGLNNARYFFFL 208

Score = 43 (6.5 bits), Expect = 1.4e-22, Sum P(2) = 1.4e-22
Identities = 10/35 (28%), Positives = 17/35 (48%)

Query: 257 VFMLGFVV-VLSFLLGGYLLSVLYLAATNQTNEW 290

VF++ + VL L GY ++Y T + +W

Sbjct: 254 VFLISLICSVLVLCCLLGYEFFLVYAGYTTNESEKW 288

Pedant information for DKFZphfbr2_72112, frame 3

Report for DKFZphfbr2_72112.3

```

[LENGTH]      344
[MW]           39677.23
[pI]           7.26
[HOMOL]        TREMBL:SPBC13G1_7 gene: "SPBC13G1.07"; product: "hypothetical protein"; S.pombe
chromosome II cosmid c13G1. 3e-17
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YDR126w] 1e-16
[FUNCAT]       03.07 pheromone response, mating-type determination, sex-specific proteins
[S. cerevisiae, YDR264c] 8e-05
[FUNCAT]       10.05.99 other pheromone response activities [S. cerevisiae, YDR264c]
8e-05
[PIRKW]        transmembrane protein 4e-15
[SUPFAM]       ankyrin repeat homology 1e-10
[SUPFAM]       unassigned ankyrin repeat proteins 1e-10
[PROSITE]      MYRISTYL 4
[PROSITE]      CK2_PHOSPHO_SITE 3

```

DKFZphfbr2_72112

group: nucleic acid management

Summary DKFZphfbr2_72112 encodes a novel 344 amino acid protein with similarity to YDR126w and other *S. cerevisiae* proteins.

The novel protein contains a myc-type, helix-loop-helix dimerization domain signature. This helix-loop-helix domain mediates protein dimerization and has been found in proteins such as the myc family of cellular oncogenes, proteins involved in myogenesis and vertebrate proteins that bind specific DNA sequences in various immunoglobulin chains enhancers. Therefore, the protein could be a novel DNA-binding protein.

The new protein can application in modulating gene expression.

similarity to YDR126w ;
membrane regions: 2

similarity to YDR126w

complete cDNA complete cds, EST hits

Sequenced by LMU

Locus: unknown

Insert length: 1270 bp

Poly A stretch at pos. 1251, no polyadenylation signal found

```

1  GGGGGCGCCC GGGAGGCGCC GGAGCCAGC GGCTGGCGCC AGATCCAGGC
51 TCCTGGAAGA ACCATGTCCG GCAGCTACTG GTCATGCCAG GCACACACTG
101 CTGCCCCAGA GGAGCTGCTG TTTGAATTAT CTGTGAATGT TGGGAAGAGG
151 AATGCCAGAG CTGCCGGCTG AAAATTACCC AACCAAGAGA AATCTGCAGG
201 ATGGACTTTC TGGTCCTCTT CTTGTTCTAC CTGGCTTCGG TGCTGATGGG
251 TCTTGTCTT ATCTGCGTCT GCTCGAAAAC CCATAGCTTG AAAGGCCTGG
301 CCAGGGGAGG AGCACAGATA TTTTCTGTA TAATTCCAGA ATGTCTTCAG
351 AGAGCCGTGC ATGGATTGCT TCATTACCTT TTCCATACGA GAAACACAC
401 CTTCAATGTC CTGCACCTGG TCTTGCAAGG GATGGTTTAT ACTGAGTACA
451 CCTGGGAAGT ATTTGGCTAC TGTCAGGAGC TGGAGTTGTC CTTGCATTAC
501 CTTCTCTGCG CCTATCTGCT GCTAGGTGTA AACCTGTTTT TTTTCACCCT
551 GACTTGTGGA ACCAATCCTG GCATTATAAC AAAAGCAAAT GAATTATTAT
601 TTCTTCATGT TTATGAATTT GATGAAGTGA TGTTCCTCAA GAACGTGAGG
651 TGCTCTACTT GTGATTTAAG GAAACCAAGT CGATCCAAGC ACTGCAGTGT
701 GTGTAACCTG TGTGTGCACC GTTTCGACCA TCACTGTGTT TGGGTGAACA
751 ACTGCATCGG GGCCTGGAAC ATCAGCTACT TCCTCATCTA CCTCTTGACC
801 TTGACGGCCT CGGCTGCCAC CGTCGCCATT GTGAGCACCA CTTTCTGGT
851 CCACTTGGTG GTGATGTCAG ATTTATACCA GGAGACTTAC ATCGATGACC
901 TTGGACACCT CCATGTTATG GACACGGTCA TTCTTATTCA GTACCTGTTC
951 CTGACTTTTC CACGGATTGT CTTCATGCTG GGCTTTGTCG TGGTCCTGAG
1001 CTTCTCTCTG GGTGGCTACC TGTTGTCTGT CCTGTATCTG GCGGCCACCA
1051 ACCAGACTAC TAACAGAGTG TACAGAGGTG TCTGGGCTCG GTGCCAGCGT
1101 TGTCCCCTTG TGGCTGGGCC TCCGTCAGCA GAGCCCCAAG TCCACCGGAA
1151 CATTCACCTC CATGGGCTTC GGAGCAACCT TCAAGAGATC TTTCTACCTG
1201 CCTTTCCATG TCATGAGAGG AAGAAACAAG AATGACAAGT GTATGACTGC
1251 CAAAAAAAAA AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 201 bp to 1232 bp; peptide length: 344
Category: similarity to unknown protein

.....

Report for DKFZphfbr2_72d13.3

```
[LENGTH]          165
[MW]               17393.73
[pI]               7.80
[BLOCKS]           BL00068A Malate dehydrogenase proteins
[KW]               TRANSMEMBRANE 2
[KW]               LOW COMPLEXITY 29.70 %
```

```
SEQ MTRLCLPRPEAREDPIVPVPPRGLGAGEGSGSPVRPPVSTWGPSWAQLLDSVLWLGA LGLT
SEG . . . . .
PRD ccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhccccc
MEM
```

```
SEQ      IQAVFSTGTPALLLLLVSF LTFDLHRPAGHTLPQRKLLTRGSQSGAGEGPQQEALLLQ
SEG      .....XXXXXXXXXXXXX..... XXXXXXXXXXXXXXXXX...
PRD      eeeeeccccchhhhhhhhhhhhhhhcccccccccccccccccccccccccchhhhhh
MEM      MMMMMMMMMMMMMMMMMM
```

```

SEQ      MGTVSGQLSLQDALLLLMGLGPLLRACGMPLTLGLAFLHPWA
SEG      .....XXXXXXXXXXXXXXXXXXXXX.....
PRD      hcccccehhhhhhhhhhhhhhccccchhhhhhhccccce
MEM      MMTMMMMMMMMMMMMMMMMMMMMMM

```

(No Prosite data available for DKFZphfbr2 72d13.3)

(No Pfam data available for DKFZphfbr2_72d13.3)

DKF2phfbr2_72d13

group: brain derived

DKF2phfbr2_72d13 encodes a novel 165 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

seems to be testis specific 9 of 10 EST hits are from testis libraries

Sequenced by LMU

Locus: unknown

Insert length: 723 bp

Poly A stretch at pos. 704, no polyadenylation signal found

```
1 AGGGGGGGTA TGGGGGAGGG GGAGACTCTG CAGGAGCCTA ATTCCCCACT
51 CTGAGCTCAC CCTTCTGTCT GCCCGGGCCC TACCCCTTCC CCTACTCTCA
101 CCCTTATAAT CCTTTTCAGC ACTAGGTCTT CCCGTCACCT CCACCTCTCT
151 CCATGACCCG GCTCTGCTTA CCCAGACCCG AAGCACGTGA GGATCCGATC
201 CCAGTTCCCTC CAAGGGGCCT GGGTGCTGGG GAGGGGTCAG GTAGTCCAGT
251 GCGTCCACCT GTATCCACCT GGGGCCCTAG CTGGGCCAG CTCCTGGACA
301 GTGTCCTATG GCTGGGGGCA CTAGGACTGA CAATCCAGGC AGTCTTTTCC
351 ACCACTGGCC CAGCCCTGCT GCTGCTTCTG GTCAGCTTCC TCACCTTTGA
401 CCTGCTCCAT AGGCCCGCAG GTCACACTCT GCCACAGCGC AAACCTTCTCA
451 CCAGGGGCCA GAGTCAGGGG GCCGGTGAAG GTCCTGGACA GCAGGAGGCT
501 CTACTCCTGC AAATGGGTAC AGTCTCAGGA CAACTTAGCC TCCAGGACGC
551 ACTGCTGCTG CTGCTCATGG GGCTGGGCCC GCTCCTGAGA GCCTGTGGCA
601 TGCCTTTGAC CTTGCTTGGC CTGGCTTTCT GCCTCCATCC TTGGGCCTGA
651 GAGCCCCTCC CCACAATCA GTGTCCTTCA AATATACAAT GACCACCCTT
701 CTTCAAAAAA AAAAAAAAAA AAC
```

BLAST Results

Entry HS860F19 from database EMBLNEW:

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 860F19

Score = 2059, P = 1.1e-85, identities = 423/434

2 exons

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 153 bp to 647 bp; peptide length: 165

Category: putative protein

Classification: no clue

```
1 MTRLCLPRPE AREDPVPVPP RGLGAGEGSG SPVRPPVSTW GPSWAQLLDS
51 VLWLGLALGT IQAVFSTTGP ALLLLLVSL TFDLLHRPAG HTLPQRKLLT
101 RGQSQGAGEG PGQQEALLQ MGTVSGQLSL QDALLLLLMG LGPLLACGM
151 PLTLLGLAFC LHPWA
```

BLASTP hits
.

No BLASTP hits available

Alert BLASTP hits for DKF2phfbr2_72d13, frame 3

No Alert BLASTP hits found

Prosites for DKFZphfbr2_72b18.2

PS00001	24->28	ASN_GLYCOSYLATION	PDOC00001
PS00001	160->164	ASN_GLYCOSYLATION	PDOC00001
PS00001	483->487	ASN_GLYCOSYLATION	PDOC00001
PS00001	583->587	ASN_GLYCOSYLATION	PDOC00001
PS00001	646->650	ASN_GLYCOSYLATION	PDOC00001
PS00004	309->313	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	347->351	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	106->109	PKC_PHOSPHO_SITE	PDOC00005
PS00005	201->204	PKC_PHOSPHO_SITE	PDOC00005
PS00005	246->249	PKC_PHOSPHO_SITE	PDOC00005
PS00005	257->260	PKC_PHOSPHO_SITE	PDOC00005
PS00005	265->268	PKC_PHOSPHO_SITE	PDOC00005
PS00005	307->310	PKC_PHOSPHO_SITE	PDOC00005
PS00005	341->344	PKC_PHOSPHO_SITE	PDOC00005
PS00005	351->354	PKC_PHOSPHO_SITE	PDOC00005
PS00005	418->421	PKC_PHOSPHO_SITE	PDOC00005
PS00005	435->438	PKC_PHOSPHO_SITE	PDOC00005
PS00005	438->441	PKC_PHOSPHO_SITE	PDOC00005
PS00005	442->445	PKC_PHOSPHO_SITE	PDOC00005
PS00005	459->462	PKC_PHOSPHO_SITE	PDOC00005
PS00005	466->469	PKC_PHOSPHO_SITE	PDOC00005
PS00005	471->474	PKC_PHOSPHO_SITE	PDOC00005
PS00005	520->523	PKC_PHOSPHO_SITE	PDOC00005
PS00005	548->551	PKC_PHOSPHO_SITE	PDOC00005
PS00005	565->568	PKC_PHOSPHO_SITE	PDOC00005
PS00005	592->595	PKC_PHOSPHO_SITE	PDOC00005
PS00005	651->654	PKC_PHOSPHO_SITE	PDOC00005
PS00006	46->50	CK2_PHOSPHO_SITE	PDOC00006
PS00006	257->261	CK2_PHOSPHO_SITE	PDOC00006
PS00006	285->289	CK2_PHOSPHO_SITE	PDOC00006
PS00006	301->305	CK2_PHOSPHO_SITE	PDOC00006
PS00006	303->307	CK2_PHOSPHO_SITE	PDOC00006
PS00006	313->317	CK2_PHOSPHO_SITE	PDOC00006
PS00006	448->452	CK2_PHOSPHO_SITE	PDOC00006
PS00006	459->463	CK2_PHOSPHO_SITE	PDOC00006
PS00006	477->481	CK2_PHOSPHO_SITE	PDOC00006
PS00006	497->501	CK2_PHOSPHO_SITE	PDOC00006
PS00006	573->577	CK2_PHOSPHO_SITE	PDOC00006
PS00006	592->596	CK2_PHOSPHO_SITE	PDOC00006
PS00006	672->676	CK2_PHOSPHO_SITE	PDOC00006
PS00006	681->685	CK2_PHOSPHO_SITE	PDOC00006
PS00006	706->710	CK2_PHOSPHO_SITE	PDOC00006
PS00007	101->108	TYR_PHOSPHO_SITE	PDOC00007
PS00007	348->356	TYR_PHOSPHO_SITE	PDOC00007
PS00008	7->13	MYRISTYL	PDOC00008
PS00008	176->182	MYRISTYL	PDOC00008
PS00008	192->198	MYRISTYL	PDOC00008
PS00008	198->204	MYRISTYL	PDOC00008
PS00008	274->280	MYRISTYL	PDOC00008
PS00008	663->669	MYRISTYL	PDOC00008
PS00009	335->339	AMIDATION	PDOC00009
PS00013	186->197	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphfbr2_72b18.2)

Sbjct: 239 DPERIYEFKSVGNSSTLSHDSSDEEELL 266

Pedant information for DKFZphfbr2_72b18, frame 2

Report for DKFZphfbr2_72b18.2

[LENGTH] 715
 [MW] 80300.63
 [pI] 6.37
 [HOMOL] TREMBL:SPBC16A3_11 gene: "SPBC16A3.11"; product: "hypothetical protein";
 S.pombe chromosome II cosmid c16A3..5e-30
 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision
 repair) [S. cerevisiae, YDR419w] 2e-15
 [FUNCAT] 1 genome replication, transcription, recombination and repair [M.
 genitalium, MG360] 3e-13
 [PIRKW] SOS mutagenesis 2e-11
 [PIRKW] DNA repair 2e-11
 [PIRKW] induced mutagenesis 2e-11
 [SUPFAM] umuC protein 3e-29
 [PROSITE] MYRISTYL 6
 [PROSITE] AMIDATION 1
 [PROSITE] CAMP_PHOSPHO_SITE 2
 [PROSITE] CK2_PHOSPHO_SITE 15
 [PROSITE] PROKAR_LIPOPROTEIN 1
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 21
 [PROSITE] ASN_GLYCOSYLATION 5
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 4.20 %

SEQ MELADVGAASSQGVHDQVLPTPNASSRVIVHVDLDCFYAQVEMISNPELKDKPLGVQQK
 SEG
 PRD ccc

SEQ YLVVTCNYEARLGVKKLMNVDAKEKCPQLVLVNGEDLTRYREMSYKVTELEEFSPV
 SEG
 PRD ccc

SEQ ERLGFDENFVDLTEMVEKRLQQLQSDLSAVTVSGHVYNNQSINLLDVLHIRLLVGSQIA
 SEG
 PRD ecc

SEQ AEMREAMYNQLGLTGAGVASNKLAKLVSGVFKPNQQTVLLPESQHLIHSNLHIKEIP
 SEG
 PRD hhhhhhhhhhhcc

SEQ GTGYKTAKCLEALGINSVRDLQTFSPKILEKELGISVAQRIQKLSFGEDNSPVILSGPPQ
 SEG
 PRD ccc

SEQ SFSEEDSFKKCTSEVEAKNIEELLASLLNRVCQDGRKPHTVRLIIRYSSSEKHYGRESR
 SEG
 PRD ccc

SEQ QCPIPSHVIQKLTGNVDVMTMVDILMKLFRNMVNVKMPFHLTLVSVCFNKLALNTAK
 SEG
 PRD ccc

SEQ KGLIDYYLMPSLSTTSRSGKHSFKMKDTHMEDFPKDKETNRDPLPSGRIESTRTRESPLD
 SEG
 PRD hhhheeecc

SEQ TTNFSKEKDINEFPLCSLPEGVQEVSKQLPVDIQEILSGKSREKFQKGGSVSCPLHAS
 SEG
 PRD ccc

SEQ RGVLSFFSKKQMIDIPINPRDLSSSKQVSSVSPCEPGTSGFNSSSSSYMSSQKDYSYYL
 SEG
 PRD hcc

SEQ DNRLKDERISQGPKEPQGFHTNSNPAVSAFHSFPNLQSEQLFSRNHTTDSHKQTVATDS
 SEG
 PRD hhhhhhhhhhhcc

SEQ HEGLTENREPDSVDEKITFPSDIDPQVFYELPEAVQKELLAEWKRTGSDFHIGHK
 SEG
 PRD ccc

 Entry HS086339 from database EMBL:
 human STS WI-11064.
 Score = 1523, P = 3.0e-64, identities = 327/343

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 50 bp to 2194 bp; peptide length: 715
 Category: similarity to known protein

```

1 MELADVGAAG SSQGVHDQVL PTPNASSRVI VHVLDLCFYA QVEMISNPCL
51 KDKPLGVQOK YLVVTCNYEA RKLGVKKLMN VRDAKEKCPQ LVLVNGEDLT
101 RYREMSYKVT ELLEEFSPVV ERLGFDENFV DLTEMVEKRL QQLQSDLSA
151 VTVSGHYVNN QSINLLDVLH IRLLVGSQIA AEMREAMYNQ LGLTGCAGVA
201 SNKLLAKLVS GVFKPNQQT VLLPESQHLI HSLNHIKEIP GIGYKTAKCL
251 EALGINSVRD LQTFSPKILE KELGISVAQR IQKLSFGEDN SPVILSGPPQ
301 SFSEEDSFKK CTSEVEAKNK IEELLASLLN RVCQDGRKPH TVRLIIRYS
351 SEKHYGRESR QCPIPSHVIQ KLGTGNYDVM TPMVDILMKL FRNMVNVKMP
401 FHLTLLSVCF CNLKALNTAK KGLIDYYLMP SLSTTSRSGK HSFKMKDTHM
451 EDFPKDKETN RDLPLSGRIE STRTRESPLD TTNFSKEKDI NEFPLCSLPE
501 GVDQEVSKQL PVDIOEELS GKSREKFOGK GSVSCPLHAS RGVLSFFSKK
551 QMQDIPINPR DHLSSSKQVS SVSPCEPGTS GFNSSSSSYM SSQKDYSYYL
601 DNRLKDERIS QGPKEPQGFH FTNSNPAVSA FHSFPNLQSE QLFSRNHTTD
651 SHKQTVATDS HEGLTENREP DSVDEKITFP SDIDPQVFYE LPEAVQKELL
701 AEWKRTGSDF HIGHK
  
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_72b18, frame 2

PIR:H64747 DNA-damage-inducible protein dinP - Escherichia coli, N = 2, Score = 212, P = 4.2e-27

PIR:H69963 DNA-damage repair protein homolog yqjH - Bacillus subtilis, N = 2, Score = 230, P = 5.2e-26

>PIR:H69963 DNA-damage repair protein homolog yqjH - Bacillus subtilis
 Length = 414

HSPs:

Score = 230 (34.5 bits), Expect = 5.2e-26, Sum P(2) = 5.2e-26
 Identities = 47/112 (41%), Positives = 73/112 (65%)

Query: 27 SRVIVHVLDLCFYAQVEMISNPCLKDKPLGV-----QQKYLVTTCNYEARKLGVKKLMNV 81
 SR+I III+D+ FYA VEM +P L+ KP+ V ++K +VVTC+YEAR GVK M V
 Sbjct: 5 SRIIFHIDMNSFYASVEMAYDPALRGKPVAVAGNVKERKGI VVTCSYEARARGVKT TMPV 64

Query: 82 RDAKEKCPQLVLVNGEDLTRYREMSYKVTLEEFSPVVERLGFDENFVDLTE 134
 AK CP+L+++ + RYR S + +L E++ +VE + DE ++D+T+
 Sbjct: 65 WQAKRHCP ELIVLP-PNFDYRNSSRAMFTILREYTDLVEPV SIDE GYMDMTD 116

Score = 137 (20.6 bits), Expect = 5.2e-26, Sum P(2) = 5.2e-26
 Identities = 43/148 (29%), Positives = 75/148 (50%)

Query: 178 QIAAEMREAMYNQLGLTGCAGVASNKLLAKLVSGVFKPNQQT VLLPESQHLI HSLNHIK 237
 + A E++ + +L L G+A NK LAK+ S + KP T+L ++ L +
 Sbjct: 125 ETAKEIQSRLQKELLPLSSIGIAPNKFLAKMASDMKKPLGITILRRQVPDILWPLP-VG 183

Query: 238 EIPGIGYKTAKCLEALGINSVRDLQTFSPKILEKELGISVAQRIQKLSFGEDNSPVILSG 297
 E+ G+G KTA+ L+ LGI+++ +L L++ LGI+ R++ + G. ++PV
 Sbjct: 184 EMHGVGKKTA EKLG LGIHTIGELAADEHSLKRL LGIN-GPRLKNKANGIHAPV---- 238

Query: 298 PPQSFSEEDSFKKCTSEVEAKNKIEELL 325
 P+ E S ++ + EELL

DKF2phfbr2_72b18

group: nucleic acid management

DKF2phfbr2_72b18 encodes a novel 715 amino acid protein with similarity to E. coli DNA-damage-inducible protein dinP and other proteins induced by DNA-damage.

The novel protein is similar to dinP of E. coli, yqjH of B. subtilis, dinP of M. tuberculosis and T19K24.15 of A. thaliana. The dinB/P pathway is a second SOS-pathway in E. coli. Therefore the new gene seems to be involved in DNA repair.

The new protein can find application in modulating DNA repair and mutagenesis.

similarity to DNA damage induced genes

complete cDNA, complete cds, potential start at Bp 49, EST hits
localisation primer site B is missing!

Sequenced by LMU

Locus: /map="416.0 cR from top of Chr18 linkage group"??

Insert length: 2475 bp

Poly A stretch at pos. 2452, polyadenylation signal at pos. 2431

```
1 GGGGGAGGAA GCGGGCGGCG ACGACGAGGA AGACGCCGAG GCCTGGGCCA
51 TGGAACTGGC GGACGTGGGG GCGGCAGCCA GCTCGCAGGG AGTTCATGAT
101 CAAGTGTTGC CCACACCAAA TGCTTCATCC AGAGTCATAG TACATGTGGA
151 TCTGGATTGC TTTTATGCAC AAGTAGAAAT GATCTCAAAT CCAGAGCTAA
201 AAGACAAACC TTTAGGGGTT CAACAGAAAT ATTTGGTGGT TACCTGCAAC
251 TATGAAGCTA GGAAGACTTG AGTTAAGAAA CTTATGAATG TCAGAGATGC
301 AAAAGAAAAG TGTCCACAGT TGGTATTAGT TAATGGAGAA GACCTGACCC
351 GCTACAGAGA AATGTCTTAT AAGGTTACAG AATTACTGGA AGAATTTAGT
401 CCAGTTGTTG AGAGACTTGG ATTTGATGAA AATTTTGTGG ATCTAACAGA
451 AATGGTTGAG AAGAGACTAC AGCAGCTGCA AAGTGATGAA CTTCTGCGG
501 TGACTGTGTC GGTTCATGTA TACAATAATC AGTCTATAAA CCTGCTTGAC
551 GTCTTGACAC TCAGACTACT TGTGGATCTC CAGATTGCAG CAGAGATGCG
601 GGAAGCCATG TATAATCAGT TGGGGCTCAC TGGCTGTGCT GGAGTGGCTT
651 CTAATAAACT GTTGGCAAAA TTAGTTTCTG GTGTCTTTAA ACCAAATCAA
701 CAAACAGTCT TATTACCTGA AAGTTGTCAA CATCTTATTC ATAGTTTGAA
751 TCACATAAAG GAAATACCTG GTATTGGCTA TAAACTTGCC AAATGTCTTG
801 AAGCACTGGG TATCAATAGT GTGCGTGAIC TCCAAACCTT TTCACCCAAA
851 ATTTTAGAAA AAGAATTAGG AATTTCAGTT GCTCAGCGTA TCCAAAAGCT
901 CAGTTTTGGA GAGGATAACT CCCCTGTGAT ACTCTCAGGA CCACCTCAGT
951 CCTTTAGTGA AGAAGATTCA TTTAAAAAAT GTACATCTGA AGTTGAAGCT
1001 AAAAATAAGA TTGAAGAACT ACTTGCTAGT CTTTAAACA GAGTATGCCA
1051 AGATGGAAGG AAGCCTCATA CAGTGAGATT AATAATCCGT CGGTATTCCCT
1101 CTGAGAAGCA CTATGGTCGT GAGAGTCGTC AGTGCCCTAT TCCTTCACAT
1151 GTAATTCAGA AATTAGGGAC AGGAAATTAT GATGTGATGA CCCCAATGGT
1201 TGATATACTT ATGAAACTTT TTCGAAATAT GGTGAATGTG AAGATGCCAT
1251 TTCACCTTAC CCTTCTAAGT GTGTGCTTCT GCAACCTTAA AGCACTAAAT
1301 ACTGCTAAGA AAGGCTTAT TGATTATTAT TTAATGCCAT CATTATCAAC
1351 TACTTCACGC TCTGGCAAGC ACAGTTTAA AATGAAAGAC ACTCATATGG
1401 AAGATTTTCC CAAAGACAAA GAAACAAACC GGGATTTCCCT ACCAAGTGGA
1451 AGAATTGAAA GTACAAGAAC TAGGGAGTCT CCACTAGATA CCACAAATTT
1501 TTCTAAAGAA AAAGACATTA ATGAATTCCC ACTCTGTTCA CTTCTGAAG
1551 GTGTTGACCA AGAAGTCTCC AAGCAGCTTC CAGTAGATAT TCAAGAAGAA
1601 ATCCTTTCTG GAAATCTAG GGAATAATTT CAAGGGAAAG GAAGTGTGAG
1651 TTGTCCATTA CATGCCTCTA GAGGAGTATT ATCTTTCTTT TCTAAAAAAC
1701 AAATGCAAGA TATTCCCATTA ATCCTAGAG ATCATTTATC CAGTAGCAAA
1751 CAGGTATCCT CTGTATCTCC TTGTGAACCG GGAACATCAG GCTTTAATAG
1801 CAGTAGTTCT TCTTACATGT CTAGCCAAA GATTATTCA TATTATTTAG
1851 ATAATAGATT AAAAGATGAA CGAATAAGTC AAGGACCTAA AGAACCTCAA
1901 GGATTTCCACT TTAACAAATC AAACCTTGCT GTGTCTGCTT TTATTTCATT
1951 TCCAAACTTG CAGAGTGAGC AACTTTTCTC CAGAAACCAC ACTACAGATA
2001 GCCATAAGCA AACAGTAGCA ACAGACTCTC ATGAAGGACT TACAGAAAAT
2051 AGAGAGCCAG ATCTGTTGA TGAGAAAATT ACTTTCCCTT CTGACATTGA
2101 TCCTCAAGTT TTCTATGAAC TACCAGAAGC AGTACAAAAG GAACTGCTGG
2151 CAGAGTGGA GAGAACAGGA TCAGATTTC ACATTGGACA TAAATAAGCA
2201 TATTCAGCAA AAAGGTCTGA AAAGCAAGGG AATACCATTA TTTTCGGATT
2251 AGCGGTTTAT TAAGCTCTTC TATATTAAAC ACTAATAGAT ATTCAATAAC
2301 GGAGTAAACT GTCCAGATA AAGCAAGAAT AGTTGCAAGA AGTAAATTCT
2351 GGCACAAAGC GTAAAAATAT AACAGAAGAA ATAATGTAA ATACTATCTT
2401 TTATGTCTAA AGCCATTTTA TATTACTTTT CAATAAAAAG AATATCATGG
2451 TCAAAAAAAA AAAAAAAA AAAAC
```

BLAST Results

Peptide information for frame 1

ORF from 202 bp to 897 bp; peptide length: 232
Category: putative protein

1 MPSSLWDRFSS SSTSSSPSSL PRTPTPDRPP RSAWGSATRE EGFDRSTSLE
51 SSDCESLDSS NSGFGPEEDT AYLDGVSLPD FELLSDPEDE HLCANLMQLL
101 QESLAQARLG SRRPARLLMP SQLVSQVGKE LLRLAYSEPC GLRGALLDVC
151 VEQGKSCHSV GQLALDPSLV PTFQLTLVLR LDSRLWPKIQ GLFSSANSFP
201 LPGFSQSLTL STGFRVIKKK LYSSEQLPIE EC

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_71o20, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_71o20, frame 1

Report for DKFZphfbr2_71o20.1

[LENGTH] 232
[MW] 25354.60
[pI] 4.87
[PROSITE] MYRISTYL 2
[PROSITE] CK2_PHOSPHO_SITE 6
[PROSITE] GLYCOSAMINOGLYCAN 1
[PROSITE] PKC_PHOSPHO_SITE 1
[KW] All_Alpha
[KW] LOW_COMPLEXITY 17.67 %

SEQ MPSSLWDRFSSSSTSSSPSSLPRTPTPDRPPRSAWGSATREEGFDRSTSLESSDCESLDSS
SEGXX
PRD ccc

SEQ NSGFGPEEDTAYLDGVSLPDFELLSDPEDEHLCANLMQLLQESLAQARLGSRPARLLMP
SEG xx.....
PRD ccc

SEQ SQLVSQVGKELLRLAYSEPCGLRGALLDVCVEQGKSCHSVGQLALDPSLVPTFQLTLVLR
SEG
PRD ccc

SEQ LDSRLWPKIQGLFSSANSFPLPGFSQSLTLSTGFRVIKKKLYSSEQLPIEEC
SEG
PRD ccc

Prosite for DKFZphfbr2_71o20.1

PS00002	62->66	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	111->114	PKC_PHOSPHO_SITE	PDOC00005
PS00006	3->7	CK2_PHOSPHO_SITE	PDOC00006
PS00006	38->42	CK2_PHOSPHO_SITE	PDOC00006
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	52->56	CK2_PHOSPHO_SITE	PDOC00006
PS00006	77->81	CK2_PHOSPHO_SITE	PDOC00006
PS00006	85->89	CK2_PHOSPHO_SITE	PDOC00006
PS00008	141->147	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_71o20.1)

DKFZphfbr2_71o20

group: brain derived

DKFZphfbr2_71o20 encodes a novel 232 amino acid protein without similarity to known proteins.

No informative BLAST results: No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits
on genomic level encoded by AC006186 (3 exons)

Sequenced by GBF

Locus: /map="10q22.1"

Insert length: 1768 bp

Poly A stretch at pos. 1742, polyadenylation signal at pos. 1726

```
1  GGGGGCAGCA  GGCCAAGGGG  GAGGTGCGAG  CGTGGACCTG  GGACGGGTCT
51  GGGCGGCTCT  CGGTGGTTGG  CACGGGTTCC  CACACCCATT  CAAGCGGCAG
101 GACGCACTTG  TCTTAGCAGT  TCTCGCTGAC  CGCGCTAGCT  GCGGCTTCTA
151 CGCTCCGGCA  CTCTGAGTTC  ATCAGCAAAC  GCCCTGGCGT  CTGTCTTCAC
201 CATGCCTAGC  CTTTGGGACC  GCTTCTCGTC  GTCGTCCACC  TCCTCTTCGC
251 CCTCGTCCTT  GCCCCGAAC  CCCACCCAG  ATCGGCCGCC  GCGCTCAGCC
301 TGGGGGTCGG  CGACCCGGGA  GGAGGGGTTT  GACCCTCCCA  CGAGCCTGGA
351 GAGCTCGGAC  TGCGAGTCCC  TGGACAGCAG  CAACAGTGGC  TTCGGGCCGG
401 AGGAAGACAC  GGCTTACCTG  GATGGGGTGT  CGTTGCCCGA  CTTCGAGCTG
451 CTCAGTGACC  CTGAGGATGA  AACTTGTGT  GCCAACCTGA  TGCAGCTGCT
501 GCAGGAGAGC  CTGGCCCAGG  CGCGGCTGGG  CTCTCGACGC  CCTGCGCGCC
551 TGCTGATGCC  TAGCCAGTTG  GTAAGCCAGG  TGGGCAAAGA  ACTACTGCGC
601 CTGGCCTACA  GCGAGCCGTG  CGGCCTGCGG  GGGCGCTGCG  TGGACGTCTG
651 CGTGGAGCAG  GGCAAGAGCT  GCCACAGCGT  GGGCCAGCTG  GCACTCGACC
701 CCAGCCTGGT  GCCCACCTTC  CAGCTGACCC  TCGTGCTGCG  CCTGGACTCA
751 CCACTCTGGC  CCAAGATCCA  GGGGCTGTTT  AGCTCCGCCA  ACTCTCCCTT
801 CCTCCCTGGC  TTCAGCCAGT  CCCTGACGCT  GAGCACTGGC  TTCCGAGTCA
851 TCAAGAAGAA  GCTGTACAGC  TCGGAACAGC  TGCCCATGGA  GGAGTGTGTA
901 ACTTCAACCT  GAGGGGGCCG  ACAGTGCCCT  CCAAGACAGA  GACGACTGAA
951 CTTTTGGGGT  GGAGACTAGA  GGCAGGAGCT  GAGGGACTGA  TTCCAGTGGT
1001 TGGAAAAGTG  AGGCAGCCAC  CTAAAGTGGA  GGTGGGGGAA  TAGTGTGTTT
1051 CAGGAAGCTC  ATTGAGTTGT  GTGCGGCTGG  CTGTGCATTG  GGGACACATA
1101 CCCCTCAGTA  CTGTAGCATG  AAACAAAGGC  TTAGGGGCCA  ACAAGGCTTC
1151 CAGCTGGATG  TGTGTGTAGC  ATGTACCTTA  TTATTTTGT  TACTGACAGT
1201 TAACAGTGGT  GTGACATCCA  GAGAGCAGCT  GGGCTGCTCC  CGCCCCAGCC
1251 TGGCCCAGGG  TGAAGGAAGA  GGCACGTGCT  CCTCAGAGCA  GCCGGAGGGA
1301 AGGGGGAGGT  CGGAGGTCGT  GGAGGTGGTT  TGTGTATCTT  ACTGGTCTGA
1351 AGGGACCAAG  TGTGTTTGT  GTTTGTTTGT  TATCTGTTT  TTCTGATCGG
1401 AGCATCACTA  CTGACCTGTT  GTAGCAGCT  ATCTTACAGA  CGCATGAATG
1451 TAAGAGTAGG  AAGGGGTGGG  TGTCAGGGAT  CACTTGGGAT  CTTTGACACT
1501 TGAAAAATTA  CACCTGGCAG  CTGCGTTTAA  GCCTTCCCC  ATCGTGTAAT
1551 GCAGAGTTGA  GCTGGCAGGG  GAGGGGCTGA  GAGGGTGGGG  GCTGGAACCC
1601 CTTCCCGGGA  GGAGTGCCAT  CTGGGTCTTC  CATCTAGAAC  TGTGTTACATG
1651 AAGATAAGAT  ACTCACTGTT  CATGAATACA  CTTGATGTT  AAGTATTAAG
1701 ACCTATGCAA  TATTTTAC  TTTTCTAATA  AACATGTTT  TTTAAACAAA
1751 AAAAAAAAAA  AAAAAAAA
```

BLAST Results

Entry AC006186 from database EMBLNEW:

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 10 clone

CRI-JC2048 map 10q22.1: HTGS phase 1, 4 unordered pieces.

Score = 6512, P = 0.0e+00, identities = 1326/1345

3 exons

Medline entries

No Medline entry

	++ + L+NLG++++ +HG+M+Q +R+ +++F++ +L++TDV++R	
Query	277 QRTALLLRNLGFTAIP LHGQMSQSKRLGSLNKFKAKARSILLATDVASR	325
HMM	GIDIPdVNHVINYDMPWNPEqYIQRIGRTgRIG*	
	G+DIP V++V+N+D+P ++ +YI+R+GRT+R+G	
Query	326 GLDIPHVDVVVNF DIPTHSKDYIHRVGRTARAG	358

SEQ PRD	VQSAVIVGGIDSMSSQSLALAKKPHIIATPGRLIDHLENTKGFNLRAKYLVMDADRIL eeeeeeecchhhhhhhhhhhccceeeeeeccccccccccccccccccceehhhhhhhh
SEQ PRD	NMDFETEVDKILKVIPDRKTFLSATMTKKVQKLQRAALKNPVKCAVSSKYQTVEKLQ hhcchhhhhhhhhhhccchhhhhhhhhccchhhhhhhhhhhhhccceeeeeeccccchhhh
SEQ PRD	YYIFIPSKFKDYLVIYNELAGNSFMIFCSTCNNORTALLLRNLGFTAIPLHGQMSQS hhhhhhhhhhhhhhhhhhhhhhccceeeeeeccchhhhhhhhhhhcccccceeeccccchh
SEQ PRD	KRLGSLNKFKAKARSILLATDVASRGLDIPHDVVVNFDPHPSKDYIHRVGRGARAGRS hhhhhhhhhhhhhhhhcchhhhhhhhhccccceeeeeeccccccccceeecccccccccc
SEQ PRD	GKAITFVTQYDVELFQRIEHLIGKKLPGFPTQDDEVMMLTERVAEAGRFAARMELREHGEK ceeeeeeecchhhhhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhhhh
SEQ PRD	KKRSREDAGDNDDETEGAIGVRNKGAGGKKMKRGR hhhhcccccccccccccccccccccccccccccccccccccc

Prosite for DKF2phfbr2 6017.3

PS000001	274->278	ASN_GLYCOSYLATION	PDOC000001
PS000004	421->425	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	25->28	PKC_PHOSPHO_SITE	PDOC000005
PS000005	72->75	PKC_PHOSPHO_SITE	PDOC000005
PS000005	209->212	PKC_PHOSPHO_SITE	PDOC000005
PS000005	229->232	PKC_PHOSPHO_SITE	PDOC000005
PS000005	276->279	PKC_PHOSPHO_SITE	PDOC000005
PS000005	300->303	PKC_PHOSPHO_SITE	PDOC000005
PS000005	354->357	PKC_PHOSPHO_SITE	PDOC000005
PS000005	360->363	PKC_PHOSPHO_SITE	PDOC000005
PS000005	400->403	PKC_PHOSPHO_SITE	PDOC000005
PS000006	9->13	CK2_PHOSPHO_SITE	PDOC000006
PS000006	25->29	CK2_PHOSPHO_SITE	PDOC000006
PS000006	186->190	CK2_PHOSPHO_SITE	PDOC000006
PS000006	368->372	CK2_PHOSPHO_SITE	PDOC000006
PS000006	391->395	CK2_PHOSPHO_SITE	PDOC000006
PS000006	424->428	CK2_PHOSPHO_SITE	PDOC000006
PS000008	66->72	MYRISTYL	PDOC000008
PS000008	71->77	MYRISTYL	PDOC000008
PS000008	116->122	MYRISTYL	PDOC000008
PS000008	120->126	MYRISTYL	PDOC000008
PS000008	128->134	MYRISTYL	PDOC000008
PS000009	382->386	AMIDATION	PDOC000009
PS000017	68->76	ATP_GTP_A	PDOC000017
PS000039	172->181	DEAD_ATP_HELICASE	PDOC000039

Pfam for DKFZphfbr2 6017.3

HMM_NAME	DEAD and DEAH box helicases	
HMM	*gLpPWILrNiyeMGFEkPTPIQQQAIpIiLEGRDVMACAQTGSGKTAAF G ++ +++++++G++KPT+IQ +AIP++L+GRD+++ A TGSGKT+AF	
Query	30 GVTVDVLC EACDQLGWTKPTKIQIEAIPALAQGRDIIGLAETGSGKGTGAF	78
HMM	lIPMLQHI dwdPwpqpPQdPrALILAPTRELAMQIQEEcrkFgkHMNgIR ++P+L ++++P + ++AL+L+PTRELA QI+E++++G++++ ++	
Query	79 ALPILNALLET P-----QR-LFALVLTPTRELAFCISEQFEALGSSIG-VQ	122
HMM	ImcIYGGtnMRdQMRmLeRgPPhIVATPGRGLIDHIER.gtl dLDrIeML ++I+GG ++ +_Q L+++P HI+IATPGRGLIDH+E+ ++L+++++L	
Query	123 SAVIVGGIDSMSQSLALAKKP-HII IATPGRGLIDHLENTKGFNLRLKYL	171
HMM	VMDEADRLMDMGFIDQIRrImrqIPMpwnRQTMMFSATMPdeIqELArRf VMDEADR+L+M+F+ +++++I++ IP ++R T +FSATM++++Q+L+R+	
Query	172 VMDEADRILNMDFETEV D KILKVIP--RDRKTF LFSATMTKKVQKLQRAA	219
HMM	MRNPiRInIdMdElTtnEnIkQwYiyVerEMWkfdclcrLIE* ++NP+ ++ +++++T++ ++Q+YI+++ + K +L+++++	
Query	220 LKNPVKCAVSSKYQTVE-KLQQYIIFIP-SKFKD TYLVYILN	259

HMM_NAME	Helicases conserved C-terminal domain
HMM	*EileeWLknlgIrvmyIHGdMpOeERdeIMddFNnGEynVLICtDVGqqr

+ G + K GG+ GR
 Sbjct: 459 SGRFRKMGIKSMGGRGGSGGGR 480

Pedant information for DKFZphfbr2_6ol7, frame 3

 Report for DKFZphfbr2_6ol7.3

[LENGTH] 455
 [MW] 50646.80
 [pI] 9.18
 [HOMOL] PIR:S40731 ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans
 1e-167
 [FUNCAT] 04.01.04 rrna processing [S. cerevisiae, YHR065c] 1e-127
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YHR065c] 1e-127
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YHR169w] 2e-79
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YLL008w] 1e-71
 [FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YMR290c] 4e-66
 [FUNCAT] j mrna translation and ribosome biogenesis [H. influenzae, HI0231 RNA] 1e-63
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YJL033w] 1e-58
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YDL084w] 1e-55
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae,
 YOR204w] 5e-55
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR204w] 5e-55
 [FUNCAT] 1 genome replication, transcription, recombination and repair [H.
 influenzae, HI0892] 9e-48
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YLR276c] 2e-45
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YDR194c] 4e-42
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL064c] 7e-16
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YMR190c] 7e-12
 [FUNCAT] 11.10 cell death [S. cerevisiae, YMR190c] 7e-12
 [FUNCAT] r general function prediction [M. jannaschii, MJ1401] 5e-06
 [BLOCKS] BL00175B Phosphoglycerate mutase family phosphohistidine proteins
 [BLOCKS] BL000390 DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039C DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039B DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039A DEAD-box subfamily ATP-dependent helicases proteins
 [PIRKW] nucleus 4e-60
 [PIRKW] RNA binding 7e-69
 [PIRKW] DEAD box 7e-69
 [PIRKW] transmembrane protein 9e-41
 [PIRKW] DNA binding 3e-55
 [PIRKW] recf recombination pathway 3e-11
 [PIRKW] ATP 1e-126
 [PIRKW] purine nucleotide binding 7e-69
 [PIRKW] P-loop 1e-126
 [PIRKW] hydrolase 1e-55
 [PIRKW] protein biosynthesis 7e-69
 [PIRKW] ATP binding 3e-61
 [SUPFAM] ATP-dependent RNA helicase eIF-4A 8e-06
 [SUPFAM] WW repeat homology 4e-58
 [SUPFAM] translation initiation factor eIF-4A 7e-69
 [SUPFAM] DEAD/H box helicase homology 1e-126
 [SUPFAM] recQ helicase homology 5e-12
 [SUPFAM] ATP-dependent RNA helicase homology 8e-06
 [SUPFAM] unassigned DEAD/H box helicases 1e-126
 [SUPFAM] ATP-dependent RNA helicase DBP1 4e-60
 [SUPFAM] ATP-dependent RNA helicase DHH1 1e-58
 [SUPFAM] recQ protein 3e-11
 [SUPFAM] tobacco ATP-dependent RNA helicase DB10 4e-58
 [SUPFAM] Bloom's syndrome helicase 5e-12
 [PROSITE] DEAD_ATP_HELICASE 1
 [PROSITE] ATP_GTP_A 1
 [PROSITE] MYRISTYL 5
 [PROSITE] AMIDATION 1
 [PROSITE] CAMP_PHOSPHO_SITE 1
 [PROSITE] CK2_PHOSPHO_SITE 6
 [PROSITE] PKC_PHOSPHO_SITE 9
 [PROSITE] ASN_GLYCOSYLATION 1
 [PFAM] Helicases conserved C-terminal domain
 [PFAM] DEAD and DEAH box helicases
 [KW] Alpha_Beta

SEQ MAAPEEHDSPTASQPIVEEEETKTFKDLGVTDVLCACDQLGWTKPTKIQIEAIPALQ
 PRD cccccccccccccchhhhhhhhhhhccccchhhhhhhhhhhcccccccccccccccccc

SEQ GRDIIGLAETGSGKTGAFALPILNALLETQRLFALVLTPTRELAFQISEQFEALGSSIG
 PRD cceeeeeeccccccccchhhhhhhhhhhccccceeeeeeccccchhhhhhhhhhhhhhhhhcc

Peptide information for frame 3

ORF from 27 bp to 1391 bp; peptide length: 455
 Category: strong similarity to known protein

```

1 MAAPEEHDSP TEASQPIVEE EETKTFKDLG VTDVLC EACD QLGWTKPTKI
51 QIEAIPALQ GRDIIGLAET GSGKTGAFAL PILNALLETQ QRLFALVLTQ
101 TRELAFOISE QFEALGSSIG VQSAVIVGGI DSMSQSLALA KKPHEIIATP
151 GRLLDHLNT KGFNLRLKY LVMDEADRIL NMDFETEVDK ILKVIPRDRK
201 TFLFSATMTK KVQKLQRAAL KNPVKCAVSS KYQTVEKLQQ YYIFIPSKFK
251 DTYLVYILNE LAGNSEMIFC STCNNTQRTA LLLRNLGFTA IPLHGQMSQS
301 KRLGSLNKEK AKARSILLAT DVASRGLDIP HVDVVVNFEDI PTHSKDYIHR
351 VGR TARAGRS GKAITFVTQY DVELFQRIEH LIGKKLPGFP TQDDEVMLLT
401 ERV AEAQRFA RMELREHGEK KRSREDAGD NDDTEGAIGV RNKVAGGKMK
451 KRKGR

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_6017, frame 3

PIR:S40731 ATP-dependent RNA helicase homolog T26G10.1 - *Caenorhabditis elegans*, N = 1, Score = 1497, P = 1.6e-153

PIR:S46713 hypothetical protein YHR065c - yeast (*Saccharomyces cerevisiae*), N = 1, Score = 1154, P = 3.6e-117

TREMBL:ATH010462_1 gene: "RH10"; product: "RNA helicase"; *Arabidopsis thaliana* mRNA for DEAD box RNA helicase, RH10, N = 1, Score = 1122, P = 8.9e-114

TREMBL:AC002985_2 product: "R27090_2"; Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence., N = 1, Score = 950, P = 1.5e-95

>PIR:S40731 ATP-dependent RNA helicase homolog T26G10.1 - *Caenorhabditis elegans*

Length = 489

HSPs:

Score = 1497 (224.6 bits), Expect = 1.6e-153, P = 1.6e-153
 Identities = 283/442 (64%), Positives = 364/442 (82%)

```

Query:   19 EEEETKTFKDLGVTDVLC EACDQLGWTKPTKIQIEAIPALQGRDIIGLAETGSGKTGAF 78
      /E+ K+F +LGV+ LC+AC +LGW KP+KIQ A+P ALQG+D+IGLAETGSGKTGAF
Sbjct:   39 EDVKEKSFAELGVSQPLCDACQRLGWMKPSKIQQAALPHALQGDVIGLAETGSGKTGAF 98

Query:   79 ALPILNALLETQRLFALVLTPTRELAFOISEQFEALGSSIGVQSAVIVGGIDSMSQSLA 138
      A+P+L +LL+ PQ F LVLTPTRELAFOI +QFEALGS IG+ +AVIVGG+D +Q++A
Sbjct:   99 AIPVLQSLLDHPQAFFCLVLTPTRELAFOIQQFEALGSGIGLIAAVIVGGVDMAAQAMA 158

Query:   139 LAKKPHEIIATPGRLIDHLNTKGFNLRLKYLVMDEADRILNMDFETEVDKILKVIPRD 198
      LA++PHII+ATPGRL+DHLNTKGFNL+ALK+L+MDEADRILNMDFE E+DKILKVIPR+
Sbjct:   159 LARRPHIIVATPGRLVDHLNTKGFNLKALKFLIMDEADRILNMDFEVELDKILKVIPRE 218

Query:   199 RKTFLFSATMTKKVQKLQRAALKNPVKCAVSSKYQTVEKLQQYYIFIPSKFKDTYLVYIL 258
      R+T+LFSATMTKKV KL+RA+L++P + +VSS+Y+TV+ L+Q+YIE+P+K+K+TYLVY+L
Sbjct:   219 RRTYLFSAATMTKKVSKLERASLRDPARVSVSSRYKTVDNLKQHYIFVPNKYKETYLVYLL 278

Query:   259 NELAGNSEMIFCSTCNNTORTALLLRNLGFTAIPHLHGQMSQSKRLGSLNKEKAKARSILL 318
      NE AGNS ++FC+TC T + A++LR LG A+PLHGQMSQ KRLGSLNKEK+KAR IL+
Sbjct:   279 NEHAGNSAIVFCATCATTMQIAVMLRQLGMQAVPLHGQMSQEKRLGSLNKEKSKAREILV 338

Query:   319 ATDVASRGLDIPHDVVVNFEDIPTHSKDYIHRVGR TARAGRS GKAITFVTQYDVLEFQRI 378
      TDVA+RGLDIPHDV+V-N+D+P+ SKDY+HRVGR TARAGRS G AIT VTQYDVE +Q+I
Sbjct:   339 CTDVAARGLDIPHDVDMVINYDMPSQSKDYVHRVGR TARAGRS G IAITVVTQYDVEAYQKI 398

Query:   379 EHLIGKKLPGFPTQDDEVMLTERVAEAQRFA RMELREHGEKKK-----RSREDAGDNDND 433
      E +GKKL + ++EVM+L ER EA AR+E++E EKKK R +D GD ++
Sbjct:   399 EANLGKKLDEYKCVENEVMVLVERTQEATENARIEMKEMDEKKKSGKKRRQNDDFGDTTEE 458

Query:   434 TEGAIGVRNKVAGGKMKRKRGR 455

```

DKFZphfbr2_6017

group: nucleic acid management

DKFZphfbr2_6017 encodes a novel 455 amino acid protein with strong similarity to DEAD-box ATP-dependent RNA helicases YHR065c and T26G10.1.

The *S. cerevisiae* protein YHR065c is required for maturation of the 35S RNA primary transcript.

The new protein can find application in modulating rRNA maturation.

strong similar to RNA helicases

complete cDNA, complete cds, EST hits
probable start at Bp 27 matches kozak consensus ANNatgG
involved in maturation of r-RNA ??
YHR065c/Rrp3p is involved in maturation of the 35S primary transcript
Drslp cold-sensitive mutation has slow 27S to 25S pre-rRNA
conversion and is deficient in 60S ribosomal subunits

Sequenced by AGOWA

Locus: unknown

Insert length: 1840 bp

Poly A stretch at pos. 1815, polyadenylation signal at pos. 1793

```
1 GGGGACTTCC GGAGACCTCA CACAAGATGG CGGCACCCGA GGAACACGAT
51 TCTCCGACCG AAGCGTCCCA GCCGATTGTG GAAGAGGAGG AAACATAAAC
101 ATTTAAAGAC CTGGGTGTGA CAGATGTGTT GTGTGAAGCT TGTGACCACT
151 TGGGATGGAC AAAACCCACC AAGATTCAGA TTGAAGCTAT TCCTTTGGCC
201 TTACAAGGTC GTGATATCAT TGGGCTTGCA GAAACTGGCT CTGGAAAGAC
251 AGGCGCCTTT GCTTTGCCCA TTCTAAACGC ACTGCTGGAG ACCCCGCAGC
301 GTTTGTTTGC CCTAGTTCTT ACCCCGACTC GGGAGCTGGC CTTTCAGATC
351 TCAGAGCAGT TTGAAGCCCT GGGGTCCTCT ATTGGAGTGC AGAGTGTGT
401 GATTGTAGGT GGAATTGATT CAATGTCTCA ATCTTTGGCC CTTGCAAAAA
451 AACCACATAT AATAATAGCA ACTCCTGGTC GACTGATTGA CCACTTGGAA
501 AATACGAAAG GTTTCAACTT GAGAGCTCTC AAATACTTGG TCATGGATGA
551 AGCCGACCGA ATACTGAATA TGGATTTTGA GACAGAGGTT GACAAGATCC
601 TCAAAGTGAT TCCTCGAGAT CGGAAAACAT TCCTCTTCTC TGCCACCATG
651 ACCAAGAAGG TTCAAAAACCT TCAGCGAGCA GCTCTGAAGA ATCCTGTGAA
701 ATGTGCCGTT TCCTCTAAAT ACCAGACAGT TGAAAAATTA CAGCAATATT
751 ATATTTTAT TCCCTCTAAA TTCAAGGATA CCTACCTGGT TTATATTCTA
801 AATGAATTGG CTGGAACCTC CTTTATGATA TTCTGCAGCA CCTGTAATAA
851 TACCCAGAGA ACAGCTTTGC TACTGCGAAA TCTTGGCTTC ACTGCCATCC
901 CCTCCATGG ACAAATGAGT CAGAGTAAGC GCCTAGGATC CCTTAATAAG
951 TTAAAGGCCA AGGCCCGTTC CATCTTCTA GCAACTGACG TTGCCAGCCG
1001 AGGTTTGGAC ATACCTCATG TAGATGTGGT TGTCAACTTT GACATTCCTA
1051 CCCATTCCAA GGATTACATC CATCGAGTAG GTCGAACAGC TAGAGCTGGG
1101 CGCTCCGGAA AGGCTATTAC TTTTGTCA CAGTATGATG TGGAACTCTT
1151 CCAGCGCATA GAACACTTAA TTGGGAAGAA ACTACCAGGT TTTCCAAAC
1201 AGGATGATGA GTTTATGATG CTGACAGAAC GCGTCGCTGA AGCCCAAAGG
1251 TTTGCCCGAA TGGAGTTAAG GGAGCATGGA GAAAAGAAGA AACGCTCGCG
1301 AGAGGATGCT GGAGATAATG ATGACACAGA GGGTGCTATT GGTGTCAGGA
1351 ACAAGGTGGC TGGAGGAAAA ATGAAGAAGC GGAAAGGCCG TTAATCACTT
1401 TTATGAAGGC TCGAGTTCTG CTGTTCTGTA AAAGAAAATT GGAGAAATGAA
1451 ACCTGCTCCA ACAGAGATCA TGAGACTGAA ATTGGTCAGA ATTCTCTCCA
1501 GAATGTGCTC AGCTAATTCA GTATTCTTCC CCATTCTGGG TTGGAGTTTA
1551 CTGCAGAGTA ATTCTTACAG TGCTGATGTC AAGACTGTTA CTGTTCTTCG
1601 ACTTTGATTG CTGCTCATG ACATGAGTAG GGTGTGCTCT TCTGTCACTT
1651 CACACAGACC TTTTGCCTTT TTTAGCTGCA AGTCAAGGAC TAGGTTGATG
1701 ATGCCCCATG CCTGTAATTG TAAAGAAGCT TGGACATCTG CAAATGATAT
1751 TTAAACCATC TTGGCTTGTG CTTTATTCAA ACTAATGTGA AACAATAAAT
1801 TTAAATATTA TTTTAAAG AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

PS00005	149->152	PKC_PHOSPHO_SITE	PDOC00005
PS00005	258->261	PKC_PHOSPHO_SITE	PDOC00005
PS00006	248->252	CK2_PHOSPHO_SITE	PDOC00006
PS00006	258->262	CK2_PHOSPHO_SITE	PDOC00006
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	171->177	MYRISTYL	PDOC00008
PS00008	268->274	MYRISTYL	PDOC00008
PS00009	41->45	AMIDATION	PDOC00009
PS00009	45->49	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_6i20.1)

51 RGHKGERQRG TRPRLGFEGG QTPFYIRIPK YGFNEGHSFR RQYKPMNLNR
 101 LOYLIDLGRV DPSQPIDLTQ LVNDRGVTIQ PLKRDYDVQL VEEGADTFDA
 151 KVNIEVQLAS ELAIAAIEKN GGVVTTAFYD PRSLDIVCKP VPFFLRGQPI
 201 PKRMLPPEEL VPYYTDAKNR GYLADPAKFP EARLELARKY GYLDPDITKD
 251 ELFKMLCTRK DPRQIFFGLA PGWVVMADK KILKPTDENL LKYYTS

BLASTP hits

Entry S63258 from database PIR:
 ribosomal protein L15 precursor, mitochondrial - yeast (*Saccharomyces cerevisiae*)
 Length = 322
 Score = 259 (91.2 bits), Expect = 2.0e-22, P = 2.0e-22
 Identities = 71/200 (35%), Positives = 106/200 (53%)

Entry H70161 from database PIR:
 ribosomal protein L15 (rplO) - Lyme disease spirochete
 Length = 145
 Score = 173 (60.9 bits), Expect = 4.8e-13, P = 4.8e-13
 Identities = 45/140 (32%), Positives = 73/140 (52%)

Alert BLASTP hits for DKFZphfbr2_6i20, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_6i20, frame 1

Report for DKFZphfbr2_6i20.1

[LENGTH] 296
 [MW] 33495.98
 [PI] 9.98
 [HOMOL] TREMBL:AF067212_1 gene: "F37F2.1"; *Caenorhabditis elegans* cosmid F37F2. 1e-38
 [FUNCAT] 05.01 ribosomal proteins [*S. cerevisiae*, YNL284c] 7e-15
 [FUNCAT] 30.16 mitochondrial organization [*S. cerevisiae*, YNL284c] 7e-15
 [FUNCAT] j mna translation and ribosome biogenesis [*M. genitalium*, MG169] 1e-06
 [BLOCKS] BL00475D
 [BLOCKS] BL00475B Ribosomal protein L15 proteins
 [PIRKW] ribosome 2e-13
 [PIRKW] mitochondrion 2e-13
 [PIRKW] protein biosynthesis 2e-13
 [SUPFAM] *Escherichia coli* ribosomal protein L15 4e-06
 [PROSITE] MYRISTYL 3
 [PROSITE] AMIDATION 2
 [PROSITE] CK2_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 4
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 12.50 %

SEQ MAGPLQGGGARALDLLRGLPRVSLANLKPNGSKKPERPRGRRRGRKCGRGHKGERQRG
 SEGXXX
 PRD ccc
 SEQ TRPRLGFEGGQTPFYIRIPKYGFNEGHSFRRQYKPMNLRLQYLIDLGRVDPSQPIDLTQ
 SEG
 PRD ccc
 SEQ LVNDRGVTIQPLKRDYDVQLVEEGADTFDAKVNIEVQLASELAIAAIEKNGGVVTTAFYD
 SEG
 PRD ecc
 SEQ PRSLDIVCKPVFFLRGQFIPKRMLPPEELVPYYTDAKNRGYLADPAKFPPEARLELARKY
 SEG
 PRD ccc
 SEQ GYLDPDITKDELFKMLCTRKDPRQIFFGLAPGWVVMADKKILKPTDENLLKYYTS
 SEG
 PRD ccc

Prosite for DKFZphfbr2_6i20.1

PS00005 33->36 PKC_PHOSPHO_SITE PDOC00005
 PS00005 88->91 PKC_PHOSPHO_SITE PDOC00005

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 134 bp to 1351 bp; peptide length: 406
 Category: similarity to unknown protein

```

1 MAENGKNCDO RRVAMNKEHH NGNFTDPSSV NEKKRREREE RQNIWLWRQP
51 LITLQYFSLE ILVILKEWTS KLWHRQSIVV SFLLLLAVLI ATYYVEGVHQ
101 QYVQRIEQF LLYAYWIGLG ILSSVGLGTG LHTFLLYLGP HIASVTLAAY
151 ECNSVNFPEP PYPDQIICPD EEGTEGTIFL WSIISKVRIE ACMWGIGTAI
201 GELPPYFMMAR AARLSGAEPD DEEYQEFEEF LEHAESAQDF ASRAKLAVQK
251 LVQKVGFFGI LACASIPNPL FDLGITCGH FLVPFWTFFG ATLIGKAIK
301 MHIQKIFVII TFSKHIVEQM VAFIGAVPGI GPSLQKPFQE YLEAQRQKLH
351 HKSEMGTPQG ENWLSWMFEK LVVVMVCYFI LSIINSMAQS YAKRIQRLN
401 SEEKTK

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfd2_3i13, frame 2

TREMBL:CEY37D8A_20 gene: "Y37D8A.22"; *Caenorhabditis elegans* cosmid
 Y37D8A, N = 1, Score = 905, P = 8.8e-91

TREMBL:ATAC98_2 gene: "YUP8H12.2"; *Arabidopsis thaliana* chromosome 1
 YAC yUP8H12 complete sequence., N = 1, Score = 470, P = 1.1e-44

PIR:H71412 hypothetical protein - *Arabidopsis thaliana*, N = 1, Score =
 293, P = 6e-24

>TREMBL:CEY37D8A_20 gene: "Y37D8A.22"; *Caenorhabditis elegans* cosmid
 Y37D8A
 Length = 457

HSPs:

Score = 905 (135.8 bits), Expect = 8.8e-91, P = 8.8e-91
 Identities = 167/317 (52%), Positives = 228/317 (71%)

```

Query:   38 REERQNIWLWRQPLITLQYFSLEILVILKEWTSKLWHRQSIVVSFLLLLAVLIATYYVEG 97
          R ER+ IV WR+P I + Y +EI + E K+ +++++ + + + + Y+ G
Sbjct:   93 RMERETIVFWRPHVIVIPYALMEIAHLAVELFFKILAHKTVLLLTAISIGLAVYGYHAP 152

Query:   98 VHQQYVQRIEKQFLLYAYWIGLGILSSVGLGTGLHTFLLYLGP HIASVTLAAYECNSVNF 157
          HQ++VQ IEK L ++W+ LG+LSS+GLG+GLHTFL+YLGPHIA+VT+AAAYEC S++F
Sbjct:   153 AHQEHVQTIKHLWWSWWVLLGLVSSIGLGLHTFLIYLGPHIAAVTMAAYECQSLDF 212

Query:   158 PEPYPDQIICPDDEEGTEGTIFLWSIISKVRIEACMWGIGTAIGELPPYFMARAARLSGA 217
          P+PPYP+ I CP + + F W I++KVR+E+ +WG GTA+GELPPYFMARAAR+SG
Sbjct:   213 PQPPYPESIQCPSTKSSIAVTF-WQIVAKVRVESLLWGAGTALGELPPYFMARAARISGQ 271

Query:   218 EPDDEEYQEFEEFLE-HAESAQD----FASRAKLAVQKLVQKVGFFGILACASIPNPLFD 272
          EPDDEEY+EF E++ ES D RAK V+ + ++GF GIL ASIPNPLFD
Sbjct:   272 EPDDEEYREFLELMNADKESDADQKLSIVERAKSWVEHNIHRLGFPGILLFASIPNPLFD 331

Query:   273 LAGITCGHFLVPFWTFFGATLIGKAIKMHQKIFVITFSKHIVEQMVAFIGAVPGIGP 332
          LAGITCGHFLVPFW+FFGATLIGKA++KMH+Q FVI+ FS H E V + +P +GP
Sbjct:   332 LAGITCGHFLVPFWSFFGATLIGKALVKMHVQMFGVILAFSDHHAENFVKILEKIPAVGP 391

Query:   333 SLQKPFQEYLEAQRQKLH 350
          +++P + LE QR+ LH
Sbjct:   392 YIRQPIDLLEKQRKALH 409

```

Pedant information for DKFZphfd2_3i13, frame 2

Report for DKFZphfd2_3i13.2

```
SEQ      ENWLSWMFEKLVVVMVCYFILSIINSMASQSYAKRIQQLRNSEEKTK
SEG
PRD      cchhhhhhhhhhhheehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc
MEM
```

PS00001	23->27	ASN_GLYCOSYLATION	PDOC00001
PS00005	69->72	PKC_PHOSPHO_SITE	PDOC00005
PS00006	29->33	CK2_PHOSPHO_SITE	PDOC00006
PS00006	215->219	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00008	120->126	MYRISTYL	PDOC00008
PS00008	126->132	MYRISTYL	PDOC00008
PS00008	173->179	MYRISTYL	PDOC00008
PS00008	195->201	MYRISTYL	PDOC00008
PS00008	197->203	MYRISTYL	PDOC00008
PS00008	259->265	MYRISTYL	PDOC00008
PS00008	275->281	MYRISTYL	PDOC00008
PS00008	325->331	MYRISTYL	PDOC00008
PS00008	329->335	MYRISTYL	PDOC00008
PS00008	356->362	MYRISTYL	PDOC00008

399

DKFZphfkd2_3ol7

group: metabolism

DKFZphfkd2_3ol7 encodes a novel 72 amino acid protein with similarity to bos taurus NADH-ubiquinone oxidoreductase B33 subunit (EC 1.6.5.3) (EC 1.6.99.3).

NADH:ubiquinone oxidoreductase is the first enzyme in the respiratory electron transport chain of mitochondria. It is a membrane-bound multi-subunit protein. The bovine heart enzyme contains about 40 different polypeptides. The novel protein is the human orthologue of bovine B22.

The new protein can find application in modulation of the respiratory electron transport chain pathways of mitochondria.

strong similarity to bovine NADH-UBIQUINONE OXIDOREDUCTASE B22 subunit

complete cDNA, complete cds, EST hits,
in frame stop codon at ~274 will be checked
ESTs HS1291620/AA883920 show no stop codon at this side

Sequenced by BMF2

Locus: unknown

Insert length: 693 bp
Poly A stretch at pos. 670, polyadenylation signal at pos. 659

```

1 CAGCAGGCGT GCAGTTTCCC GGCTCTCCGC GCGGCCGGGG AAGSTCAGCG
51 CCGTAATGGC GTTCTTGCGG TCGGGACCCT ACCTGACCCA TCAGCAAAAG
101 GTGTTGCGGC TTTATAAGCG GCGGCTACGC CACCTCGAGT CGTGGTGCGT
151 CCAGAGAGAC AAATACCGAT ACTTTGCTTG TTTGATGAGA GCCCGGTTTG
201 AAGAACATAA GAATGAAAAG GATATGGCGA AGGCCACCCA GCTGCTGAAG
251 GAGGCCGAGG AAGAATTCTG GTAACGTCAG CATCCACAGC CATACTCTT
301 CCCTGACTCT CCTGGGGGCA CCTCCTATGA GAGATACGAT TGCTACAAGG
351 TCCCAGAATG GTGCTTAGAT GACTGGCATC CTTCTGAGAA GGCAATGTAT
401 CCTGATTACT TTGCCAAGAG AGAACAGTGG AAGAAACTGC GGAGGGAAAG
451 CTGGGAACGA GAGGTTAAGC AGCTGCAGGA GGAAACGCCA CCTGGTGGTC
501 CTTTAACTGA AGCTTTGCCC CTGCCCCGAA AGGAAGGTGA TTTGCCCCCA
551 CTGTGGTGGT ATATTGTGAC CAGACCCCGG GAGCGGCCCA TGTAGAAAGA
601 GAGAGACCTC ATCTTTCATG CTTGCAAGTG AAATATGTGA CAGAACATGC
651 ACTTGCCCTA ATAAAAATC AGTAAAAAAA AAAAAAAAAA AAA

```

BLAST Results

Entry S28256 from database PIR:
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine
>TREMBL:MIBTCIB22_1 gene: "cI-B22"; product: "NADH-ubiquinone
oxidoreductase complex B22 subunit"; B.taurus mitochondrion cI-B22
mRNA for B22 subunit of the NADH-ubiquinone oxidoreductase complex
Score = 933, P = 5.2e-93, identities = 163/179, positives = 172/179,
frame +2

Medline entries

92389317
Sequences of 20 subunits of NADH:ubiquinone oxidoreductase from RT bovine heart mitochondria.
Application of a novel strategy for RT sequencing proteins using the polymerase chain reaction

Peptide information for frame 2

ORF from 56 bp to 271 bp; peptide length: 72
Category: strong similarity to known protein

```

1 MAFLASGPYL THQKVLRLY KRALRHLESW CVQRDKYRYF ACLMRARFEE
51 HKNEKDMAKA TQLLKEAEEE FW*ROHPQPY IFPDSPGGTS YERYDCYKVP
101 EWCLDDWHPS EKAMYPDYFA KREQWKKLRR ESWEREVKQL QEETPPGGPL
151 TEALPPARKE GDLPPLWYI VTRPRERPM

```

BLASTP hits

Sequences producing significant alignments:

(bits) Value

sp|Q02369|NI2M_BOVIN|OD36CE17281FB735 (NDUFB9...)NADH-UBIQUINONE... 141 7e-34
 tr|U41534|Q18036|D34BCCB6E8FBCD5F (C16A3.4)SIMILAR TO NADH-UBIQ... 53 3e-07

>sp|Q02369|NI2M_BOVIN|OD36CE17281FB735 (NDUFB9...)NADH-UBIQUINONE
 OXIDOREDUCTASE B22 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)
 (COMPLEX I-B22) (CI-B22).[BOS TAURUS]
 Length = 178

Score = 141 bits (351), Expect = 7e-34
 Identities = 63/71 (88%), Positives = 68/71 (95%)

Query: 2 AFLASGPYLTHQQKVLRLYKRALRHLESWCVQDKYRYFACLMRARFEEHKNEKDMAKAT 61
 AFL+SG YLTHQQKVLRLYKRALRHLESWC+ RDKYRYFACLR+RARF+EHKNEKDM KAT
 Sbjct: 1 AFLSSGAYLTHQQKVLRLYKRALRHLESWCIRHDKYRYFACLLRARFDEHKNEKDMVKAT 60

Query: 62 QLLKEAEEFEW 72

QLL+EAEEFEW

Sbjct: 61 QLLREAEEFEW 71

>tr|U41534|Q18036|D34BCCB6E8FBCD5F (C16A3.4)SIMILAR TO
 NADH-UBIQUINONE OXIDOREDUCTASE B22.[CAENORHABDITIS
 ELEGANS]
 Length = 163

Score = 52.7 bits (124), Expect = 3e-07
 Identities = 25/64 (39%), Positives = 41/64 (64%), Gaps = 1/64 (1%)

Query: 10 LTHQOKVLRLYKRALRHLESWCVQDKYRYFACLMRARFEEHKNEKDMAKATQLLKEAE 68
 L+H+QKV RLYKR LR +++W + + R+ C++RARF+ + +E D K+ LL +
 Sbjct: 12 LSHRQKVTRLYKRCLREVDNWWYGGNNLEVRFQKCIIRARFDANAEVDTRKSQILLADGC 71

Query: 69 EEFEW 72

+ W

Sbjct: 72 RQLW 75

Alert BLASTP hits for DKFZphfkd2_3o17, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_3o17, frame 2

Report for DKFZphfkd2_3o17.2

[LENGTH] 72
 [MW] 8839.28
 [pI] 9.26
 [HOMOL] PIR:S28256 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine
 2e-34
 [KW] All_Alpha

SEQ MAFLASGPYLTHQQKVLRLYKRALRHLESWCVQDKYRYFACLMRARFEEHKNEKDMAKA
 PRD cccccccchhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhhhcchhhhhh
 SEQ TQLLKEAEEFEW
 PRD hhhhhhhhhccc

(No Prosite data available for DKFZphfkd2_3o17.2)

(No Pfam data available for DKFZphfkd2_3o17.2)

DKFZphfkd2_46a6

group: kidney derived

DKFZphfkd2_46a6 encodes a novel 315 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of kidney-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: /map="228.6 cR from top of Chr15 linkage group"

Insert length: 2774 bp

Poly A stretch at pos. 2751, polyadenylation signal at pos. 2732

```
1 CTCGCCAGCG CAGCTATGGC TGCTGGCGTA CCCTGTGCGT TAGTCACCAG
51 CTGCTCCTCC GTCTTCTCAG GAGACCAGCT GGTCCAACAT ACCCTTGGAA
101 CAGAAGATCT TATTGIGGAA GTGACTTCCA ATGATGCTGT GAGATTTTAT
151 CCCTGGACCA TTGATAATAA ATACTATTCA GCAGACATCA ATCTATGTGT
201 GGTGCCAAAC AAATTTCTTG TTAAGTCAGA GATTGCAGAA TCTGTCCAAG
251 CATTGTGGGT TTAATTTGAC AGCACACGAA AATCGGGCCT TGATAGTGTC
301 TCCTCATGGC TTCCACTGGC AAAAGCATGG TTACCTGAGG TGATGATCTT
351 GGTCTGCGAT AGAGTGTCTG AAGATGGTAT AAACCGACAA AAAGCTCAAG
401 AATGGAGCCT CAAACATGGC TTTGAATTGG TAGAATTAG TCCAGAGGAG
451 TGGCCTGAGG AGGATGATGA CTTCCCAGAA TCTACAGGAG TAAAGCGAAT
501 TGTCCAAGCC CTGAATGCCA ATGTGTGGTC CAATGTAGTG ATGAAGAATG
551 ATAGGAACCA AGGCTTTAGC CTCTCAACT CATTGACTGG AACAAACCAT
601 AGCATTGGGT CAGCAGATCC CTGTCAACCA GAGCAACCCC ATTTGCCAGC
651 AGCAGATAGT ACTGAATCCC TCTCTGATCA TCGGGGTGGT GCATCTAACA
701 CAACAGATGC CCAGGTGTAT AGCATTGTGG ATCCCATGTT AGATCTGGAT
751 ATTCAAGAAT TAGCCAGTCT TACCACTGGA GGAGGAGATG TGGAGAATTT
801 TGAAAGACCC TTTTCAAAGT TAAAGGAAAT GAAAGACAAC GCTGCCACGC
851 TTCTCTATGA GCAAAGAAAA GTGCATGCAG AAAAGGTGGC CAAAGCATTC
901 TGGATGGCAA TCGGGGGAGA CAGAGATGAA ATTGAAGGCC TTTTCATCTGA
951 TGGAGAGCAC TGAATTATTC ATACTAGGGT TTGACCAACA AAGATGCTAG
1001 CTGTCTCTGA GATACCTCTC TACTCAGCCC AGTCATATTT TGCCAAAATT
1051 GCCCTTATCA TGTGGCTGCT CTGACTTGTT TATAGGGTCC CCTTAATTTT
1101 AGTTTTTAGT AGGAGGTTAA GGAGAAATCT TTTTTTCTCT CAGTATATTG
1151 TAAGAGAGTG AGGAATACAG TGATAGTAAT GAGTGAGGAT TTCTTAAATA
1201 TACTTTTTTT TTGTTCTAGG AATGAGGGTA GGATAAATCT CAGAGGTCTG
1251 TGTGATTTAC TCAAGTTGAA GACAACCTCC AGGCCATTCC TGGTCAACCT
1301 TTTAAGTAGC ATTTCCAGCA TTCACACTTG ATACTGCACA TCAGGAGTTG
1351 TGTACACCTT CCGGGTGAT TTGGGTTTTC TCCATTCAAG GAGCTTGATG
1401 CTCTGAGCTA TGATGCTTTT ATTGGGAGGA AAGGAGGCAG CTGCAGAATT
1451 GATGTGAGCT ATGTGGGGCC GAACTCTCAC CCCGCAGCTA ACTCTCTACC
1501 TAAGAAAATG CCTCTGGGCA TTCTTTTGAA GTATAGTGTC TGAGCTCATG
1551 CTAGAAAGAA TCAAAAAGCC AGTGTGGATT TTAGGCTGT AATAAATGAG
1601 GCAAAGGATT TCTATTCCAG TGGGAAGGAA ACCTCTCTAC TGAGTTGTGG
1651 GGGATATGTT GTATGTTAGA GAGAACCTTA AGGAGTCCTT GTATGGGCCA
1701 TGGAGACAGT ATGTGATAAC ATACCGTGAT TTTTCATGAAG AAATCTTCT
1751 GTCCTAGAGT TCTCCCTGTC TGCTTGAGAT GCCAGAGCTG TGTGTTGCA
1801 CACCTGCAAA ACAAGGCACA TTTCCCTCTT TCTCTTTAAA GCCAAAGAGA
1851 GATCACTGCC AAGTGGGAG CACTAAGGGG TGGGTGGGGA AGTGAAATGT
1901 TAGCGATGTA ATTCTGAGC ACCTTGTTTT TCTTCCAAGG TTCGTAGCTC
1951 CTCTCTGCCC TTCCAAGCCT GTAACCTCGG AGGACTATCT TTTGTCTCT
2001 ATCCTTTGTC TTGTTAGAGT GGGTCAGCCC CAGAGGAACT GATAAGCAAA
2051 TGGCAAGTTT TAAAGGAAG AGTGGAAAGT ACTGCAATA AAAATCCTTA
2101 TTTGTTTTTG TAGACTTTGT AATGCATATC ATTAGCCCTC ACTGTGATCA
2151 TTAAGTGTGT GGCTCTGAAC TGGCACATAG TACAGTGGAT GGAAGGTGCC
2201 CGCACACAGC CTGAGAACTG GTTCTGGCCT AGGTGGGCTC TAGAACCATT
2251 TACACAGCAT GAAAGAAACA GGTGGGTTA GGAGCAGAAA GAAATAAGGC
2301 TCACACCCCT CCAGACACTA CCTTATAAGC ACTGCAGAAC CTGAAACAGA
2351 TGGCAGAAAG AATGGAATGC TACAGGGGCC AGCAGGAGTG ACCACAGGGA
2401 GGGGACAGCT CAGTACTGAG AGCATTGAGG AAGAGGCTTT CCAGGGAACA
2451 CTGGACATTG CTTAGTGACC TTTTGTTCCT TTTTCTTTTA TTTTCTTTTA
2501 CTGTTCTGAA AGACTTTGAG TCTGTGGTTC ACCACCAGCC CATCAGTGTT
2551 TCTTTGAGGT GATTGCATTA GGGAAAGTTG CTCTGGGATT GCAAAAAAAA
2601 AAAAAAGGTG GAACATGTTT TCCTTAAAGG ATGGAAGCTT TTAGAAAATA
2651 TACTAGGCCA TCTGGTTAGA AAAAACAGAC CAGACTAGAA AAAGCTGTGA
```

2701 ATTTGATTTT GTAGATTAAA CAAAGCCAGA TGATTAAAAT GTGATTTATT
2751 TATAAAAAAA AAAAAAAAAA AAAA

BLAST Results

Entry HS463358 from database EMBL:
human STS WI-14364.
Length = 472
Minus Strand HSPs:
Score = 1605 (240.8 bits), Expect = 5.0e-68, P = 5.0e-68
Identities = 347/361 (96%)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 16 bp to 960 bp; peptide length: 315
Category: putative protein
Classification: unset

1 MAAGVPCALV TSCSSVFSGD QLVQHTLGTE DLIVEVTSND AVRFYPWTID
51 NKYYASADINL CVVPNKFLVT AEIAESVQAF VVYFDSTRKS GLDSVSSWLP
101 LAKAWLPEVM ILVCDRVSED GINRQKAQEW SLKHGFELVE LSPEELPEED
151 DDFPESTGVK RIVQALNANV WSNVVMKNDR NQGFSLNLSL TGTNHSIGSA
201 DPCHPEQPHL PAADSTESLS DHRGGASNTT DAQVDSIVDP MLDLDIQELA
251 SLTTGGGQVE NFERPFSKLG EMKDKAATLP HEQRKVHAEK VAKAFWMAIG
301 GDRDEIEGLS SDGEH

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_46a6, frame 1

PIR:T04362 probable GTP-binding protein yptm3 - maize, N = 1, Score =
87, P = 0.21

PIR:S71585 GTP-binding protein GB2 - Arabidopsis thaliana, N = 1, Score
= 86, P = 0.27

>PIR:T04362 probable GTP-binding protein yptm3 - maize
Length = 210

HSPs:

Score = 87 (13.1 bits), Expect = 2.4e-01, P = 2.1e-01
Identities = 34/160 (21%), Positives = 67/160 (41%)

Query: 48 TIDNKYYASADINLCVVPNKFL-VTAEIAESVQAFVVYFDSTRKSGLDVSSWLPLAKAWL 106
TIDNK I F +T ++ +D TR+ + ++SWL A+
Sbjct: 49 TIDNKPIKLOIWDTAGQESFRSITRSYYRGAAGALLVYDITRRETFNHLASWLEDAROHA 108
Query: 107 PE---VMIL--VCDRVSEGINRQKAQEWSLKHGFELVELSPEELPEEDDDDFESTGVKR 161
VM++ CD ++ ++ +++ +HG +E S + ++ F ++ G
Sbjct: 109 NANMTVMLIGNKCDLSHRRVSYEEGEQFAKEHGLVFMEASAKTAQNVEEAFIKTAGT-- 166
Query: 162 IVQALNANVWSNVVMKNDRNQGFSLNLSLTGTNHSIGSADPC 203
I + + ++ N G+++ NS G S A C
Sbjct: 167 IYKKIQDGIFDVSNESNGIKVGAVPNSSGGGAGSSSQAGGC 208

Pedant information for DKFZphfkd2_46a6, frame 1

Report for DKFZphfkd2_46a6.1

[LENGTH] 315

{MW} 34505.54
{pI} 4.55
{KW} Alpha_Beta
{KW} LOW_COMPLEXITY 6.67 %

```
SEQ  MAAGVPCALVTSCSSVFSGDQLVQHTLGTEDLIVEVTSNDAVRFPWTIDNKYY SADINL
SEG  .....
PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccce

SEQ  CVVPNKFLVTAEIAESVQAFVVFDFSTRKSGLDVSSWLPLAKAWLPEVMILVCDRVSED
SEG  .....
PRD  eeccccchhhhhhhhhheeeeecccccccccccccccccccccccccccccccccccccc

SEQ  GINRQKAQEWSLKHGFELVELSPEELPEEDDDFPESTGVKRIVQALNANVWSNVVMKNDR
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  cchhhhhhhhhhhccccccccccccccccccccccccccccchhhhhhhhhcccccccccccc

SEQ  NQGFSLLNSLTGTNHSIGSADPCHPEQPHLPAADSTESLSDHRGGASNTTDAQVDSIVDP
SEG  .....
PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccch

SEQ  MLDLDIQELASLTGGGDVENFERPFPSKLEMKDKAATLPHEQRKVHAEKVAKAFWMAIG
SEG  .....
PRD  hhhhhhhhhhhccccccccccccchhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhhhc

SEQ  GDRDEIEGLSSDGEH
SEG  .....
PRD  ccccccccccccccc
```

(No Prosite data available for DKFZphfkd2_46a6.1)

(No Pfam data available for DKFZphfkd2_46a6.1)

DKFZphfkd2_46b10

group: kidney derived

DKFZphfkd2_46b10.1 encodes a novel 315 amino acid protein with similarity to C.elegans cosmid F25B5.3

The novel protein contains a HTH-LYSR-family PROSITE pattern. Proteins of the lysR family are bacterial transcriptional regulatory proteins which bind DNA using a helix-turn-helix motif. Most of these proteins are transcription activators and usually negatively regulate their own expression. They all possess a potential 'helix-turn-helix' DNA-binding motif in their N-terminal section. The 'helix-turn-helix' motif is missing in DKFZphfkd2_46a6.1. No informative BLAST results, no predictive PFAM or SCOP motive.

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to C.elegans F25B5.3

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: unknown

Insert length: 1285 bp

Poly A stretch at pos. 1266, no polyadenylation signal found

```
1 CAGTCTACGC GAGCTGCCTG TTTTTCCT GCTTGGACGC GCATGAGGGC
51 CCCGTCCATG GACCGCGCGG CCGTGGCGAG GGTGGGCGCG GTAGCGAGCG
101 CCAGCGTGTG CGCCCTGGTG GCGGGGGTGG TGCTGGCTCA GTACATATTC
151 ACCTTGAAGA GGAAGACGGG GCGGAAGACC AAGATCATCG AGATGATGCC
201 AGAATTCAG AAAAGTTCAG TTCGAATCAA GAACCCTACA AGAGTAGAAG
251 AAATTATCTG TGGTCTTATC AAAGGAGGAG CTGCCAAACT TCAGATAATA
301 ACGGACTTTG ATATGACACT CAGTAGATTT TCATATAAAG GGAAAAGATG
351 CCCAACATGT CATAATATCA TTGACAACTG TAAGCTGGTT ACGGATGAAT
401 GTAGAAAAAA GTTATTGCAA CTAAAGGAAA AATATTACGC TATTGAAGTT
451 GATCCTGTTC TTAAGCTTGA AGAGAAGTAC CCTTATATGG TGGAAATGGTA
501 TACTAAATCA CATGGTTTGC TTGTTTCAAG AGCTTTACCA AAAGCTAAAC
551 TTAAGAAAT TGTGGCAGAA TCTGACGTTA TGCTCAAAGA AGGATATGAG
601 AATTTCTTTG ATAAGCTCCA ACAACATAGC ATCCCGTGT TCATATTTTC
651 GGCTGGAATC GCGCATGTAC TAGAGGAAGT TATTCGTCAA GCTGGTGTTC
701 ATCATCCCAA TGTCAAAGTT GTGTCCAATT TTATGGATTT TGATGAAACT
751 GGGGTGCTCA AAGGATTTAA AGGAGAACTA ATTCATGTAT TTAACAAACA
801 TGATGGTGCC TTGAGGAATA CAGAAATTTT CAATCAACTA AAAGACAATA
851 GTAACATAAT TCTTCTGGGA GACTCCCAAG GAGACTTAAG AATGGCAGAT
901 GGAGTGGCCA ATGTTGAGCA CATTCTGAAA ATTGGATATC TAAATGATAG
951 AGTGGATGAG CTTTATAGAA AGTACATGGA CTCTTATGAT ATTGTTTTAG
1001 TACAAGATGA ATCATTAGAA GTAGCCAACCT CTATTTTACA GAAGATTCTA
1051 TAAACAGCA TTCTCAAGA AGACCTCTCT CCTGTGGGTG CAATTCAACT
1101 GTTCATCCGT TCATCTTGCT GAGAGACTTA TTTATAATAT ATCCTTACTC
1151 TCGAAGTGTT CCCTTTGTAT AACTGAAGTA TTTTCAGATA TGGTGAATGC
1201 ATTGACTGGA AGCTCCTTTT CTCCACCTCT CTCAACACAC TCCTCACCCT
1251 ATCTTTTAAC CCATTTAAAA AAAAAAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 43 bp to 1050 bp: peptide length: 336
Category: similarity to unknown protein
Classification: unset
Prosites motifs: HTH_LYSR_FAMILY (16-47)

```

1 MRAPSMDRAA VARVGAVASA SVCALVAGVV LAQYIFTLKR KTGRKTKIIE
51 MMPEFQKSSV RIKNPTRVEE IICGLIKGGA AKLQIITDFD MTLRSRFSYKG
101 KRCPTCHNII DNCKLVTDEC RKKLLQLKEK YYAIEVDVPL TVEEKYPYMV
151 EWYTKSHGLL VQQALPKAKL KEIVAESDVM LKEGYENFED KLOQHSIPVF
201 IFSAGIGDVL EEVIRQAGVY HPNVKVVSNF MDEFETGVLK GFKGELIHVF
251 NKHDGALRNT EYFNQLKDNS NIILLGDSQG DLRMADGVAN VEHLKIGYL
301 NDRVDELLEK YMDSYDIVLV QDESLEVANS ILQKIL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfd2_46b10, frame 1

SWISSPROT:YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III., N = 1, Score = 524, P = 2.2e-50

TREMBL:AC005499_12 gene: "T6A23.12"; Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence., N = 2, Score = 194, P = 1.4e-26

>SWISSPROT:YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III.

Length = 376

HSPs:

Score = 524 (78.6 bits), Expect = 2.2e-50, P = 2.2e-50
Identities = 112/300 (37%), Positives = 174/300 (58%)

```

Query:   44 RKTKEIEMMPEFQ--KSSVRIKNPTRVEEIIICGLIKGGA AKLQIITDFD MTLRSRFSYK-G 100
          +KT ++ ++ + + + + +PT V + ++ GGA K +I+DFD TLSRF+ + G
Sbjct:   73 KKTQVPLLMNYLLGEEQILVADPTA VAAKLRKMVVGAGKTVVISDFDYTL SRFANEQG 132

Query:   101 KRCPTCHNIID-NCKLVTDECRKLLQLKEKYYAIEVDVPLTVEEKYPYMVVEWYTKSHGL 159
          +R T H + D N + E +K + LK KYY IE P LT+EEK P+M +W+ SH L
Sbjct:   133 ERLSTTHGVFDDNVMLRKPELGQKFVDLKNKYPIEFSPNLTMEEEKIPHMEKWWGTSHSL 192

Query:   160 LVQQALPKAKLKEIVAESDVM LKEGYENFEDKLOQHSIPVFIFSAGIGDVLEEVIRQA-G 218
          +V + K +++ V +S ++ K+G E+F + L H+IP+ IFSAGIG+++E ++Q G
Sbjct:   193 IVNEKFSKNTIEDFVRQSRIVFDGAEFDIEALDAHNIPLVIFSAGIGNIIEYFLQQLG 252

Query:   219 VYHPNVKVVSNFMDDEFETGV LKGFKEGELIHVFENKHDGAL-RNTEYFNQLKDNSNIILLGD 277
          N +SN + FDE F LIH F K+ + + T +F+ + N+ILLGD
Sbjct:   253 AIPRNTHFISNMILFDEDDNACAFSEPLIHTFCKNSSVIQKETSFFHDIAGRVNVILLGD 312

Query:   278 SQGDLRMADGVANVEHLKIGYLNDRVDEL--LEKYMDSYDIVLVQDESLEVANSILQKI 335
          S GD+ M GV LK+GY N +D+ L+ Y + YDIVL+ D +L VA I+ I
Sbjct:   313 SMGDIHMDVGVERDGP TLKVGYYNGSLDDTAALQHYEEVYDIVLIHDPTLNVAQKIVDII 372

```

Pedant information for DKFZphfd2_46b10, frame 1

Report for DKFZphfd2_46b10.1

```

[LENGTH]      336
[MW]           37948.37
[pI]           6.67
[HOMOL]       SWISSPROT:YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III.
[PROSITE]     HTH_LYSR_FAMILY 1
[KW]          TRANSMEMBRANE 2
[KW]          LOW_COMPLEXITY 7.44 %

```

```

SEQ MRAPSMDRAAVARVGAVASASVCALVAGVVLAQYIFTLKRKTGRKTKIEMMPEFQKSSV
SEG .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD cccchhhhhcchhhhhhhheehhhhhhhhhhhhhhhhhhhhhhhhhhhccceeehhhhhhhhhe
MEM .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

```

```

SEQ RIKNPTRVEEIIICGLIKGGA AKLQIITDFD MTLRSRFSYKGKRCPTCHNIIDNCKLVTDEC
SEG .....
PRD eeccccchhhhhhhhhhhcccccceeeccccccccccccccccccccccccccccchhhhhh
MEM .....

```

```
SEQ  RKKLLQLKEKYAIEVDPVLTVEEKYPYMVEWYTKSHGLLVQQALPKAKLKEIVAESDVM
SEG  .....
PRD  hhhhhhhhhhhheeeccccccccccchhhhhccccchhhhhccchhhhhhhhhhhcc
MEM  .....

SEQ  LKEGYENFFDKLQQHSIPVFI FSAGIGDVLEEVI RQAGVYHPNVKVVS NFMD FDETGV LK
SEG  .....
PRD  cccccchhhhhhhhhccccccccccccchhhhhhhhhcccccccccccccccccccc
MEM  .....MMMMMMMMMMMMMMMMMM.....

SEQ  GFKGELIHVFNKHDGALRNTEYFNQLKDNSNIILLGDSQGDLRMADGVANVEHILKIGYL
SEG  .....
PRD  eccceeeeeccccccccccchhhhhhhhhceeecccccccccccccccccccccccccc
MEM  .....

SEQ  NDRVDELLEKYMDSYDIVLVQDESLEVANSILOKIL
SEG  .....
PRD  cchhhhhhhhhhhheeeecchhhhhhhhhccc
MEM  .....
```

Prosites for DKF2phfkd2_46b10.1

PS00044 16->47 HTH_LYSR_FAMILY PDOC00043

(No Pfam data available for DKF2phfkd2_46b10.1)

DKFZphfkd2_46d13

group: kidney derived

DKFZphfkd2_46d13 encodes a novel 506 amino acid protein with weak similarity to KE03 protein

The novel protein contains a RGD site.

No informative BLAST results; No predictive prosite, pfam or SCOP motive

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to KE03 protein

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: /map="227.6 cR from top of Chr1 linkage group"

Insert length: 3346 bp

Poly A stretch at pos. 3328, polyadenylation signal at pos. 3308

```
1 CTCTCGCGAG AGGAGCAAGA GGAAGATGGC CGTGCCCTGT TTTTCGGTGT
51 AAGGCAGCAG ACGGCGGCTG CGACGGCGAG ACTGAGATCC TGGTGTCTGT
101 GGCACCTGAG TTCTAGCTTC CCCCAGCGAG CGCGCGTCCC TCGTGCCTA
151 GGCAGAGAGCC GGCTCTTCCC CGGGAGATGC GTTTGTCCCA GGCTCGGGGG
201 CTCAGTGGGA GTTCATGCTG CGCTGGAGGC TCTTGGCCAC CGCTCTAATC
251 GCCTTGTGCC GCCGCAGCGC CAGCTCCGTC GCCAGCGGTG AGCCTCCCGA
301 TTCCCCCCTT TGCCCTTGGC GGCGGGGATG ACCGGGGAGA AGATCCGCTC
351 ACTGCGGAGG GACCACAAGC CCAGCAAAGA AGAAGGGGAC CTGCTGGAGC
401 CCGGGGATGA AGAAGCGGCG GCTGCCCTCG GCGGTACCTT TACCAGAAGC
451 AGGATTGGCA AGGGCGGCAA AGCTTGTCTA AAGATCTTCA GTAACCATCA
501 CCACCGGCTA CAGCTGAAGG CAGCTCCGCG CTCCTCCAAT CCCCCCGGCG
551 CCGCGGCTCT GCGCTGCGAC AATTCTCTCG TGAATGCCAA CTCCCACTCC
601 CCGGCCCTTC TGGCCGGCAC CAACCCCGTT GCTGTCTCTG CGGATGGAGG
651 CAGTTGCCCC GCACACTACC CGGTGCACGA GTGCGTCTTC AAGGGGGATG
701 TGAGGAGACT CTCTCTCTC ATCCGCACGC ACAATATCGG GCAGAAAGAT
751 AATCACGGAA ATACTCTTTT ACACCTTGCT GTGATGTTAG GAAATAAAGT
801 TACAGCTCTT TTGAGGAAGC TTAAGCAGCA ATCCAGGGAA AGTGTGTAAG
851 AAAAACGACC TCGATTATTA AAAGCCCTGA AAGAGCTAGG TGACTTTTAT
901 CTAGAACTTC ACTGGGATTT TCAAAGCTGG GTGCCCTTAC TTTCCCGAAT
951 TCTGCCTTCC GATGCATGTA AAATATACAA ACAAGGTATC AATATCAGGC
1001 TTGACACAAC TCTCATAGAC TTTACTGACA TGAAGTGCCA ACGAGGGGAT
1051 CTAAGCTTCA TTTCAATGG GGATGCGGCG CCCTCTGAAT CTTTTGTAGT
1101 ATTAGACAAT GAACAAAAAG TTTATCAGCG AATACATCAT GAGGAATCAG
1151 AGATGGAAAC AGAAGAAGAG GTGGATATTT TAATGAGCAG TGATATTTAC
1201 TCTGCAACTT TATCAACAAA ATCAATTCTT TTCACGCGTG CCCAGACAGG
1251 ATGGCTTTTT CGGGAAGATA AAACAGAAAG AGTAGGAAAC TTTTGGCAG
1301 ACTTTTACCT GTTGAATGGA CTGTATATAG AATCAAGGAA AAGAAGAGAA
1351 CATCTCAGTG AAGAGGATAT TCTTCGAAAT AAGGCCATCA TGGAGAGTTT
1401 GAGTAAAGGT GGAACATATA TGGAAACAGAA TTTTGAAGCG ATTCGAAGAC
1451 AGTCTCTTAC ACCGCCTCCT CAGAACACTA TTACATGGGA AGAATATATA
1501 TCTGCTGAAA ATGGAAGGAG TCCTCATCTG GGTAGAGAAT TGGTGTGCAA
1551 AGAGAGTAAG AAAACGTTTA AAGCTACGAT AGCCATGAGC CAGGAATTTC
1601 CCTTAGGGAT AGAGTTATTA TTGAATGTTT TAGAAGTAGT AGCTCCCTTC
1651 AAGCACTTTA ACAAGCTTAG AGAATTTGTT CAGATGAAGC TTCTCCAGG
1701 CTTTCTCTGA AAATTAGATA TACCTGTGTT TCCCAACAAT ACAGCCACTG
1751 TGAATTTTCA GGAGTTTCGA TACGATGAAT TTGATGGCTC CATCTTTACT
1801 ATACCTGATG ACTACAAGGA AGACCCAAGC CGTTTTCTCT ATCTTTAACT
1851 GACGTGGAAG AGGATGCCGT CTAACCAAGG AAAGAAAATA CAGAGACCTT
1901 AGAAGTGGAT CCAAAATAGAA GGGACAAATG CTTTCAGTGA AGAAAAGGGA
1951 ATTACACATT GAATCGACAC ATCAGTAATA CGATACAGTG AAATGGGCCT
2001 CTAATAAGAA TTTCAGCGAG TTTTCTGATG TGCCATTTT TGTCTTTTAA
2051 AAAATATACA TATTATAAAT GTAATAGTTT GACACATTAA TGACCCTAAG
2101 ACCTGCGTAT GTGAAGCAGC TATGAGTGCT GTGATTTGTT TTTAAAAATT
2151 TTTTACACTT TTGTTGAAAT ATATATGCAT ATAAATATAT CTATATCTAT
2201 ATCTATATCT AAAACACTCC TGGACCATTA ACGTAAATTA AATGTCTTAA
2251 GAGATATGGA GCCCTTTTAA ACTTGTCATC TTTATGCAAG GTGACATTTA
2301 TAAATATTCC TTGAGAGCTT GTTTTCATAA AATGTAACAT ATGTAACATT
2351 ATGTATAGTT CAGTAATTTG AATGTTTGTT CAATATAATG AACTAGAAGG
2401 AATGCAATTT TCTGTAGATG AATGAACCAA ATGGTAACCA TTAACAATTT
2451 GCATTATATAT GTTGCAATAC ATTTCAAGAG GAGCGTTTCA TCTGCAGGGA
2501 ATAAGGTACC TCCTTTAGCA CCTTAGTGCA ATTCATTGTG GTGCTATTGT
2551 TTTTACCTG AATGTTTGTT ACTAATCTTC CTTTCATAGA ACCTCTATTT
2601 TTTTTTTTTC TAAACTTGAG TTTGAGTCCT TGTATGGTC ATCATAAGGT
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2651 AATGGTTAGC ATGTTTAAAG ATATTCCTCT TCCAAATCTC AGCACTTTAA
2701 AAAAAAATCC AAATTTTAA ACTTGCTTCC TAATAAGTAC ACATCGGTCT
2751 GATTATTTTG TTTGTTTTTA GTAGAAATAG GATGCATTGG TGTCAGTTTT
2801 AAAAAACAAT ACACATATTT TGGACAACCC TACATATTTA ATCCTTTCAA
2851 AATAAGATAA AAACATTTTA TATGCTAACA GAATATATTT GTTACAAGTT
2901 AAAGTCCAGA AGTATACACA AGATTGATTA CTCCTATTAT TTTTTTTAAA
2951 TCACAGGAAA ATATTGATTT CATTGTCTCC AAAGTGATAA AATCTTGTAT
3001 TACTCATTTT TGCACCTAAA ATTTTCTTAA TTTATTCCAA GGTGGTTTGA
3051 AGGTCCAAGT ATGAAAATAA ATTAGGGGGA TTAATGTATA ACAGTTTATA
3101 AGTATCATGT TGTATTAAAG AGCTTACTTA GATTGATGTT TTTAAAATGT
3151 ATCCTGATGA ATGTCTCAAG AATGCATCTG TCAAGTTTTT TAGACTGACC
3201 AGTAGCTTAA ACTTTTTTCA GGATTTTAGG TAATTTGAAA GGAGTTTAGA
3251 GACCTTATT GAAAATATGA TTTAAAATC CAAAGCATAA ACCGTAAGAA
3301 AAATTTTAAA TAAACATCTT TAAAGCTGAA AAAAAAAAAA AAAAAA

```

BLAST Results

Entry HS121353 from database EMBL:

human STS WI-14729.

Score = 1597, P = 1.9e-69, identities = 363/379

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 328 bp to 1845 bp; peptide length: 506
 Category: similarity to unknown protein

```

1 MTGEKIRSLR RDHKPSKEEG DLLEPGDEEA AAALGGTFTR SRIGKGGKAC
51 HKIFSNHHHR LQLKAAPASS NPPGAPALPL HNSSVTANSQ SPALLAGTNP
101 VAVVADGGSC PAHYPVHECV FKGDVRRLLS LIRTHNIGQK DNHGNTPLHL
151 AVMLGNKVTA LLRKLKQQR ESVEEKRPR LKALKELGDF YLELHWDQFQ
201 WVPLLSRILP SDACKIYKQG INIRLDTTLI DFTDMKCQRG DLSFIFNGDA
251 APSESEFVVD NEQKVYQRIH HESEMETEE EVDILMSSDI YSATLSTKSI
301 SFTRAQTGWL FREDKTERVG NFLADFYLVN GLVIESRKRR EHLSEEDILR
351 NKAIMESLSK GGNINEQNFE PIRRQSLTPP PONTITWEEY ISAENGKAPH
401 LGRELVCES KKTFFATIAM SQEFLGLIEL LLNVLEVVPV FKHFNKLREF
451 VQMKLPPGFP VKLDIPVFPT ITATVTFQEF RYDEFDGSIF TIPDDYKEDP
501 SRFPDQ

```

BLASTP hits

Entry CEC01F1_3 from database TREMBL:

gene: "C01F1.6"; Caenorhabditis elegans cosmid C01F1.

Score = 371, P = 4.5e-61, identities = 69/138, positives = 96/138

Entry CEC18F10_9 from database TREMBL:

gene: "C18F10.7"; Caenorhabditis elegans cosmid C18F10.

Score = 383, P = 3.4e-39, identities = 103/349, positives = 182/349

Entry AF064604_1 from database TREMBL:

product: "KE03 protein"; Homo sapiens KE03 protein mRNA, partial cds.

Score = 348, P = 8.3e-32, identities = 95/295, positives = 148/295

Alert BLASTP hits for DKFZphfkd2_46d13, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_46d13, frame 1

Report for DKFZphfkd2_46d13.1

```

[LENGTH]      506
[MW]           57003.12
[pI]           6.40

```


(HOMOL) TREMBL:CEC18F10_9 gene: "C18F10.7"; Caenorhabditis elegans cosmid C18F10. 2e-35

[BLOCKS] BL01288E
 [PROSITE] RGD 1
 [PROSITE] MYRISTYL 7
 [PROSITE] CAMP_PHOSPHO_SITE 2
 [PROSITE] CK2_PHOSPHO_SITE 9
 [PROSITE] PKC_PHOSPHO_SITE 6
 [PROSITE] ASN_GLYCOSYLATION 1
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 7.51 8

SEQ MTGEKIRSLRRDHKPSKEEGDLLEPGDEEAAAALGGTFTRSRIKGKGKACHKIFSNHHHR
 SEGXXXXXXXXXXXXX.....
 PRD ccc

SEQ LQLKAAPASSNPPGAPALPLHNSSVTANSQSPALLAGTNPVAVVADGGSCPAHYPVHECV
 SEGXXXXXXXXXXXXX.....
 PRD hhhhhhcc

SEQ FKGDVRRLLSLIRTHNIGQKDNHGNTPLHLAVMLGNKVTALLRKLKQSQRESVEEKRPRL
 SEG
 PRD ecc

SEQ LKALKELGDFYLELHWDFQSWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRG
 SEG
 PRD hhhhhhcc

SEQ DLSFIFNGDAAPSESFVLDNEQKVYQRIHHEESEMETEEVDILMSSDIYSATLSTKSI
 SEGXXXXXXXXXXXXX.....
 PRD ccc

SEQ SFTRAQTGWLFRDQKTERVGNFLADFYLVNGLVIESRKRREHLSEEDILRNKAIMESLSK
 SEG
 PRD ecc

SEQ GGNIMEQNFEPIRRQSLTPPPQNTITWEEYISAENGKAPHLGRELVCESKKTFRKATIAM
 SEG
 PRD ccc

SEQ SQEFPLGIELLLNVLEVAPFKHENKLREFVQMKLPPGFPVKLDIPVFPTITATVTFQEF
 SEG
 PRD hcc

SEQ RYDEFDGSIFTIPDDYKEDPSRFPDL
 SEG
 PRD ccc

Prosites for DKFZphfkd2_46d13.1

PS00001	82->86	ASN_GLYCOSYLATION	PDOC00001
PS00004	126->130	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	373->377	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	8->11	PKC_PHOSPHO_SITE	PDOC00005
PS00005	296->299	PKC_PHOSPHO_SITE	PDOC00005
PS00005	316->319	PKC_PHOSPHO_SITE	PDOC00005
PS00005	336->339	PKC_PHOSPHO_SITE	PDOC00005
PS00005	410->413	PKC_PHOSPHO_SITE	PDOC00005
PS00005	413->416	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	172->176	CK2_PHOSPHO_SITE	PDOC00006
PS00006	228->232	CK2_PHOSPHO_SITE	PDOC00006
PS00006	274->278	CK2_PHOSPHO_SITE	PDOC00006
PS00006	278->282	CK2_PHOSPHO_SITE	PDOC00006
PS00006	344->348	CK2_PHOSPHO_SITE	PDOC00006
PS00006	386->390	CK2_PHOSPHO_SITE	PDOC00006
PS00006	476->480	CK2_PHOSPHO_SITE	PDOC00006
PS00006	491->495	CK2_PHOSPHO_SITE	PDOC00006
PS00008	35->41	MYRISTYL	PDOC00008
PS00008	46->52	MYRISTYL	PDOC00008
PS00008	108->114	MYRISTYL	PDOC00008
PS00008	138->144	MYRISTYL	PDOC00008
PS00008	155->161	MYRISTYL	PDOC00008
PS00008	320->326	MYRISTYL	PDOC00008
PS00008	487->493	MYRISTYL	PDOC00008
PS00016	239->242	RGD	PDOC00016

(No Pfam data available for DKFZphfkd2_46d13.1)

DKFZphfkd2_46j20

group: metabolism

DKFZphfkd2_346j20 encodes a novel 224 amino acid protein similar to 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase.

The new protein seems to be the human ortholog of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase.

The new protein can find application in modulating the homoprotocatechuate degradative pathway and as a enzyme for biotechnologic production processes.

strong similarity to 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase

complete cDNA, complete cds, EST hits,
potential start at Bp 16 matches kozak consensus ANCatgG
strong similarity to proteins of worm plant archea and bacteria
2-hydroxyhepta-2,4-diene-1,7-dioate isomerase is part of
the tyrosine metabolism (degradation of tyrosine late step) EC 5.3.1.-
complete cds according to similar C.elegans and A.thaliana protein

Sequenced by MediGenomix

Locus: unknown

Insert length: 1706 bp

Poly A stretch at pos. 1686, polyadenylation signal at pos. 1667

```
1  CACTTGATGG GAATCATGGC AGCATCCAGG CCATTGTCCC GCTTCTGGGA
51  GTGGGGAAG AACATCGTCT GCGTGGGGAG GAACTACGCG GACCAAGTCA
101 GGGAGATGCG CAGCGCGGTG TTGAGCGAGC CCGTGTGTTT CCTGAAGCCG
151 TCACAGGCGT ACGCCGCCGA GGGCTCGCCC ATCCTCATGC CCGCGTACAC
201 TCGCAACCTG CACCACGAGC TGGAGCTGGG CGTGGTGATG GGCAAGCGCT
251 GCCGCGCAGT CCCCGAGGCT GCGGCCATGG ACTACGTGGG CGGCTATGCC
301 CTGTGCCTGG ATATGACCGC CCGGGACGTG CAGGACGAGT GCAAGAAGAA
351 GGGGCTGCCC TGGACTCTGG CGAAGAGCTT CACGGCGTCC TGCCCGGTCA
401 GCGCGTTCTG GCCCAAGGAG AAGATCCCTG ACCCTCACA GCTGAAGCTC
451 TGGCTCAAGG TCAACGGCGA AUTCAGACAG GAGGGTGAGA CATCCTCCAT
501 GATTTTTTTC ATCCCTTACA TCATCAGCTA TGTTTCTAAG ATCATAACCT
551 TGAAGAAGG AGATATTATC TTGACTGGGA GCCTCAAGGG AGTTGGACCG
601 GTTAAAGAAA ACGATGAGAT CGAGGCTGGC ATACACGGGC TGGTCAGTAT
651 CACATTTTAA GTGGAAAAGC CAGAATATTG AGTTATTCTT TAACAAGTTT
701 CGAGAGAGAA GGGAGCAAGA CAAGAGCAAG CAACGGCTAT TAAATGTCAC
751 AATCCTTTAA TTAGAAACCA TTTATTGGCC GGACGCGGTG GCTCACGCCT
801 GTAATCGCAG CACTTTGGGA GGCCGAGGCG GGCGGCTCAC GACGTCAGGA
851 GATCCAGACC ATCTTGGCTA ACAGGGTGAA ACCCGGTCTC TACTAAAAAT
901 ACAAAAAATT AGCCGGGCGT GGTGCGGGGC GCCTGTAGTC CCAGCTACTC
951 TGGAGGCTGA GGCAGGAGAA TCAATTGAAC CCGGGAGGCG GAGCTTACAG
1001 TGAGCTGAGA TTGCGCCACT GTACTCCTGG GCAACAGCGA GACTCCGTCT
1051 CAAAAA AAAA AAAA AAAA AGAAACCAT TATTTTAAAA ATGATTAGAT
1101 TGCTATGCCT CAACTCATAG AAGATGAACC CTCAAGAAA ACGTGAAGTA
1151 GAACGGGTGG GCCAGAAATG AAAACAGGCA AGTAAAGTAT TTCTTCGGAA
1201 AACATTTTAT CAAACCAAT GTTAAAAAGA CTTTCCTTTT GTAAAACTGG
1251 ATTAGAGAAG ACTTTTCAGT GGGTTATCTC TAGGATGATC AGTAGTTCAG
1301 CACTTAAAAA CTGCAGAGAA AACTGAAAGT TATGTTCCAG ATAACCTTCC
1351 GTTGTTTACC AAATTTTCTT AGATTTGGTC ATCATCAGGA AGCATTTGTA
1401 AAAATAAAAA TCTCCACAAA TTACTGGCCC ATCTCGGACT TGCTGAATCA
1451 ATTTGATAGG ATTAATCTCC AGTGAAGCTG TGTTTACAGG GCATTCCAAG
1501 TGATTCCTAT CAGGAAATGT GAAAAACACT CCGTACATA ATCGGTTAAT
1551 TTAATAATTT ACTTAATAAG TGAACAAGTA ATGAAGATTT CACCTGTTTA
1601 CTTAGGGTAT CTACCCAGAC CCATCGATTG TGAGTTCGGG AGATGATTTT
1651 GAAATTACTG TTTTCCAAT AAAGGTGCTC CCTTCCAAAA AAAAAAAAAA
1701 AAAAAA
```

BLAST Results

No BLAST result

Medline entries

94039092: Purification, nucleotide sequence and some properties of a bifunctional isomerase/decarboxylase from the homoprotocatechuate degradative pathway of *Escherichia coli* C.

Peptide information for frame 1

ORF from 7 bp to 678 bp; peptide length: 224
Category: strong similarity to known protein

```

1 MGIMAASRPL SRFWEWGKNI VCVGRNYADH VREMRSVLS EPVLFKLPST
51 AYAPEGSPIL MPAYTRNLHH EELGVVMGK RCRAVPEAAA MDYVGGYALC
101 LDMTARDVQD ECKKKGLPWT LAKSFASCP VSAFVPKEKI PDPHKLKLWL
151 KVNGLRQEG ETSSMIFSIP YIISYVSKII TLEEGDIILT GTPKGVGPVK
201 ENDEIEAGIH GLVSMTEKVE KPEY

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfk2_46j20, frame 1

PIR:S44919 ZK688.3 protein - *Caenorhabditis elegans*, N = 1, Score = 537, P = 8.7e-52

PIR:D71109 probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase - *Pyrococcus horikoshii*, N = 1, Score = 529, P = 6.1e-51

PIR:C71425 hypothetical protein - *Arabidopsis thaliana*, N = 1, Score = 519, P = 7e-50

PIR:A64864 probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase b1180 - *Escherichia coli*, N = 1, Score = 474, P = 4.1e-45

>PIR:S44919 ZK688.3 protein - *Caenorhabditis elegans*
Length = 214

HSPs:

Score = 537 (80.6 bits), Expect = 8.7e-52, P = 8.7e-52
Identities = 99/211 (46%), Positives = 138/211 (65%)

```

Query: 10 LSRFWEWGKNI VCVGRNYADH VREMRSVLS EPVLFKLPST AY APEGSPIL MPAYTRNLH 69
      L+ F IVCVGRNY DH E+ +A+ +P+LF+K ++ EG PI+ P +NLH
Sbjct: 4 LAGFRNLATKIVCVGRNYKDHALELGNAIPKKPMLFVKT VNSFIVEGEPIVAPPGCQNLH 63

Query: 70 HELELGVVMGKRCRAVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWT LAKSF TASC 129
      E+ELGVV+ K+ + ++ AMDY+GGY + LDMTARD QDE KK G PW LAKSF SC
Sbjct: 64 QEVELGVVISKKASRISKSDAMDYIGGYTVALDMTARD FQDEAKKAGAPWFLAKSFDGSC 123

Query: 130 PVSAFVPKEKIPDPHKLKLWLKVNGLRQEGETSSMIFSIPYIISYVSKII TLEEGDIIL 189
      P+ F+P IP+PH ++L+ K+NG+ +Q T MIF IP ++ Y ++ TLE GD++L
Sbjct: 124 PIGGLPVS DIPNPHDVELFCKINGK DQRCRTDVMIFDIPTLLEYTTQFFTLEVGDVVL 183

Query: 190 TGTPKGVGPVKENDEIEAGIHGLVSMTEKVE 220
      TGTP GV + D IE G+ ++ F V+
Sbjct: 184 TGTPAGVT KINSGDVIEFGLTDKLNKFN VQ 214

```

Pedant information for DKFZphfk2_46j20, frame 1

Report for DKFZphfk2_46j20.1

```

[LENGTH] 224
[MW] 24843.07
[PI] 6.96
[HOMOL] PIR:S44919 ZK688.3 protein - Caenorhabditis elegans 8e-55
[FUNCAT] r general function prediction [M. jannaschii, MJ1656] 9e-40
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YNL168c] 4e-38
[EC] 5.3.3.10 5-Carboxymethyl-2-hydroxymuconate delta-isomerase 1e-35
[PIRKW] isomerase 1e-35
[PIRKW] intramolecular oxidoreductase 1e-35
[SUPFAM] 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase 1e-46
[PROSITE] MYRISTYL 4
[PROSITE] AMIDATION 1

```

```

{PROSITE}    CK2_PHOSPHO_SITE    2
{PROSITE}    PKC_PHOSPHO_SITE    3
{KW}         Alpha_Beta

```

```

SEQ    MGIMAASRPLSRFEWGNIVCVGRNYADHVREMRSAVLSEPVLFLLKPSTAYAPEGSPIL
PRD    cccccccccchhhhhccceeeeeeccchhhhhhhhhccccccccceeecccccccccccccc

SEQ    MPAYTRNLHHELELGVVMGKRCRAVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWT
PRD    cccccchhhhhheeeccccccccchhhhhhhheeeeeeccchhhhhhhhhhhcccccc

SEQ    LAKSFTASCPVSAFVPKEKIPDPHKLKLWLKVNDELQGEGETSSMIFSIPYIISYVSKII
PRD    cccccccccceeeccccccccceeeccccccccccccceeechhhhhhhhhhh

SEQ    TLEEGDIILTGTGPKGVGPVKENDEIEAGIHGLVSMTFKVEKPEY
PRD    hccccceeeccccccccccccceeecccccccccccccc

```

Prosites for DKFZphfd2_46j20.1

PS00005	104->107	PKC_PHOSPHO_SITE	PDOC00005
PS00005	192->195	PKC_PHOSPHO_SITE	PDOC00005
PS00005	216->219	PKC_PHOSPHO_SITE	PDOC00005
PS00006	104->108	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00008	2->8	MYRISTYL	PDOC00008
PS00008	75->81	MYRISTYL	PDOC00008
PS00008	116->122	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008
PS00009	78->82	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfd2_46j20.1)

DKFZphfkd2_46k19

group: transcription factors

DKFZphfkd2_46k19.3 encodes a novel 130 amino acid protein similar to rat Dcoh, a bifunctional protein-binding transcriptional co-activator.

Dcoh is a bifunctional protein, complexed with bipterin. It serves as dimerization cofactor of hepatocyte nuclear factor-1 and catalyzes the dehydration of the bipterin cofactor of phenylalanine hydroxylase.

The new protein can find application in modulating/blocking the expression of genes controlled by the hepatocyte nuclear factor-1.

strong similarity to pterin-4-alpha-carbinolamine dehydratase

potential start at Bp 102 according to similar proteins,
both genomic sequences are from chromosome 5,

Sequenced by MediGenomix

Locus: map="5"

Insert length: 5641 bp

Poly A stretch at pos. 5617, polyadenylation signal at pos. 5598

```
1 CAGCCCTCGG CAGACGGCCA ATGGCGGCGG TGCTCGGGGC GCTCGGGGCG
51 ACGCGGCGCT TGTTCGCGGC GCTGCGAGGC CAGAGCCTAG GGCTAGCGGC
101 CATGTCATCA GGTACTCACA GGTTCATTGC AGAGGAGAGG AACCAAGCTA
151 TACTTGACCT TAAAGCAGCA GGATGGTCGG AATTAACTGA GAGAGATGCC
201 ATCTACAAAG AATTCTCCTT CCACAATTTT AATCAGGCAT TTGGCTTTAT
251 GTCCCGAGTT GCCCTACAAG CAGAGAAGAT GAATCATCAC CCAGAATGGT
301 TCAATGTATA CAACAAGGTC CAGATAACTC TCACCTCACA TGAAGTGGGT
351 GAACTGACCA AAAAAGATGT GAAGCTGGCC AAGTTTATTG AAAAAGCAGC
401 TGCTTCTGTG TGATTCTTTC CAAAATACAT AAGTCTGAGA GGCTAAACTT
451 GATGGCTGTG TTAACATATG TCACGTGTAG CACAGTGGAG AAAGCAGGAT
501 ATGGCTCATA ATGACAGTGG TGAAGACCTG CGAATGAAGT TGCTAGTTAA
551 CACCTACATT AGGGTTTGAC ATAGGTCTAT GTTATGGGTC GCTGCATCTG
601 CTGGAACCTA CAGACTTTAC TATAGAGAAT CAAAGATCCC GTATCCGAAG
651 TCTATGGAAT TGCTCATGGT GGTAAATTCC AACAGAATGA AACACCAAAC
701 TTGCTTAAAG TAACCTACGT TTCAATTGTA AAGAGATATT GTCAAAATTG
751 GAGGCCCCCA GGTTCCTGTC TGTTCCAAAT CTTTGCATGA TGACAGTGGT
801 TTCTCTGATG TGGTAAAGCTT TGGCTTTCTT CTGTTTCTT TCTAAAAGAT
851 CACTGGAGTA GAGAGGAGTT AAACAGACAT GACCTTTGAC CTCTGCTATG
901 ACCTCCACAG ATAGCAAACC GGGCCGACAC ATGGTTGACG ATGTCCTTTT
951 CTACAATGAA GTTAATGAAA GTTCTGAAAA TAGTGATTAC TTTCTGCAT
1001 TGATAGGATT TAGGAAACCT CTGGATAAAT AGCTTAAGCA TGGCTGTTTA
1051 TGTTTTGTCT ATAGACAAAA AGCAGCAGCA TGTACATTGT ATTTGGACAC
1101 AAGCCTGCCT CGGTAAATAT ATTGAACAT TGGACCACTA GGGTTAGTAG
1151 GGAGCGGTCT GTACACTTTC TGATTAGCA TFCAGAAACA TTCTAGGTGG
1201 ACTCTGTAGC TTTCACTTTT GTAAAGTTAT CGGAAAAACA TCGGGAGGGT
1251 TTGGCCATCA TATGTGAGCT TTGTGTTTCA ATGCCAGTTA CTCAGGATTA
1301 GTGAAATTAAT GACTGTCCAG AGGACTTCAG GGTCAACCAAG CTGCTGCACC
1351 TGCCATTGGC TGACTCTCCC CGGCTATCTG TGGCTGAGAT GGTGCTGCTT
1401 AGGTACAGCA GAGCATGAGC TGCTGTCTGA AGGGCACAGG AGATGGCCCT
1451 TGGGCTTCTC ATCCCAGGAT GCCTGCCCTG CCCACCAATC CATGAGAAGA
1501 TATGTATGAT TTCAGTAGGC CCTGGATCAG CTTGTACCTT CTGGTTTCTT
1551 GTTTGCTTTC CACTCACTCA GCTGGAGTTT CATTTCACGA CTAAAGTCTT
1601 CATCATTTGG TFCAGAAACA GCATTCACTT GTGGCTGTGC TGATGTAGTA
1651 CACCAAGAAC AACTGGGCTC TTCTCTGTCA CTTTCAGTGG GCTACCTTCC
1701 CTCACCTCTC CAAGCAGCAT GAAAGAATTC TTTACATTTT TAATCTCTTT
1751 TTTGTTTTTC CCTGAAAGTA TGCTTTGGTG CTTAAAGAGA GAAGTCACAA
1801 AAGTATACTA CTGAGTTTCC TGGAGATGAA ATCCTGTTGT CCTTAGCTAT
1851 GTGAATGAGC ACAGGGATCC CTGATGCCAT TATTTTGTAT ATTCATACGG
1901 CACACACTTA CTGAGGCTCT TCTGTGTGCC CTAGGGGATT GAGCACAGTG
1951 ACATATCAGG GCAGGTAGAA ACAGATGGAG AGCTGATGCG GGCTGTCTTA
2001 GAGCAGCTGC CCCAGGAGGC CCCTGTGGAT GGATGTTGGG CAGGAGCCCT
2051 GAGACGTTAG GGGCATATAA CTAAGGAGCA TAGCAGGAGT TATAGGAGGA
2101 GCTGATCCCT GAGGGAACA ATCAAGACCG AGAAGATGGC GCTAAAGTTT
2151 GAATTGTGGG GACATTAATC ACGGTGATT TTAACCTTTT GCTGTTGATG
2201 ATTTTAAATG GAGAAAATGA GTACGTAAGA TGTTATTTCC CAGTTCAGTA
2251 TATAGGTTGC CCACAAAGTA TTTTCTTACC ATGAATGGTC ATATATACTT
2301 GTTGTAGAAT ACCAGGGACA GCAGATGAGG TGGGGTAGTT ACTTCCTTTT
2351 CTTACAGCCC AAGAACTTTG GTGTCCAGGA GATTGACCAA TTTAGCCACT
2401 GAGCATTTAA TACAACACAG GGCTACCCAG ATCCCACTGT CCTGATTTGC
2451 CCTGAAAGCC AAAGGAGTCA GGAGAAGGTG AGTGGGGTGA ATATATTAAT
2501 CCTGAGAGTT GAACAGAGCA AAAATCCCTA TTACTTTTGT ACTTAAACA
```

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2551 TCTCTGCCAC ATGTGCTCAC TCTTTATATT CTGTTTAGGT GGTTTATATG
2601 TGCACATCCC ATCCTATGCC TGCAGTAGC CAACTCAGGG TTTATATTGC
2651 CTCCTTTCTT TTTTCTTTTT TTTTTTTTTT TTTTAAGAGA TGGGGTCTCG
2701 TTCTGTCATG CAGACTGGAG TGCAGTGGT TGATCACAGC TCATTGTAAC
2751 CTCCAACGCC TGGACTGAAG TGATCCTCCT GCCTTGGCCT CTCTGGTAGC
2801 TGGGACTACA GGTGCATGCC ACCACACCCA CCTAATTTTT TTTATTTTAA
2851 TTTTITGTAG AGACAGTCTC ACTATCTTGC TCGGGCTGGT CCTGAACCTC
2901 TGGGCTCAAG TTATCTTGCT GCCTCAGCCT CCCATGGGTA ATCTTTATTT
2951 CCTTTTTTTT TTTTTTTTGG AGATGGAGTT TCGCTCTTGT CGCCCAGGCT
3001 GGAGTGCAAT GGCACGATCT TGGCTCACTG CAGTCTCCAC CTCCTGGGTT
3051 CAGGTGATTC TCCATCCTCG GCCTACTGAG TAGCTGAGAT TACAGGCAAC
3101 TGCCACCATG CGCGGCTAAT TTGTGATTTT TTTTITAGTA AGAGATGGGG
3151 TTTTCGCCATG TTGGCCGGAC TGGTCTTAGA CTCCTGACCT CAAGCGACCT
3201 GCCTGCCTTG GCCTCCCAA GTGCTGGGAT TACAGGCATG AGCCGCTATG
3251 CCTCGTCGCT GATTTTTATT TCTTATTTTT TTTTITAGTA TGGGGGTCTC
3301 ACTATGCTGC TCAGGCTGAT CTCAAACTCC TGGCCTCAAG TGATCCTCCC
3351 ACCTTAGCCT CCCAAGTTGC TGGGATTATA AGTGTGAGCC ACTATCCCTA
3401 CCTCACTATT ACCTTCTTTG CTCTCTTGT TTTCTTTTGT TCTAAGTCAA
3451 ACCCATCACA ATCTTTTCTT GTCCCTCCAG GTGTTTTCCA GTGCTGTGCC
3501 CTGGATGTGC TCTCTTCTC TTAGAGCCCA GAGAACTTGC TTTTCCCTCT
3551 TATATATGAC CCTTAACTTT TTCTAACACA TTATTAAGGG CCTGTGTCTA
3601 TCAGCTGGGG GCACCTCTTG AAGGGAGGGC CTTTGTGTGG TCTGTTTCTA
3651 GTGACTTCCA GCTTTAACCC AGAGCCTCAT GATTGCTGGG TGCCCATAGC
3701 CTTTGTGCTG AATGGAGGCA CTCAGTCTCC TTGGGAAGAG AGAATCCATG
3751 ATAGACCCAC TTGGGAGCTC CCCACTTCAG GGGCCTACAC ACTGGTAATG
3801 CAACAGAATG CCCAAGAGTG ACCTCATAAA GCAAGGATTC CCTTCGTGGC
3851 CCCCTCTCTG CTGCCCTCA GAATCCAGAC GCTAAGGAAA ATCCCTAAGC
3901 AGAGATTTTC TGTGGATGTC TAAAAGCAAG GAATAAAAGT TGAAAATTTG
3951 GAAATGTGCT CAACACCGTC ACCAGCGCCA CTCGAGAGTC ATTTCTAGTT
4001 CACCACTTGA CACTACATCG GTGGGATTTT GCCCAACATT CAAGAAATTT
4051 AAGTAAATAT TATCTATCTC CATTGCCTGT TAAGAAATGT GCTAGTAGAA
4101 GTGTGAGGGC AGGGGTGTCAG TGTCTCTCA GCCTCTTCCC TCAGATACTC
4151 GTCTGCTTAC CAAAATAAGT TGCATGTCCT TGACAATCTG GTTCTATGA
4201 TTGTGAGGCG TGGCATGCTA TTACCTTTAT GTGCCCTGTA GACTTGAATG
4251 ACCAGTTTGA CCAGTTTGAC TGTAGATAA TCAGAAGGCT TTTCTCTTTT
4301 TTTATAATAG ACCCATCTC AAATCAGATA ATGAAAATTA CATATCTTGA
4351 TATATTAGAA AAGTATATAC ATTCTGGCTG GGCACGGTGG CTCACGCTG
4401 TAATCCCTGC ACTTTGAGAG GCTGGGGCGG ATCACTTGAG GTCAGGAGTT
4451 TGAGACCGGC CTGGCCAGCG TGGCGAAACC CCATCTCTAC TAAAAATACA
4501 CAGATTAGCC CGGAGTGATG GTGTGCACCT GTTGTCCCAG CTAAGCAGGA
4551 TCCTGAGGCA GGAGAATCCC TTTAACCTGG GGGCGAAGG TTGCAAGTGA
4601 CCAGGATTGC ACCACTGCAC TCCAGCCTGG GTGACGGAAC GGGACTCTGT
4651 CTCAGAAAAA AAAAAAAGA AGAGGAAAAA GAAAAATATA TATTCTATAT
4701 TTTTAACTAT TATGAGAATG TGTTCATTTC ATTTGTAACA TATAATGGGA
4751 AACAGTAATA CGTACTCTGA GAAAAATTGC AAAGCACAGA TAAATGGAAA
4801 TAAACAGGAA AAAGAATCAC CTATAACCTC ACCATCCATA GACAGACACT
4851 GTTAAAAATT TGGCATATTT CCTGCTGATT TTTTCTACTG CTGATTTTGT
4901 CACAGGTGAG ATAAATTTGA ACAGAGAATT TTGTATCTTT GGTTTTGTG
4951 TTTGCTGCA CAAAAAACA AAAGATATAA AAATGGATCA TAAACATTTT
5001 TCTAAATCCT GAAAAGTGCA TAGACATATT TTAGTGCTGT TATTTACAAA
5051 GATGGACATA CCATAATTTA CTTACACAGT CCTTTTGTG AGATGTTTAA
5101 GTTGTTTTCA AGCTTCTCAG TGCTGGAAAA AATACTGAGA TAGACATGTT
5151 TAGTTGAAGT TATTTCAATT CAGCTTATAT TATCTTGGT CAGAGAATGA
5201 ATGGTTCTCA GGCTTTTCAA AAGAGCTGGT CAGTTTTTAT GCCTCTGGCA
5251 GTTTTGTAGA GTGCTCAATC ATACTACACT GTTGCCAGCA TTAGATCTTA
5301 TCACATTTAA GTCAATGCTA ATTTTATAAA CAAAAACAAT GGTTTACTT
5351 TGCACTCTCC TGATTGGTGT TGCTGTAGAA CATATTTGGA GAAGTTTGTT
5401 TGTCTTTGGT GTTTATTCCA TGAATAGATT GTGTGCCAT TTTCTCTTGG
5451 GCTATTACGT TTTTATTAC TGATGTGAGC ATGTGTATGG GTGATTATTT
5501 GATGATTATC AGTTTGTCTT AGTAGACTGG CAATATTTAG TCTTGCTGTC
5551 ACTGTGTTCC CAGTGCCAAC TAGATTGCTT GATATGTAGT TGCCACTCAA
5601 TAAAGATTTG TTGAGTCAAT GAAAAAATAA AAAAAAATAA A

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BLAST Results

Entry AC004764 from database EMBL:
Homo sapiens chromosome 5, P1 clone 255g5 (LBNL H61), complete
sequence.
Score = 11057, P = 0.0e+00, identities = 2217/2224
Bp 428-5625 of cDNA == Bp 2912-8107 of AC004764

Entry HSAC1555 from database EMBL:
Homo sapiens (subclone 1_d8 from BAC H75) DNA sequence, complete
sequence.
Score = 575, P = 5.1e-30, identities = 115/115
Bp -240- 430 of cDNA == HSAC1555 splice pattern

Phenylalanine hydroxylase-stimulating protein/pterin-4
alpha-carbinolamine dehydratase from rat and human liver.
Purification, characterization, and complete amino acid
sequence.

Identity of 4a-carbinolamine dehydratase, a component of the phenylalanine hydroxylation system, and DCoH, a transregulator of homeodomain proteins.

Crystal structure of DCoH, a bifunctional, protein-binding transcriptional coactivator

ORF from 21 bp to 410 bp; peptide length: 130
Category: strong similarity to known protein

1 MAAVLGALGA TRRLAALRG QSLGLAAMSS GTHRLIAEER NQAILDLKAA
51 GWSELSEDA IYKEFSFHNF NQAFGMSRV ALQAEKMNNH PEWFNVYNKV
101 OITLTSHDCG ELTKKDKVLA KFIKAAASV

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_46k19, frame 3

No Alert BLASTP hits found

Pedant information for DKFZph.fkd2 46k19, frame 3

Report for DKF2phfkd2_46k19.3

```
[LENGTH]          130
[MW]              14377.56
[pI]              9.17
[HOMOL]           PIR:A47189 pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) - rat 4e-34

[FUNCAT]          01.07.99 other vitamin, cofactor, and prosthetic group activities [S.
cerevisiae, YHL018w] 5e-04
[SCOP]            dldchg_4.38.1.1.1 Pterin-4a-carbinolamine dehydratas 4e-50
[EC]              4.2.1.96 Tetrahydrobiopterin dehydratase 6e-34
[PIRKW]           nucleus 6e-34
[PIRKW]           carbon-oxygen lyase 6e-34
[PIRKW]           homotetramer 6e-34
[PIRKW]           hydro-lyase 6e-34
[PIRKW]           cytosol 6e-34
[PIRKW]           acetylated amino end 6e-34
[PIRKW]           homodimer 6e-34
[SUPFAM]          pterin-4-alpha-carbinolamine dehydratase 6e-34
[PROSITE]         MYRISTYL          2
[PROSITE]         CK2_PHOSPHO_SITE      3
[PROSITE]         PKC_PHOSPHO_SITE      4
[KW]              Alpha_Beta
[KW]              3D
[KW]              LOW COMPLEXITY      14.62 %
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SEQ      MAAVLGLALGATRLLLAALRGQSLGLAAMSSGTHRLTAEERNQATILDLKAAGWSELSEDA
SEG      .XXXXXXXXXXXXXXXXXXXXX.....
1dchB    .....CCCCHHHHHHHHHHHHHHHCCCEEECCCE
SEQ      IYKEFSFHNFNQAFGFMSRVALQAEKMNHHPEWFNVYNKVQITLTSHDCGELTKKDVKLA
SEG      .
1dchB    EEEEECCCHHHHHHHHHHHHHHHHHHHHHCCCCCEEETTTEEEEECBTTTTBTCCHHHHHH
SEQ      KFIKAAASV

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SEG
ldchB HHHHHHHHHH

Prosites for DKFZphfkd2_46k19.3

PS00005	11->14	PKC_PHOSPHO_SITE	PDOC00005
PS00005	32->35	PKC_PHOSPHO_SITE	PDOC00005
PS00005	56->59	PKC_PHOSPHO_SITE	PDOC00005
PS00005	113->116	PKC_PHOSPHO_SITE	PDOC00005
PS00006	56->60	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	113->117	CK2_PHOSPHO_SITE	PDOC00006
PS00008	6->12	MYRISTYL	PDOC00008
PS00008	20->26	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfkd2_46k19.3)

DKFZphfkd2_46m4

group: signal transduction

DKFZphfkd2_46m4.3 encodes a novel 198 amino acid putative GTP-binding protein related to the SAR-1 family of Ras superfamily members.

SAR1 proteins are involved in vesicular transport between the endoplasmic reticulum and the Golgi apparatus.

The new protein can find clinical application in modulating the transport of vesicles to the Golgi Apparatus, thus enabling post-translational modifications of the vesicles contents. Blocking of the molecule is expected to result modulation/blocking of secretory pathways.

nearly identical to mouse GTP-binding protein

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: /map="438.9 cR from top of Chr10 linkage group"

Insert length: 2996 bp

Poly A stretch at pos. 2969, polyadenylation signal at pos. 2958

```
1 ACATCCGGCG AGTAGCTGGC GGTCCCAGGT GCTGCTGGTT AGTGTGCTCT
51 GAGGGAGGGT CCGAGCCAGC CGCTGTTTGG CCGGAGGAGC CCCTCAGGCC
101 GTAGTAAGCA TTAATAATGT CTTTCATCTT TGAGTGGATC TACAATGGCT
151 TCAGCAGTGT GCTCCAGTTC CTAGGACTGT ACAAGAAATC TGGAAACTTT
201 GTATTCTTAG GTTTGCATAA TGCAGGCAAA ACCACTCTTC TTCACATGCT
251 CAAAGATGAC AGATTGGGCC AACATGTTCC AACACTACAT CCGACATCAG
301 AAGAGCTAAC AATTGCTGGA ATGACCTTTA CAACCTTTGA TCTTGGTGGG
351 CACGAGCAAG CACGTCGCGT TTGGAAAAAT TATCTCCAG CAATTAATGG
401 GATTGTCTTT CTGGTGGACT GTGCAGATCA TTCTCGCTC GTGGAATCCA
451 AAGTTGAGCT TAATGCTTTA ATGACTGATG AAACAATATC CAATGTGCCA
501 ATCCTTATCT TGGGTAACAA AATTGACAGA ACAGATGCAA TCAGTGAAGA
551 AAAACTCCGT GAGATATTTG GGCTTTATGG ACAGACCACA GGAAAGGGGA
601 ATGTGACCTT GAAGGAGCTG AATGCTCGCC CCATGGAAGT GTTCATGTGC
651 AGTGTGCTCA AGAGGCAAGG TTACGGCGAG GGTTCCTGCT GGCTCTCCCA
701 GTATATTGAC TGATGTTTGG ACGGTGAAAA TAAAGAGTT TTAATCTCT
751 GGACTGATCC TATTCACAGC TTCCTCATCA ACTTTTCTAA TAGAACAAGG
801 ATAGCTCTCC AACCATGTCT GGCGTTGAGA AGCCAAGAGT CTCTGTCAAC
851 TCTCTCATTG CCCAGTGGTC ACATGTGCTC TTCTCCACAC TGTGGGAGG
901 TAATGCTGCC CCACGTGCTG GTGCAGGTCA GTATCCTGGG ACTTGAAGCC
951 TGGCAGGATT TGCCGGGTAA AGCTGTATGC CATCATGGGG CACCTGAAAA
1001 GAAAAACACG TCTCACCCT GTGGTTGATT CAAAAGAAAG TGATTCTATT
1051 TTITAAAGAA AGCGTTGTTA ATGTAATTGG TATCCCTCCT AACTTTTTGA
1101 GTTCACAATT TACTTGGTCC AGAGTTTTCT ATTCTTTTTT TTTTTTAAA
1151 CTAATGAATG ACATTTAGAT ACTTCATAAA ATTATGAACA GATATGGAGG
1201 CCAGAGCTCA TTTGGGTAAA CTTACTCCTG CTGAGTTAGC AGGTTGGTGA
1251 GAGAAGCTCC CCTGAGCTCA CTTGCTCTC TGACTGCCTT GGAGTAGGTG
1301 GCATAACCTT GTGCACAGAG AACTAGAAAA GGGGCAGAAC CCCGGCCTTG
1351 CAGTTGTGGC AGGTTTCCAC TGTGGTAAGC TAGGTTTATT CCTCATCAAG
1401 GAATGTGTAG CAGATTGTTT ACTGTGGAGG AGGTAATTAT AGAATGGGTT
1451 ATTGTTGTTA TTCTTACTCA TGAAGTTACA GATTTTAGCC AGTCTTTGCT
1501 TTTATACCTT TGTGAAATTT AATTTCTCTC TATAGCACCT TCCTTTTTTCG
1551 TTTTCAGTTA TCAAAAGTGA CTTTGACCTC ATAAGAGAGT TGACAACATC
1601 TCTCGTGTCA CATACTGCAG GTGCATCAGT TACTTTTSCA CAGATTCTAG
1651 GGGGACATTT TTCTGAATAG GAAGACAGGA CAAAGTTAAC AGCTTAAGGG
1701 CTCTTAATTC TGTGAGTTGA GGACTTAAAA GTATTGTAGC ATTTGTTTGG
1751 ATCCATGAAA AATGTATTCA GTGGGCTTTA AAATTTCCAT TTGCAGAATT
1801 TGGTCTCTCA GGCTGTTTGG GAGCTCTTTT TTTTACATT TTTCTCCTT
1851 GACACCTATT TTATTGGTGT TTAAGTAAA GGTAAACATC TGTAGCTTTT
1901 CCAGGTTTTT TTTTTTTTTT TTGATATGAA ATTGTCTTTC TCCATTGCAG
1951 AAATAAGCTA GGGAAACACT AACCCAAAAA CTTTCTGTAG AGCTGTTCCT
2001 TTGGAGGCAG CATCACTTAT TGGCAGTAAA GACTCAGTAT AAAAGCACCA
2051 GCATCCCTAC TTGGGTGATG GGGATTAATT TTATAGCATT CCATTTTCCT
2101 AGTGCCACAT GTGAAATTGG ATTTTGATGA TCTTAATCTA TATTCTACCC
2151 TTATAATAAA AGATCAAAAG ATATATCTCC TATGAACAGA TTGCAGATAG
2201 GAGATGAAAA GTTGGGAGGA TGCCTTTATT CTAATGTGAG GGTAGGGAAA
2251 ATGTGGATCA CATTACTGGG GTGAAGGAGG CATTGTCTTT TAGTTGGAGT
2301 TCTCATTTTT ATTCTCCAGT ACTGACTTGT GGGGAAAGCA TACTTTTTCA
2351 CTGCCAGGTA CTGAATGCAG AGGCTCAGTG AAGTATATAT GTGGGAAGTG
2401 CATGCATTTT GTTTATTAGC AAACATAGCT GGATTAAGAC GAAGTTGTTG
2451 GTTTGGAAAG GGGTTAAAGC CTTAAGTGAA CAAATCTAGC TAACAGTGAA
2501 TGAAGTAGGT AATATAACTT GCATATTTTT AATTTCTCTT GGTTAAAGGT
2551 CCCCATACT TCTCTGTTCC GAGACATGAG AAGTATGATT ACTTCAGTGT
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2601 TAGTTTCTT AATTTTTTTT TTCCCCTATT TGTCCCTTGT CACTTTGTTG
2651 CAAGCTAGAA ATCTGTGGGT TATACATAGG GCAGCTCTTT GCGAAAGTGG
2701 TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT
2751 TCTTGCCCCA CGGAACACTA TTCCTATAAG ATAGCTGAAA GAAGCTGCTG
2801 TGAGGAGCTC AGCTCCAACA CAGGATCAGC ACCTTGATA GGAATCCCA
2851 TGAATTATGA CTTCTCATTC TGTTTATCA GAGTGCATAT ATGTCCTACT
2901 TCAGGAAAAG TAAAACAGTC ATTTACGAAA GAAAGTCAAT CTGTATCCTA
2951 AGCATTTTAA TAAAAGTTA AAACAAAAA AAAAAAAAAA AAAAAA

```

BLAST Results

Entry HS679348 from database EMBL:
human STS WI-16722.
Length = 265
Minus Strand HSPs:
Score = 1242 (186.4 bits), Expect = 2.8e-50, P = 2.8e-50
Identities = 260/265 (98%)

Medline entries

94085558:
Molecular analysis of SARI-related cDNAs from a mouse
pituitary cell line.

Peptide information for frame 3

ORF from 117 bp to 710 bp; peptide length: 198
Category: strong similarity to known protein

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1 MSFIFEWIYN GFSSVLOFLG LYKKSGLVF LGLDNAGKTT LLHMLKDDRL
51 GQHVPTLHPT SEELTIAGMT FTTFDLGGHE QARRVWKNYL PAINGIVFLV
101 DCADHSRLVE SKVELNALMT DETISNVPII ILGNKIDRTD AISEEKLREI
151 FGLYGQTTGK GNVTLKELNA RPMEVFMCVS LKROGYGEGF RWLSQYID

```

BLASTP hits

Entry S39543 from database PIR:
GTP-binding protein - mouse
Length = 198
Score = 1029 (362.2 bits), Expect = 5.1e-104, P = 5.1e-104
Identities = 197/198 (99%), Positives = 198/198 (100%)

Entry SARA_MOUSE from database SWISSPROT:
GTP-BINDING PROTEIN SARA.
Length = 198
Score = 1012 (356.2 bits), Expect = 3.2e-102, P = 3.2e-102
Identities = 195/198 (98%), Positives = 196/198 (98%)

Entry CEZK180.4 from database TREMBL:
gene: "ZK180.4"; Caenorhabditis elegans cosmid ZK180.
Length = 193
Score = 679 (239.0 bits), Expect = 6.3e-67, P = 6.3e-67
Identities = 125/197 (63%), Positives = 161/197 (81%)

Alert BLASTP hits for DKFZphfkd2_46m4, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_46m4, frame 3

Report for DKFZphfkd2_46m4.3

```

[LENGTH]      198
[MW]           22367.00
[pI]           6.21
[HOMOL]        PIR:S39543 GTP-binding protein - mouse 1e-112

```

[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YPL218w] 1e-58
 [FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YPL218w] 1e-58
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YOR094w] 2e-23
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YPL051w] 4e-22
 [FUNCAT] 30.08 organization of golgi [S. cerevisiae, YDL192w] 3e-20
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YBR164c] 3e-19
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YMR138w] 2e-09
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YMR138w] 2e-09
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YHR168w] 7e-05
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YHR005c] 1e-04
 [FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YKL154w] 1e-04
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YHR005c] 1e-04
 [FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YHR005c] 1e-04
 [FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YKL154w] 1e-04
 [FUNCAT] 08.19 cellular import [S. cerevisiae, YML001w] 3e-04
 [BLOCKS] BL00395A Alanine racemase pyridoxal-phosphate attachment site proteins
 [BLOCKS] BL01019B ADP-ribosylation factors family proteins
 [BLOCKS] BL01019A ADP-ribosylation factors family proteins
 [BLOCKS] BL01020D SAR1 family proteins
 [BLOCKS] BL01020C SAR1 family proteins
 [BLOCKS] BL01020B SAR1 family proteins
 [BLOCKS] BL01020A SAR1 family proteins
 [SCOP] dlplj_ 3.25.1.3.1 cH-p21 Ras protein [human (Homo sapiens)] 7e-36
 [SCOP] dlguaa_ 3.25.1.3.10 Rap1A [Human (Homo sapiens)] 8e-40
 [SCOP] dlrrf_ 3.25.1.3.5 ADP-ribosylation factor 1 (ARF1) [rat (Rattus)] 2e-55
 [SCOP] dlhurb_ 3.25.1.3.4 ADP-ribosylation factor 1 (ARF1) [human (Homo)] 1e-58
 [SCOP] dlgota2_ 3.25.1.3.3 (1-54,171-326) Transducin (alpha subunit) [ra] 2e-33
 [SCOP] dltadb2_ 3.25.1.3.2 (1-30,152-316) Transducin (alpha subunit) 6e-36
 [PIRKW] glycoprotein 4e-19
 [PIRKW] monomer 1e-16
 [PIRKW] P-loop 3e-64
 [PIRKW] lipoprotein 4e-19
 [PIRKW] GTP binding 3e-64
 [SUPFAM] ADP-ribosylation factor 5e-22
 [PROSITE] ATP_GTP_A 1
 [PROSITE] MYRISTYL 3
 [PROSITE] SAR1 1
 [PROSITE] CK2_PHOSPHO_SITE 4
 [PROSITE] PKC_PHOSPHO_SITE 3
 [PROSITE] ASN_GLYCOSYLATION 1
 [PFAM] ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
 [KW] Alpha_Beta
 [KW] 3D

SEQ MSFIFEWIYNGFSSVLQFLGLYKSGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPT
 1hurATTTTTCC

SEQ SEELTIAGMTFTTDLGGHEQARRVWKNYLPAINIGIVFLVDCADHSRLVESKVELNALMT
 1hurA EEEEEETEEEEEEETTTTTTCCCHHHHHHHHCEEEEEEEETTTTHHHHHHHHHHHHHHHHHHH

SEQ DETISNPILILGNKIDRTDAISEEKLREIFGLYGQTTGKGNVTLKELNARPMVEFMCSV
 1hurA TTTTTTTEEEEEETTTTTTCCCHHHHHHHHCGG.....

SEQ LKRQGYGEGFRWLSQYID
 1hurA

Prosites for DKFZphfkd2_46m4.3

PS00001	162->166	ASN_GLYCOSYLATION	PDOC00001
PS00005	25->28	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00006	60->64	CK2_PHOSPHO_SITE	PDOC00006
PS00006	72->76	CK2_PHOSPHO_SITE	PDOC00006
PS00006	111->115	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	68->74	MYRISTYL	PDOC00008
PS00008	155->161	MYRISTYL	PDOC00008
PS00017	32->40	ATP_GTP_A	PDOC00017
PS01020	171->197	SAR1	PDOC00782

Pfam for DKFZphfd2_46m4.3

```

HMM_NAME      ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
HMM            *GMgWfsIFrkmWGlWNKEMRILMLGLDNAGKTTILYMLKlgEIVTTIPT
               ++ FS+++++GL++K+++++LGLDNAGKTT+L+MLK++++ ++PT
Query          9  -YNGFSSVLQFLGLYKKSGLVFLGLDNAGKTTLLHMLKDDRLGQHVPT      56
HMM            IGFNVETVeYKNIKFNVDVGGQdsIRPYWRHYYPNTDGIWVVDsADRD
               +++++E++++ ++F+++D+GG++++R++W++Y P+++GI+++VD+AD++
Query          57 LHPTSEELTIAGMTFTTDFDLGGHEQARRVWKNYLPAINGIVFLVDCADHS    106
HMM            RMeEaKqELHaMLNEEELrDAPLlIFANKQDLpgAMSesEIREaLGLHeI
               R+ E+K+EL+A++++E ++++P+LI++NK+D+ +A+SE+++RE+ GL+ +
Query          107 RLVESKVELNALMTDETISNVPIlILGNKIDRTDAISEEKLREIFGLYGQ    156
HMM            RCn.....RPWYIQMCCAvtGEGLYEGMDWLSNYInkRkK*
               +++          RP++++MC+++++G++EG++WLS+YI
Query          157 TTGKGNVTLKELNARPMEVFMCSVLKRQGYGEGFRWLSQYI-----    197

```

DKFZphfkd2_47a4

group: transcription factor

DKFZphfkd2_47a4.1 encodes a novel 280 amino acid protein with similarity to zinc finger proteins.

The new protein is a putative transcription factor with one C2H2 zinc fingers.

The new protein can find application in modulating/blocking the expression of genes controlled by this transcription factor.

similarity to C.elegans F46B6.7

potential frame shift at 1092, will be checked see BLASTX

Sequenced by MediGenomix

Locus: map="7q31"

Insert length: 1756 bp

Poly A stretch at pos. 1737, no polyadenylation signal found

```

1 CCCTTTTCTT TTCTGCCGGG TAATGGCTGC TTCCAAGACC CAGGGGGCTG
51 TCGCCCGAAT GCAGGAAGAC CGTGATGGGA GCTGCAGCAC AGTCGGGGGT
101 GTAGGTTATG GGGTAAGGAT TGTATCCTGG AGCCGCTTTC CCTGCCAGAA
151 AGTCCAGGTG GCACCACCAC TTTAGAAGGT TCTCCATCTG TGCCTTGTAT
201 TTTCTGTGAA GAACATTTTC CTGTGGCTGA ACAAGACAAA CTTCTGAAGC
251 ACATGATTAT TGAGCATAAG ATTGTCATAG CTGATGTCAA GTTGGTTGCT
301 GATTTCCAAA GGTACATTTT ATATTGGAGG AAAAGGTTCA CTGAACAGCC
351 CATCACAGAT TTTTGTAGTG TAATAAGAAT TAATCCACT GCTCCATTG
401 AAGAACAAGA GAATTATTTT TTGTTATGTG ACGTTTACC AGAAGATAGA
451 ATTCTTAGAG AAGAGCTTCA GAAACAGAGA CTGAGAGAAA TTCTGGAACA
501 ACAGCAGCAA GAACGAAATG ATAACAATTT TCATGGCGTT TGTATGTTTT
551 GCAATGAAGA ATTCCTTGGG AACAGATCTG TTATTTTGAA CCACATGGCC
601 AGAGAACATG CTTTCAACAT TGGATTGCCA GACAACATTG TAACTGCAA
651 TGAATTTTGG TGTACATTAC AGAAAAAGCT TGACAATTTG CAGTGCTTGT
701 ACTGTGAGAA GACCTTCAGG GGCAAAAATA CACTTAAAGA TCACATGAGG
751 AAAAAACAGC ATCGTAAGAT TAATCCTAAG AACAGAGAA ATGACAGATT
801 TTATGTATC AATTATTTGG AACTTGGAAA ATCGTGGGAG GAAGTTCAGT
851 TCGAAGATGA TCGGGAGTTG CTGGACCATC AGGAAGATGA CTGGTCTGAT
901 TGGGAAGAAC ACCCTGCCCTC TGCAGTCTGC TTATTTGTG AAAAGCAAGC
951 AGAAACAATT GACAAGTTCT ATGTCCACAT GGAGCATCCA CACGAATTTG
1001 ATCTTCTCAA AATAAAGTCA GAACCTGGAT TAAATTTCTA TCAGCAAGTG
1051 AAACCTGGTC ATTTTATTCG GAGGCAAGTT CACCAATGCA GATGATGGCT
1101 GCCATGTGAA GTTCAAATCC AAAGCAGACT TAAGAACTCA CATGGAAGAA
1151 ACTAAACACA CTTGCTGCTC CCCCATAGA AAGACGTGGG ATCAACTGGA
1201 GTATTATTTT CCAACCTATG AAAATGACAC TCTCCTGTGT ACACATCTG
1251 ACAGTGAAAG TGACCTGACA GCTCAGGAAC AAAATGAAA TGTTCCTATC
1301 ATCAGTGAAG ATACATCTAA ACTGTATGCT TTGAAACAAA GCAGTATTTT
1351 GAACCAAGTT CTACTATAAG AGTACTTGAA AACCTAGAAG AAACCTACCAC
1401 AGAAGCAATT TTTTATGTTT TTCTCTATG AGACAGATAT GAAAGAACAA
1451 TTTAAATTTG AACATCAACA AAAGATTGGT CCTTGGTGAA ATAACTTTT
1501 CAAAAATGAA TGTCTTTTC AAAAAATAAA GTAGAAAAAT GCACTTACTA
1551 AGAACATGAA AAAAAATGA AGTAGGAAAA TAAGATGAAG ACTTTGTATT
1601 TTGGCTGTAA ACTTTTATTG TGTGATCATC TTAAATTATC TCACTTCATT
1651 AAACTCATAA TTATATATAG AAGTATATGT CAATTACAAA GAAATGAAAT
1701 GTTCAAATTA TTTATAAACC TGATTTTCA ATCAGCGAAA AAAAAA
1751 AAAAAA

```

BLAST Results

Entry AC004112 from database EMBL:
Homo sapiens BAC clone RG313E03 from 7q31, complete sequence.
Score = 2660, P = 3.0e-241, identities = 534/535
> 10 exons

Entry AC004111 from database EMBL:
Homo sapiens BAC clone RG103H13 from 7q31, complete sequence.
Score = 598, P = 5.8e-17, identities = 128/137
1 exon

Medline entries

Peptide information for frame 1

```

1 MIEHKIVIA DVLVADFQR YILYWRKRFT EQPITDFCSV IRINSTAPFE
51 EQENYFLLCD VLPEDRLRE ELQKQRLRE LEQQQQERND NNFHGVCMFC
101 NEEFGLGRSV LINHMAREHA FNIGLPDNIV NCNEFLCTLK KLDGNLQCLY
151 CEKTRFRGKNT LKDHMRKKQH RKINPKNREY DRFYVINYLE LGKSWEEVQL
201 EDDRELLDQH EDDWSDEEH PASAVCLFCE KQAEETIEKLY VHMEDAHEFD
251 LLIKIKSELGH EDYOOVKLVN STRROVHCCR

```

Entry YB9M_YEAST from database SWISSPROT:
34.7 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.
Score = 112, P = 4.6e-04, identities = 43/165, positives = 71/165

Pedant information for DKFZphfkd2 47a4, frame 1

```
SEQ      MIIEHKIVIADVKLVADFQRYILYWRKRFEQPITDFCSVIRINSTAPFEEQENYFLLCD
SEG      .....
PRD      cccccceehhhhhhhhhhahhhhhhhhhhhhhcccccceeeecccccchhhhheeecc

SEQ      VLPEDRILREELQORLREILEOOOERNDNNFHGVCMFCNEEFLGNRSVILNHMAREHA
SEG      ....xxxxxxxxxxxxxxxkxxxxxxxxxx
PRD      cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccceeeecccccccceehhhhhhhh

SEQ      FNIGLPDNIVNCNEFLCTLOKKLNJLOCLYCEKTFRGKNTLKDHMRKKOHRKINPKNREY
```

```

SEG .....
PRD hccccccccchhhhhhhhhhhhhheeeccccccccchhhhhhhhhhhcccccccccc

SEQ DRFYVINYLELGKSWEEVQLEDDRELLDHQEDDWSDEEHPASAVCLFCEKQAETIEKLY
SEG .....
PRD ceeeeeeeccccchhhhhhhhhcchhhhhhhccccccccccccccccchhhhhhhhhhhhhhh

SEQ VHMEDAHEFDLLKIKSELGLNFYQQVKLVNFIRRVHQCRR
SEG .....
PRD hhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhhhhcccc

```

Prosites for DKFZphfkd2_47a4.1

PS00001	44->48	ASN_GLYCOSYLATION	PDOC00001
PS00001	107->111	ASN_GLYCOSYLATION	PDOC00001
PS00004	27->31	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	154->157	PKC_PHOSPHO_SITE	PDOC00005
PS00005	160->163	PKC_PHOSPHO_SITE	PDOC00005
PS00006	160->164	CK2_PHOSPHO_SITE	PDOC00006
PS00006	194->198	CK2_PHOSPHO_SITE	PDOC00006
PS00006	215->219	CK2_PHOSPHO_SITE	PDOC00006
PS00007	178->185	TYR_PHOSPHO_SITE	PDOC00007
PS00007	13->22	TYR_PHOSPHO_SITE	PDOC00007
PS00008	124->130	MYRISTYL	PDOC00008
PS00028	148->171	ZINC_FINGER_C2H2	PDOC00028

Pfam for DKFZphfkd2_47a4.1

```

HMM_NAME      Zinc finger, C2H2 type
HMM            *CpWPDCgKtFrrwsNlrRHMR..T.H*
               C + C+KTFR + +L+ HMR   H
Query          148 CLY--CEKTFRGKNTLKDHMRKK-QH      170

```

DKFZphfkd2_4b6

group: kidney derived

DKFZphfkd2_4b6 encodes a novel 133 amino acid protein with similarity to Homo sapiens clone 25003 partial CDS.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to Homo sapiens clone 25003

complete cDNA, complete cds, few EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1936 bp

Poly A stretch at pos. 1916, polyadenylation signal at pos. 1890

```
1 GGGAGACTTG CAATGAAGTT AGAATGAACA GGAGGAGTCT GCAGCTTTTC
51 AGTGCCCTGGG ATAACATATAG TTTAAAGATC ATTGTGTAAA ATAGGATTTT
101 TAGTCAGCAT GCATTGTTTT AAACCGACTA ACTGATAGCC TAAAACTTTA
151 TTTTTCGATT TTGCCAATCC TTGGAGTTTT GTTTTGCAGA ATTAAGAAAA
201 AAATGAATGT ATGATCATCT GAAAAGGGCT TTCTCTCAAT CCCACTTCAT
251 GGCATGACCT CTGCTGGATC ATTAGTTCTA GCCAGAGAAG TAGCAAAGGA
301 ACATGACCTC TGAGACCTCC CTTCCCTCAT CAGTGGGGCT GACTGAGCTG
351 GGGGCTTGAA GCCGGAGGTA ACCTTTCCTG TCGAATGTTT CTTTAGAGAA
401 TGGCAATGGT CTCTGCGATG TCCTGGGTCC TGTATTGTG GATAAGTGCT
451 TGTGCAATGC TACTCTGCCA TGGATCCCTT CAGCACACTT TCCAGCAGCA
501 TCACCTGCAC AGACCAGAAG GAGGGACGTC TGAAGTGATA GCAGCACACC
551 GATGTTGCAA CAAGAATCGC ATTGAGGAGC GGTCAACAAAC AGTAAAGTGT
601 TCCTGTCTAC CTGGAAAAGT GGCTGGAACA ACAAGAAACC GGCCTTCTTG
651 CGTCGATGCC TCCATAGTGA TTTGGAAATG GTGGTGTGAG ATGGAGCCTT
701 GCCTAGAAGG AGAAGAATGT AAGACACTCC CTGACAATTC TGGATGGATG
751 TGCGCAACAG GCAACAAAAT TAAGACCACG AGAATTCACC CAAGAACCTA
801 ACAGAAGCAT TTGTGGTAGT AAAGGAAAAC CAACCTCTTG GAAAATACAT
851 TTTGAGAATC TCAAACATCT CACATATATA CAAGCCAAAT GGATTTCTTA
901 CTTGCACTTT GACTGGCTAC CAGATAATCA CAGTGCCTTT AGTGTGTGTA
951 ACGAAATATC CTACAGTGAG AAGACACAGC GTTTTGGCAT CACCATGGAA
1001 AGTGGGCTTA AAAAAGGGTC TTCTCAGTGA AATTTTGGG CATCATGAAG
1051 AACGATCAAC TATCTTCTAA TTTGAATCTA TAGTTACTTT GTACCATTTG
1101 AAATATATGT ATATATATAT ATATAATATT TTGAAATATT ATCTATTCTC
1151 TTCAAGAAAT GAACAGTACC ACAGTTTGAG ACGGCTGGTG TACCCCTTTG
1201 AGTTTTGGAT GTTTTGTCTG TTTTGCTTTG TTTTGTAGT CATTTCCTTT
1251 TCTAACGGCA AGGAAGATAT GTGCCCTTTT GAGAATTCAA GATGGCACTG
1301 ACACGGGAAG GCCAGCTACA GGTGGACTCC TGGAAATTTGA GGCATCATAA
1351 TGATACTGAA TCAAGAACTT CTTCTGCTT CTACCAGATG GCCCAAGGAA
1401 GCACATCGTC CTGTTTTATT GCTTTCTACC CTGTGCAATA TTAGCATGCA
1451 AGCTTGGCTT ACATAGTCAT ACTTTATATT CAATTGATAT ATAATAACCG
1501 TTCTAACCTC TTCCAGGAAA ATATTTTtag AACTACTAGC TTTTCCACTT
1551 AGAAGAAAAT GAGGATTCTT AAGGGAGCCA CTCCACCATG CTATTAAGAC
1601 TCTGGCAGAG TTATGGGTAG GATATGGATC CCTACATGAA TAAGTCCTGT
1651 AAATACAATG TCTTAAGGCT TTGTATAGCT GTCCTAGACT GCAGAAATGT
1701 CCTCTGATTA AATCCAAAGT CTGGCATCGT TAACTACATA GTGCTGTAGC
1751 AACAAAGTCT ATCATGGCAT CTCTTCTAT GTTTGGTTTG CTTTTTCCAA
1801 GAGTATTACG GTCTCCTCTT GTGAGATAGG AAGGCCATGA AAACAATTAG
1851 ATTTCAAGAT GATCTATGTG ACCAAATGTT GGACGCCCTT ATTAAAGTGG
1901 TAAACAACCT CTTTCTAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

```

1 MAMVSAMSWV LYLWISACAM LLCHGSLQHT FQQHHLHRPE GGTCEVIAAH
51 RCCNKNRIEE RSQTVKCSCL PGKVAGTTRN RPSCVDASIV IWKWWCEMEP
101 CLEGECKTL PDNSGWMCAT GNKIKTTRI H PRT

```

No BLASTP hits available

TREMBLNEW:AF131851_1 product: "Unknown"; Homo sapiens clone 25003 mRNA
sequence, partial cds., N = 1, Score = 242, P = 1.7e-20

HSPs :

Query: 42 GTCEVIAAHRCCNKNRIEERSQTVKCSCLPGKVAGTTNRNPSCVDASIVWKWWCEMEPC 101
GTCE++ R ++ R QT +C+C G++AGTTR RP+CVDA I+ K WC+M PC
Sbjct: 76 GTCEIVTLDRSSQPRTTARQTARACACRKGQIAGTTTARPAACVDARIIKTKQWCDMLPC 135

Query: 102 LEGEECTLPDNSGWMCAT-GNKIKTTRI 129
LEGE C L + SGW C G +IKTT +
Sbjct: 136 LEGEGCDLLINRSWGTCTQPGGRIKTTTV 164

```
[LENGTH]      133
[MW]           15030.64
[PI]           8.49
[HOMOL]        TREMBLNEW:AF131851_1 product: "Unknown"; Homo sapiens clone 25003 mRNA
sequence, partial cds. 4e-20
[KW]           Alpha_Beta
[KW]           SIGNAL PEPTIDE 26
```

[illegible]

(No Prosite data available for DKFZphfkd2_4b6.1)

(No Pfam data available for DKFZphfk2_4b6.1)

DKFZphfkd2_4c8

group: kidney derived

DKFZphfkd2_4c8 encodes a novel 153 amino acid protein with partial similarity to huntington's associated protein HAP1.

The novel protein contains a leucine zipper involved in protein-protein interaction. No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to KIAA0549 and HAP1

potential frame shift at Bp ~1350-1500 will be checked

Sequenced by GBF

Locus: unknown

Insert length: 3182 bp

Poly A stretch at pos. 3162, polyadenylation signal at pos. 3135

```
1 GGGCTTCCCC CATAGAATTT TTCTTTTCAT TGCCCACTTT ACTGTTTGG
51 CTCCAGACTG TCGTTAAGAA TGTACAGCCT AATTCTGGTG TGTTCGGGA
101 TATTCTTCTG TCCAGTATTC TGGAAAGGCG GGGAGGCATG GCAGCGTTTT
151 ACTTGACGTT GATGGTGCTG TGAAGTCCAT TCTTTCCTCT GCAAGACTAC
201 TGACTATGCA GAAATTTATC GAAGCGGATT ATTATGAACT AGACTGGTAT
251 TATGAAGAAT GCTCGGATGT TTTATGTGCT GAAAGAGTTG GCCAGATGAC
301 TAAGACATAT AATGACATAG ATGCTGTCTC TCGGCTTCTT GAGGAGAAAG
351 AGCGGGATTT AGAATTGGCC GCTCGCATCG GCCAGTCGTT GTTGAAGAAG
401 AACAAAGACCC TAACCGAGAG GAACGAGCTG CTGGAGGAGC AGGTGGAACA
451 CATCAGGGAG GAGGTGTCTC AGCTCCGCGA TGAGCTGTCC ATGAAGGATG
501 AGCTGCTTCA GTTCTACACC AGCGCAGCGG AGGAGAGTGA GCCCGAGTCC
551 GTTTGCTCAA CCCCGTTGAA GAGGAATGAG TCGTCTCTCT CAGTCCAGAA
601 TTAATTTTCA TTGGATTCTC TTCAAAGAA GCTGAAAGAC CTTGAAGAGG
651 AGAATGTGTG ACTTCGATCC GAGGCCAGCC AGCTGAAGAC AGAGACCATC
701 ACCTATGAGG AGAAGGAGCA GCAGCTGGTC AATGACTGCG TGAAGGAGCT
751 GAGGGATGCC AATGTCCAGA TTGCTAGTAT CTCAGAGGAA CTGGCCAAGA
801 AGACGGAAGA TGCTGCCCGC CAGCAAGAGG AGATCACACA CCTGCTATCG
851 CAAATAGTTG ATTTGCAGAA AAAGGCAAAA GCTTGCGCAG TGGAAATGA
901 AGAACTTGTC CAGCATCTGG GGGCTGCTAA GGATGCCAGC CGGCAGCTCA
951 CAGCCGAGCT GCCTGAGCTG GAGGACAAGT ACSCAGAGTG CATGGAGATG
1001 CTGCATGAGG CCGCAGGAGG GCTGAAGAAC CTCGGGAACA AAACCATGCC
1051 CAATACCACG TCTCGGCGCT ACCACTCACT GGGCCTGTTT CCCATGGATT
1101 CCTTGGCAGC AGAGATTGAG GGAACGATGC GCAAGGAGCT GCAGTTGGAA
1151 GAGGCCGAGT CTCCAGACAT CACTCACCAG AAGCGTGTCT TTGAGACAGT
1201 AAGAAACATC AACCAAGTTG TCAAGCAGAG ATCTCTGACC CCTTCTCCCA
1251 TGAACATCCC CGGCTCCAAC CAGTCCTCGG CCATGAACTC CCTCCTGTCC
1301 AGCTGCGTCA GCACCCCCCG GTCCAGCTTC TACGGCAGCG ACATAGGCAA
1351 CGTCGTCTCT GACAACAAGA CCAACAGCAT CATTCTGGAA ACAGAGGCGA
1401 CCGACCTGGG AAACGATGAG CGGAGTAAGA AGCCGGGGAC GCCCGGCACC
1451 CCCAGGCTCC CACGACCTGG AGACGCGCTG GAGGCGGCTG TCCCTGCGCC
1501 GGGAGAACTA CCTCTCGGAG AGGAGGTTCT TTGAGGAGGA GCAAGAGAGG
1551 AAGCTCCAGG AGCTGGCGGA GAAGGGCGAG CTGCGCAGCG GCTCCCTCAC
1601 ACCCACTGAG AGCATCATGT CCCTGGGCAC GCACTCCCGC TTCTCCGAGT
1651 TCACCGGCTT CTCTGGCATG TCCTTCAGCA GCCGCTCCTA CCTGCCTGAG
1701 AAGCTCCAGA TCGTGAAGCC GCTGGAAGGT GATCACGCGG GGCCTCGGCC
1751 CCTCTCTGTC CTCCTGGGGG ACTCCCTTTG GTCCCTGATC CACCTGCGGA
1801 AGGCGGGGCA CCTCTGTCAC GCCTACTCCT TTTTCTTCCG CGACAGCCAC
1851 CCGCGCTGCT GGTGTGAGTT CCTCTGAGGG TGGTGTCTAG CCTAGGCCTC
1901 CGTCCCTCCC CTCTGGCTGG CAGGTGTGAC AATGCACACA TAGGCCATGA
1951 AACTCGGCCA GGAAGACAAA GCATGTGCAC TGTGGTCTTC TAGTCTTTTC
2001 CTTTGCCTTT AGAACCTTAG AAATAAAAC TTTTGTGGCG GTAGAGGCAC
2051 TGCTAACTGA TTCAAAAATT AATTAGGTTT TGCTGTGGG TGTGAGGAAT
2101 GCAGAAAATT AATGCTTTAG CTTTTCTGCA GTTTTGGTGT CGGGGAGAGG
2151 TTCCAAGCAA ACTCTATTAA ATGGGGATTT TTTTTCCTCC ATAACCACTT
2201 GAATGTGATT TGTGGGCTTA TGTGTTCTGA TTTGAACTTC ATATAGCAAG
2251 GTTGTGCTTT TTGCCAGATC CAGTATCTTC TGAGCGCGCG TCCTAGAGTC
2301 TACAATTTGG AGTCCAGGAA GGGGTGGCTG TGGAGACAAG TGAGTTTGTG
2351 ACCTCCGTAA GCCACCCTTT TTCAGGCTCA GTTCATGTGT TAGTATCAGG
2401 GGCATCTCAG ATGATTAAAC TCATGGGAAA AACTTCCTCC TTCCCTCTCT
2451 CCCTCTTGCC CTCCTGCCTC TTTTCTTTT TTTTCTTTT ATATTGGGCA
2501 CTTATAAAAT GTTTTCCCTC TACCTGTGTC TACTCTGCCA AGAGCCACCA
2551 AGTGCCTATA TTTTTCATTT TTTACTCTTT TAGTTTGGAA AGCCATATAC
2601 GTTTGAGAAG GTGTTTAAAA ACTCTGTGTT ACACCTACGA TGCAAAGCCA
2651 AATCAGAACT TCTGTAAGGC AGAACTTTCC CAACTTTAAA AAAATTATTG
```

```

2701 TCCCCTCTAG GAGCCTTCTT AGACGTTTTT TCCTAATCAC CCCCCAAAGA
2751 CATTTTAATA CCACATATAT ATTGTTTATG TACTATATGT ATATACATAA
2801 ACAATACATA AGCAATACAT CTGTGGTATT AAAATTAAAA AGAATCCAAT
2851 TATGTTTACC TCAAAAAGAAC CTGTTTTTGC TTCTTGGGAG CAATATTGCC
2901 CCTGTGAGAC TGCATGCTAT AAGGTAAGGT TGTGCTTGT AAAGACCCAA
2951 GACATGACTG GGTTCACAG TCTCCAAAGG AAGAGGGTGG GCTAGTTGT
3001 TTTTATTATT ATTTTAAAT TGTATAATTG GGGTCTTCT TAGAGTTCAG
3051 AAAAGGTATA GCTTACTCTT TTTTAATTGT TTATTAGTT GTAAGCTTAG
3101 TGATTGTTT CTGATCCACA TGTGTGTGT TCTTCAATAA AATCTTTCAT
3151 TTCTGCAATT TTAATAAAAA AAAAAAAAAA AA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 206 bp to 1531 bp; peptide length: 442
 Category: similarity to known protein
 Classification: unset
 Prosite motifs: LEUCINE_ZIPPER (139-161)

```

1 MQKFIEADYY ELDWYEECS DVLCAERVGO MTKTYNDIDA VTRLLEEKER
51 DELEAARIGQ SLLKKNKTLT ERNELLEEQV EHIREEVSQ L RHELSMKDEL
101 LQFYTSAAEE SEPESVCSTP LKRNESSSSV ONYFHLDSLO KKLKDL EEN
151 VVLRSEASQL KTETITYEEK EQQLVNDVCV ELRDANVQIA SISEELAKKT
201 EDAARQOEI THLLSQIVDL QKAKACAVE NEELVQHLGA AKDAQRLTA
251 ELRELEDKYA ECMEMLEHAQ EELKNLRNKT MPNTTSRRYH SLGLFPMDSL
301 AAEIEGTMRK ELQLEEAESP DITHQKRVFE TVRNINQVVK QRSLTSPSPMN
351 IPGSNQSSAM NSLLSSCVST PRSSFYGSDI GNVVLDNKTN SIILETEAAD
401 LGNDERSKKP GTPGTPRLPR PGDGAEAAVP APGELPLGEE VL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4c8, frame 2

PIR:S72555 huntingtin-associated protein HAP1 - human (fragment), N = 1, Score = 234, P = 8.6e-19

TREMBL:CEUT27A3_7 gene: "T27A3.1"; Caenorhabditis elegans cosmid T27A3., N = 1, Score = 226, P = 9.9e-16

PIR:S67495 huntingtin-associated protein HAP1-A - rat, N = 1, Score = 215, P = 1.6e-14

>PIR:S72555 huntingtin-associated protein HAP1 - human (fragment)
 Length = 320

HSPs:

Score = 234 (35.1 bits), Expect = 8.6e-19, P = 8.6e-19
 Identities = 66/189 (34%), Positives = 110/189 (58%)

```

Query: 109 EESEPEVCSTPLKRNE--SSSSVQNYFH---LDSLQKKLKDLEENNVVLRSEASQLKTE 163
      EE+E + C+ P + S ++ + H L++LQ+KL+ LEEEN LR EASQL T
Sbjct: 28 EEAEEDLQCAHPDAPKLISQEALLHQHCPQLEALQEKLRLLEENHQLREEASQLDT- 86

Query: 164 TITYEEKEQQLVNDVCVKELRDANVQIASISEELAKKTEDAARQOEIITHLLSQIVDLQKK 223
      E++EQ L+ +CV++ +A+ Q+A +SE L + E+ RQQ+E+ L +Q++ LQ++
Sbjct: 87 ---LEDEEQMLILECQEVSQSEASQMAELSEVLVLRLENYERQQQEVARLQAQVLKQQR 143

Query: 224 AKACAVENEELVQHLGAAKDAQRLTAEL--LRELEDKYAECE--MLHEAQEELKNL-RN 278
      + E E+L + L + K+ Q QL E L ++ AE + + + + + RN

```

Sbjct: 144 CRMYGAETEKLQKQLASEKEIQMLQEEETLPGFQETLAEELRTSLRRMISDPVYFMERN 203
 Query: 279 KTMP--NTTSRRY 289
 MP +T+S RY
 Sbjct: 204 YEMPRGDTSSLRY 216

Peptide information for frame 3

ORF from 1416 bp to 1874 bp; peptide length: 153
 Category: similarity to known protein
 Classification: unset

1 MSGVRSRGRR APPGSHDLET ALRRLSLRRE NYLSERRFFE EEQERKLQEL
 51 AEKGELRSGS LPTTESIMSL GTHSRFSEFT GFGMSFSSR SYLPEKLQIV
 101 KPLEGDHAGP RPLSVLLGDS LWSLIHLRKA GHLCHAYSFF FRDSHPRCWF
 151 EFL

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfd2_4c8, frame 3

TREMBL:AB011121_1 gene: "KIAA0549"; product: "KIAA0549 protein"; Homo sapiens mRNA for KIAA0549 protein, partial cds., N = 1, Score = 252, P = 5.5e-21

>TREMBL:AB011121_1 gene: "KIAA0549"; product: "KIAA0549 protein"; Homo sapiens mRNA for KIAA0549 protein, partial cds.
 Length = 469

HSPs:

Score = 252 (37.8 bits), Expect = 5.5e-21, P = 5.5e-21
 Identities = 57/98 (58%), Positives = 69/98 (70%)

Query: 8 GRRAPPGSHDLETALRRLSLRRENYLSERRFFEEEQERKLQELAEKGELRSGSLPTTESI 67
 G+ P G DL TAL RLSLRR+NYLSE++EE EE +RK+Q LA++ E SG +TPTES+
 Sbjct: 27 GQPGSGSDSLATALHRLSLRRQNYLSEKQFFAEWQRKIQLADQKEGVSGCVTPTESL 86
 Query: 68 MSLGTHSRFSEFTGFGMSFSSRSYLPEKLQIVKPLEG 105
 SL T SE T S S R ++PEKLQIVKPLEG
 Sbjct: 87 ASLCTTQ--SEITDLSSAS-CLRGFMPEKLQIVKPLEG 121

Pedant information for DKFZphfd2_4c8, frame 2

Report for DKFZphfd2_4c8.2

[LENGTH] 442
 [MW] 50020.14
 [pI] 4.77
 [HOMOL] TREMBL:AF040723_1 product: "neuroan1"; Homo sapiens neuroan1 mRNA, complete cds. 5e-29
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 5e-08
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YIL149c] 5e-08
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 5e-08
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YIL138c] 6e-08
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YGR130c] 2e-07
 [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 1e-06
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR356w] 1e-06
 [FUNCAT] 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1643] 1e-06
 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-06
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-06
 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 4e-06
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w] 4e-06
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YNL250w] 2e-05
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 2e-05

[FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL079c]
 5e-05
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YNL079c] 5e-05
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins
 [S. cerevisiae, YNL079c] 5e-05
 [FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YHR158c]
 1e-04
 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 1e-04
 [FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae,
 YNL272c] 3e-04
 [FUNCAT] 08.16 extracellular transport [S. cerevisiae, YNL272c] 3e-04
 [BLOCKS] BL01289B
 [BLOCKS] BL00415M Synapsins proteins
 [EC] 3.6.1.32 Myosin ATPase 2e-07
 [PIRKW] tandem repeat 2e-07
 [PIRKW] heterodimer 1e-06
 [PIRKW] endocytosis 9e-07
 [PIRKW] heart 1e-06
 [PIRKW] transmembrane protein 4e-07
 [PIRKW] zinc finger 9e-07
 [PIRKW] metal binding 9e-07
 [PIRKW] DNA binding 3e-06
 [PIRKW] muscle contraction 2e-07
 [PIRKW] acetylated amino end 3e-06
 [PIRKW] actin binding 2e-07
 [PIRKW] mitosis 1e-06
 [PIRKW] microtubule binding 1e-06
 [PIRKW] ATP 2e-07
 [PIRKW] chromosomal protein 1e-06
 [PIRKW] receptor 3e-08
 [PIRKW] thick filament 2e-07
 [PIRKW] phosphoprotein 8e-06
 [PIRKW] glycoprotein 3e-08
 [PIRKW] skeletal muscle 3e-06
 [PIRKW] DNA condensation 1e-06
 [PIRKW] alternative splicing 2e-06
 [PIRKW] coiled coil 2e-07
 [PIRKW] P-loop 2e-07
 [PIRKW] heptad repeat 4e-07
 [PIRKW] methylated amino acid 2e-07
 [PIRKW] peripheral membrane protein 9e-07
 [PIRKW] cardiac muscle 6e-06
 [PIRKW] hydrolase 2e-07
 [PIRKW] muscle 2e-06
 [PIRKW] cytoskeleton 2e-06
 [PIRKW] Golgi apparatus 4e-07
 [PIRKW] calmodulin binding 9e-07
 [SUPFAM] myosin motor domain homology 2e-07
 [SUPFAM] tropomyosin TPM1 2e-06
 [SUPFAM] giantin 4e-07
 [SUPFAM] protein kinase C zinc-binding repeat homology 2e-06
 [SUPFAM] human early endosome antigen 1 9e-07
 [SUPFAM] unassigned kinesin-related proteins 4e-07
 [SUPFAM] M5 protein 8e-08
 [SUPFAM] cytoskeletal keratin 3e-06
 [SUPFAM] myosin heavy chain 2e-07
 [SUPFAM] conserved hypothetical P115 protein 1e-06
 [SUPFAM] centromere protein E 1e-06
 [SUPFAM] pleckstrin repeat homology 2e-06
 [SUPFAM] kinesin motor domain homology 4e-07
 [PROSITE] LEUCINE_ZIPPER 1
 [KW] All_Alpha
 [KW] LOW_COMPLEXITY 6.79 %
 [KW] COILED_COIL 27.15 %

SEQ MQKFIEADYYELDWWYEECSVDLCAERVGQMTKTYNDIDAVTRLLEEKERDLELAARIGQ
 SEGxxxxxxxxxxxxxxxxxxxx
 PRD ccc
 COILSC

SEQ SLLKKNKTLTERNELLEQVEHIREEVSQRLHLSMKDELLQFYTSAAESEPESVCSTP
 SEG
 PRD hhh
 COILS ccc

SEQ LKRNESSSSVQNYFHLDSLQKKLKOLEEENVVLRSEASQLKTETITYEEKEQQLVNDVCVK
 SEG
 PRD hhh
 COILScc

DKFZphfkd2_4k14

group: intracellular transport and trafficking

DKFZphfkd2_4k14.3 encodes a novel 254 amino acid putative GTP-binding protein nearly identical to Rab6.

Rab proteins are members of the Ras superfamily of GTPases. Rab proteins are localised to the cytoplasmic side of organelles and vesicles involved in the secretory (biosynthetic) and endocytotic pathways in eukaryotic cells. Rab proteins direct the targeting and fusion of transport vesicles to their acceptor membranes.

rab6 is a ubiquitous ras-like GTPase involved in intra-Golgi transport.

The new protein can find application in modulating the transport of vesicles inside the Golgi apparatus.

strong similarity to Rab6

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 3084 bp

Poly A stretch at pos. 3061, polyadenylation signal at pos. 3043

```
1 GGGGCACTCA GCGAGTTGGG CTGCGGCGGC GCGGGCTGGG GAAGCCGAAG
51 CGCCGCGCGT GAGAGATCCC GGATACATCT GCGGTTTGGG CTCCGCCACC
101 CTCGCTCTCT CTCCCGCAGG TCTCTGAGCC GGCTGCGGAA GGAGGGAACG
151 GCCCTAGCCT TGGGAAGCCA AAGCACACCC CTGGCTCCCG CCGACACCCG
201 CCTCCTTCCC TTCCAGCCG CGGGCCTCGC TCCGTGCTCG GCTACTCTGC
251 CGGGAGGCGG CGGCGGCTGC CAGTCTGTGG CGAGCCCTGC TGCCCTCCAG
301 CCGGCTTCTT CCAGCCGGGC TCCTCCACCG GCCCTTGACG GGGCAGAGAG
351 AGCTCGGCGC CCGCCCTTCC GCTCGCCTTT TTCGTACGCC GGCTGGAGGA
401 GCATCGGTCC GGGAGGTCTC TGGGCTGAGG CGGCGACAGC TCCTCTAGTT
451 CCACCATGTC CGCGGGCGGA GACTTCGGGA ATCCGCTGAG GAAATTCAG
501 CTGGTGTTCG TGGGGGAGCA AAGCGTTGCA AAGACATCTT TGATCACCAG
551 ATTCAGGTAT GACAGTTTGT ACAACACCTA TCAGGCAATA ATTGGCATTG
601 ACTTTTTATC AAAAATATG TACTTGGAGG ATGGAACAAAT CGGGCTTCGG
651 CTGTGGGATA CGGCGGGTCA GGAACGTCTC CGTAGCCTCA TTCCAGGTA
701 CATCCGTGAT TCTGTGCAG CTGTAGTAGT TTACGATATC ACAAATGTTA
751 ACTCATTCCA GCAAATACA AAGTGGATTG ATGATGTGAG AACAGAAAGA
801 GGAAGTGATG TTATCATCAC GCTAGTAGGA AATAGAACAG ATCTTGCTGA
851 CAAGAGGCAA GTGTCAAGTT AGGAGGGAGA GAGGAAAGCC AAAGGGCTGA
901 ATGTTACGCT TATTGAAACT AGGGCAAAA CTGATACAA TCTAAAGCAG
951 CTCTTTCGAC GTGTAGCAGC AGCTTTGCCG GGAATGGAAA GCACACAGGA
1001 CGGAAGCAGA GAAGACATGA GTGACATAAA ACTGGAAGAG CCTCAGGAGC
1051 AAACAGTCAG CGAAGGGGGT TGTTCCTGCT ACTCTCCCAT GTCATCTTCA
1101 ACCCTTCCCT AGAAGCCCCC TTACTCTTTC ATTGACTGCA GTGTGAATAT
1151 TGGCTTGAAC CTTTCCCTT CATTAATAAC GTTTTGCAAT TCATCATTCG
1201 TGCTGTCTCT GTGGAGGTGA TCTATTAGCT TCACAAGCAC AAAAAAGTC
1251 AGCGTCTTCA TTATTTATAT TTTACAAAAA GCCAAATTAT TTCAGCATAT
1301 TCCGGTGATA ACTTTAAAAA TTAGATACAT TTTCTTAACA TTTTTTCTT
1351 TTTTAATGTT ATGATAATGT ACTTCAAAAT GATGGAAATC TCAACAGTAT
1401 GAGTATGGCT TGGTTAACGA GCAGTATGTT CACAGCCTGC TTTATCTCTC
1451 CTTGCTCTTC TCACCTCTCC CTTACCCCGT TCCCTATTTC CGTGTCTTCA
1501 CCTAGCCTCC CCCCCTCTCC TCAAAACAAA CAAGAGATGG CAAAGCAGCA
1551 GTCCGACCAA GCCCACTGGA ATTATCCTTT AATTTTACAG ATACCCTTG
1601 CTGTAGGCTG TGGACCAAGA TGTCAGAAAT TATTCTTGAG CACTGATGTA
1651 AATTACTTAG ATCTTCTTTG AGTTCAGAA TCAGCGATCA CGGTAGGCAG
1701 TGCTTGAATG AGAAAAGCCT CCTGGTGCAT CTTCAAAATG AGTCCTAAAG
1751 AACATACTGA GTACTTATAA GTAGCAGAAC ATAAATGTA TTTCTGACTA
1801 ACACAAATGG TCCTTTCACA TGTGCTTTAT TAGACTCTGG GAGAGAAAAG
1851 TAACCAAGTG CTTCAGAACA GGTTTTTAGT ATTTACTTCT TCATGGTAAG
1901 ATAATGAAGT TCTAATGAAC TATTTCTCCC AAGGTTTTAA AATTGTCAAG
1951 AGTTATTCTG TTTGTTTAAA AAGTAAGAAA CCTCTGTAAG CAATAGATT
2001 TGCTTGGGTT TTCTTCTTAA AAAAAATAAT ACTATGCAGG CAAGACACCA
2051 TAAAAGTTTA ATTCCTTACA GAAGAACCAG TGGAAAGATT TAAATTTGGC
2101 ACTACGATCA AAACCTACTG ATTAGCAGAA ATAACGATAT CTAAGCTTAA
2151 CCAGCAAAAG AACCTCTCAG AGAATAGCAA AAACCTTGCT CAGGACATTT
2201 GAGGTCAAAT TGAAGACGGA AGACGGAAAC CGGAAACCGT TTTCTGTAA
2251 GCGGCTAGAG CGAGATCAGG TAAGCATACA TAGTAGAGGG AAAGGAGAGA
2301 ATGGAAATAA AACTGAATAT TATGCAGATT TATGCCTTAT TTTTATGAT
2351 TTTTAAAGGT TGGGTCTTTC AGGCTGGTTT TGGTTTGTAT TAGATCTGTA
2401 TAGTTTAGTG ATTTAGTTTT ATATTTAAGC TACGATTAAT ATTTTTCTT
2451 TGGCGATATT TCTTTGCTTT TTTTTTTTAA CAACTTTCCA TTTTATAGT
```

```

2501 TTTCGTTGAA TCTATTTAGA GCTTCACCAT GGCAATATGT ATTTCCCTTA
2551 AAACACTGCA AACAAATATA CTAGGAGTGT GCCCTTTTAA TCTTTACTAG
2601 TTATTGTGAG ACTGCTGTGT AAGCTAATAA ACACATTTGT AAAAACATTG
2651 TTTGCAGGAA GAAAACTTCG AGTTACAGGT CAGGAAAAGC CTGCTGAATT
2701 TATGTTGTAA ACGTTACTTA ACACAGTATA AAGATGAAAA GACAACAAAA
2751 GTATCTTCAT ACTTCCTCAT CCCCTCATTG CAACAAAACC TTAAACTGGG
2801 AGAACCTTAG TCCCCTCTCT TTCCTCTTCC TCCTCCACTT CCCACTTATT
2851 GCCACTTGT AATATTCAGA GAGCACTTGG ATTATGGATC TGAATAGAGA
2901 AATGCTTACA GATAATCATT AGCCACATA CCAGTAACTT ATACTTAAAG
2951 ATGGGATGGA GTTATAAAGT GCTTTTATAA TCCAATATAA TTGCTAAAGG
3001 CAAGGGTTGA CTCTTTGTTT TATTTTGACA TGGCATGTCC TGAAATAAAT
3051 ATTGGTTCAC TATGAAAAAA AAAAAAAAAA AAAA

```

BLAST Results

No BLAST result

Medline entries

98382468:

Rab proteins.

97203146:

GTP-bound forms of rab6 induce the redistribution of Golgi proteins into the endoplasmic reticulum.

Peptide information for frame 3

ORF from 456 bp to 1217 bp; peptide length: 254

Category: strong similarity to known protein

Classification: unset

Prosites motifs: BACTERIAL_OPSIN_RET (45-57)

```

1 MSAGGDFGNP LRFKFLVFLG EQSVAKTSLI TRFRYDSFDN TYQAIIGIDF
51 LSKTMYLEDG TIGLRLWDTA GQERLRLSLIP RYIRDSAAA VVYDITNVNS
101 FQOTTKWIDD VTERGSDVI ITLVGNRTDL ADKROVSVEE GERKAKGLNV
151 TFIETRAKTG YNVKQLFRRV AAALPGMEST QDGSREDMSD IKLEKPQEQT
201 VSEGGCSCYS PMSSTLPQK PPYSFIDCSV NIGLNLFP SL ITFCNSSLLP
251 VSWR

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4k14, frame 3

PIR:G34323 GTP-binding protein Rab6 - human, N = 1, Score = 944, P = 6.5e-95

TREMBL:CET25G12_2 gene: "T25G12.4"; Caenorhabditis elegans cosmid T25G12., N = 1, Score = 756, P = 5.4e-75

TREMBL:NTNTRAF_1 gene: "Nt-rab6"; Nicotiana tabacum SR1 Nt-rab6 mRNA, complete cds., N = 1, Score = 698, P = 7.6e-69

TREMBL:D84314_1 product: "rab6"; Drosophila melanogaster mRNA for rab6, complete cds., N = 1, Score = 836, P = 1.9e-83

PIR:T01588 small GTP-binding protein F16B22.10 - Arabidopsis thaliana, N = 1, Score = 704, P = 1.8e-69

>PIR:G34323 GTP-binding protein Rab6 - human
Length = 208

HSPs:

Score = 944 (141.6 bits), Expect = 6.5e-95, P = 6.5e-95
Identities = 186/208 (89%), Positives = 190/208 (91%)

Query: 1 MSAGGDFGNPLRKFKLVFLGEQSVAKTSLITRFYDSFDNTYQAIIGIDFLSKTMYLEDG 60
MS GGDFGNPLRKFKLVFLGEQSV KTSITRF YDSFDNTYQA IGIDFLSKTMYLED
Sbjct: 1 MSTGGDFGNPLRKFKLVFLGEQSVGKTSITRFYDSFDNTYQATIGIDFLSKTMYLED 60

Query: 61 TIGLRLWDTAGQERLRSILIPRYIRDSAAAVVVYDITNVNSFQQTWKWIDDVTERGSDVI 120
T+ L+LWDTAGQER RSLIP YIRDS AVVVYDITNVNSFQQTWKWIDDVTERGSDVI
Sbjct: 61 TVRLQLWDTAGQERFSLIPSYIRDSAVVVYDITNVNSFQQTWKWIDDVTERGSDVI 120

Query: 121 ITLVGNRTDLADKRQVSVEEGERKAKGLNVTFIETRAKTGYNVKQLFRRVAAALPGMEST 180
I LVGN+TDLADKRQVS+EEGERKAK LNV FIET AK GYNVQLFRRVAAALPGMEST
Sbjct: 121 IMLVGNKTDLADKRQVSIIEGERKAKELNVMTFIETSAKAGYNVQLFRRVAAALPGMEST 180

Query: 181 QDGSREDMSDIKLEKPOEQTVSEGGCSC 208
QD SREDM DIKLEKPOEQ VSEGGCSC
Sbjct: 181 QDRSREDMIDIKLEKPOEQPVSEGGCSC 208

Pedant information for DKFZphfd2_4k14, frame 3

Report for DKFZphfd2_4k14.3

[LENGTH] 254
[MW] 28385.29
[pI] 7.58
[HOMOL] PIR:G34323 GTP-binding protein Rab6 - human 1e-102
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YLR262c]
7e-60
[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YLR262c] 7e-60
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae,
YOR089c] 2e-33
[FUNCAT] 08.19 cellular import [S. cerevisiae, YOR089c] 2e-33
[FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YOR089c] 2e-33
[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YOR089c]
2e-33
[FUNCAT] 09.09 biogenesis of intracellular transport vesicles [S. cerevisiae,
YGL210w] 3e-28
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YFL005w] 8e-27
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL005w]
8e-27
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YOR101w]
2e-21
[FUNCAT] 11.10 cell death [S. cerevisiae, YOR101w] 2e-21
[FUNCAT] 01.03.13 regulation of nucleotide metabolism [S. cerevisiae, YOR101w]
2e-21
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR101w] 2e-21
[FUNCAT] 03.99 other cell growth, cell division and dna synthesis activities [S.
cerevisiae, YOR101w] 2e-21
[FUNCAT] 10.04.07 g-proteins [S. cerevisiae, YOR101w] 2e-21
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YNL098c] 6e-19
[FUNCAT] 11.01 stress response [S. cerevisiae, YNL098c] 6e-19
[FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YNL098c] 6e-19
[FUNCAT] 04.07 rna transport [S. cerevisiae, YOR185c] 6e-16
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YOR185c] 6e-16
[FUNCAT] 08.01 nuclear transport [S. cerevisiae, YOR185c] 6e-16
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YPR165w] 4e-13
[FUNCAT] 10.02.07 g-proteins [S. cerevisiae, YPR165w] 4e-13
[FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YCR027c] 2e-09
[FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YLR229c] 8e-08
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins
[S. cerevisiae, YLR229c] 8e-08
[FUNCAT] 03.01 cell growth [S. cerevisiae, YNL180c] 1e-05
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YOR094w] 5e-05
[BLOCKS] BL01115A GTP-binding nuclear protein ran proteins
[SCOP] dlas3_2 3.29.1.4.12 Transducin (alpha subunit), insertion domain 1e-32
[SCOP] dlmh1_ 3.29.1.4.2 Rac1 [Human (Homo sapiens)] 2e-51
[SCOP] d5p21_ 3.29.1.4.1 cH-p21 Ras protein [human (Homo sapiens)] 7e-53
[SCOP] dlhura_ 3.29.1.4.8 ADP-ribosylation factor 1 (ARF1) [human (Homo sapiens)] 1e-46
[SCOP] dla2kc_ 3.29.1.4.5 Ran Nuclear transport factor-2 (NTF2) [Do 6e-60
nucleus 2e-14
[PIRKW] cell cycle control 5e-15
[PIRKW] membrane trafficking 3e-71
[PIRKW] endoplasmic reticulum 1e-29
[PIRKW] phosphoprotein 1e-29
[PIRKW] prenylated cysteine 2e-36
[PIRKW] signal transduction 5e-15
[PIRKW] transforming protein 5e-30
[PIRKW] purine nucleotide binding 1e-28
[PIRKW] alternative splicing 1e-18
[PIRKW] P-loop 3e-71

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[PIRKW]      lipoprotein 2e-36
[PIRKW]      proto-oncogene 1e-20
[PIRKW]      methylated carboxyl end 1e-20
[PIRKW]      membrane protein 1e-29
[PIRKW]      GTP binding 3e-71
[PIRKW]      thiolester bond 1e-29
[PIRKW]      Golgi apparatus 1e-29
[SUPFAM]     ras transforming protein 1e-76
[PROSITE]    BACTERIAL_OPSIN_RET 1
[PFAM]       Ras family (contains ATP/GTP binding P-loop)
[KW]         Alpha_Beta
[KW]         3D

```

```

SEQ      MSAGGDFGNPLRKFKLVFLGEQSVAKTSLITRFRYDSFDNTYQAIIGIDFLSKTMYLEDG
lkao-    .....CEECEEEECTTTTCHHHHHHHHHHCCCCCTTTTC-EEEEEEEEETTE

SEQ      TIGLRLWDTAGQERLRLSLIPRYIRDSAAAVVYDITNVNSFQOTTKWIDDVTERGSDVI
lkao-    EEEEEEEECTTTTCHHHHHHHHHHCCCEEEEEETTTHHHHHHHHHHHHHHHHTTTCCC

SEQ      ITLVGNRTDLADKRQVSVEEGERKAKGLNVTFTIETRAKTGYNVKQLFRRVAAALPGMEST
lkao-    EEEEEETTTTGGGCCCHHHHHHHHHHCCCEEEECTTTTHHHHHHHHHHH.....

SEQ      QDGSREDMSDIKLEKPOEQTVSEGGCSCYSPMSSSTLPQKPPYSFIDCSVNIGLNLFPSL
lkao-    .....

SEQ      ITFCNSSLLPVSWR
lkao-    .....

```

Prosites for DKFZphfd2_4k14.3

```

PS00327      45->57  BACTERIAL_OPSIN_RET  PDOC00291

```

Pfam for DKFZphfd2_4k14.3

```

HMM_NAME      Ras family (contains ATP/GTP binding P-loop)

HMM            *KLVIGDSGVGKSCLLIRFTQNeFnEeYIPTIGvDFYtKTIIDGKtIK
Query          15  KLVFLGEQSVAKTSLITRFRYDSFDNTYQAIIGIDFLSKTMYLEDGTIG      63

HMM            LQIWDTAGQERYRsMRPMYYRGAMGFMVYDITNRqSFENIrNWweEIrR
Query          64  LRLWDTAGQERLRLSLIPRYIRDSAAAVVYDITNVNSFQOTTKWIDDVRT      113

HMM            HCDrDENVPIMLVGNKCDLEDQROVStEEGQeFAREWGAIPFMETSAKTN
Query          114  ERG--SDVIITLVGNRTDLADKRQVSVEEGERKAKGLN-VTFIETRAKTG      160

HMM            iNVEEAFMEIvReIlqrMqe.q.NgteNinidQpsrnrk...rCCCIM*
Query          161  YNVKQLFRRVAAALPGMESTODGSREDMSDIKLEKPOEQTVSEGGCS-C      208

```

DKFZphfkd2_4m11

group: transmembrane protein

DKFZphfbr2-4m11 encodes a novel 159 amino acid protein with weak similarity to the putative membrane protein YMR034c of *S. cerevisiae*.

The novel protein contains 4 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of kidney-specific genes and as a new marker of neuronal cells.

weak similarity to YMR034c

complete cDNA, complete cds, no EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1749 bp

Poly A stretch at pos. 1727, polyadenylation signal at pos. 1713

```
1 GGGGTCCTCA AAGCCGCCGG AGCAACCCCC AGGTCTTTAC TTTACAATCG
51 GCAATTTGAC TTGCTCTGCT GCATGCTCTGG AGGGACCAAG GAAAGTGTGG
101 AGACGCTCCA AGGATTAGGT GATCGGAGCT TGAAAAGAAA AAAAGCCAAA
151 CAAATAACA AAACCCACCC ACCCTAACGA ATATGAGGCT GCTGGAGAGA
201 ATGAGGAAAG ACTGGTTCAT GGTCCGAATA GTGCTGGCGA TCGCTGGAGC
251 TAAACTGGAC CCGTCCATAG GGTGAATCG GCGACCACTG AAGCCAGAAA
301 TAACTGTATC CTACATTGCT GTTGCAACAA TATTCTTTAA CAGTGGACTA
351 TCATTGAAAA CAGAGGAGCT GACCACTGCT TTGGTGCATC TAAAACTGCA
401 TCTTTTATT CAGATCTTTA CTCTTGCATT CTCCACAGCA ACAATATGGC
451 TTTTCTTCA GCTTTTATCA ATCACACCCA TCAACGAATG GCTTTTAAAA
501 GGTTCGAGA CAGTAGGTTG CATGCCTCCG CCTGTGTCTT CTGCAGTGAT
551 TTTAACCAAG GCAGTTGGTG GAAATGAGGC AGCTGCAATA TTTAATTCAG
601 CTTTGGGAAG TTTTGGGTA AGTAAACATA GTTAACTTG TCTATTACAA
651 CTTTGTCTGT GATATTGTGT ATATGAAAGA TTTAGTGAAA GCTGGATTG
701 TTTTACTCTT TGGTTAAGTA TAAAAATTGT TGAATCTTTT CATGTGCCAG
751 TATCCATACC CTGAAGAAAA GTAGTTAATG AATAAAGCAA ATGTTCTCTT
801 ACAATATATT TTGGAGGTTT GGATTTTAAA ATTCCATTTA ATGAATTCAA
851 GGAATCAATT AAAACACTAT GTGTCTCCTT ATAGAGGTTA TGTCATATATA
901 TTGATCATTT AATGACGTCT TTTAGATTAT TATTATTTTG TATCATGGGA
951 CTGAGGATTT TGAAAAGGAA ACATGACCCA GCTGGTCAGA AAGGGAATGC
1001 TAATTTACTT GTTGACATGC CATTATTTT GTACATTTCA CTGTCAAAGA
1051 AGCTACTGGC TTGGATGCTT CTGAGAAATC TATGTGAGAA AAAATTTGAA
1101 AGGAAGATAT GACTAATGAG TAATTGCAA GTAAATGTTG TATCTATATA
1151 TATATATATA TAAAGATTCA AAAGTAGTTC AGCTTTCATA AGTAGAACCA
1201 ATATAAGGAC GTTGTTTTAG CATTTTTAAAT CATTATTTT AAATAAATGA
1251 TGTAACAGAG GCTTGATTTG TGTTATGAAA GATTGAGAAA CTAAATTTTC
1301 TGTTGATTTA ATTTTGTGT GCCTTAAAC TTTGTAAAT TCCTGAAGTT
1351 AATTATCATA TTGTACTTTT TGGGGCATAA CTCATTAGCA GATATGTAGT
1401 GCAGTGATTT ACAATAAAT GAGAGTAAAA TCAGTGATGT ATAACTAGT
1451 TCATGAGTCT AGGTAAAATA TCAATTACCT CTGTTTAAAA TGCTCTGTTA
1501 ATTATTATTG TATGTATTTA AATGTAGTTA AAGCTTTTAA ACATGTTGTT
1551 ACATAGTGTT AATTCTACAC AGTGCTACAC AGCTTTTAGT GTCACATAGC
1601 CTTACAGAGT TTATAATGAT GTAGCATCTG CAAAATATAT GCATAGCTTA
1651 TATCCTATTT TTATAGAGCC AGTAATGGTT TTTGTGATGC TGTATTACTT
1701 CTGGGTTTGA GACAATAAAG TCTGTTTAAC AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

```

1  MRLLERMARD  WFMVGIVLAI  AGAKLEPSIG  VNGGPKLPEI  TVSYIAVATI
51 FFNSGLSLKT  EELTSALVHL  KHLHFIQIFT  LAFFPATIWL  FLQLLSITPI
101 NEWLLKGLQT  VGCMPPPVS   AVILTAVGG  NEAAAFNSA  FGSFLVSKHS
151 LTCLLQLLL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4ml1, frame 3

PIR:A65015 yfeH protein - Escherichia coli (strain K-12), N = 1, Score = 131, P = 4.2e-08

```
>PIR:S53951 probable membrane protein YMR034c - yeast (Saccharomyces
cerevisiae)
Length = 434
```

HSPs :

Score = 171 (25.7 bits), Expect = 3.2e-12, P = 3.2e-12
Identities = 38/144 (26%), Positives = 72/144 (50%)

```

Query:      5  EPMRKDWFMVGIVLAIAGAKLEPSIGVNGGPLKPEITVSYIAVATIFFNSGLSLKTEELT 64
             E ++  WF + + + I A+ P+  +GG +K + ++ Y VA IF  SGL +K+  L
Sbjct:     18  EFLKSQWFFICLAILIARFANFADGGGLIKQYSIGYGCVAIFLQSGGLGMKSRSLM 77

Query:     65  SALVHLKLHLFIQIFTLAFFPATIWLF---LQLLSITPINEWLLKGLQTVGCMPPPVSSA 121
             + +++ + H  I + +      + ++ F  ++ +      I++W+L GL      P  V+S
Sbjct:     78  ANMLNWRHAHATILVLSFLITSSIVYGCCAVKAANDPKIDDWVLIGLILTATCPTTVASN 137

Query:    122  VILTKA VGGNEAAAFNSAFGSFL 145
             VI+T      GGN      +      G+ L
Sbjct:    138  VIMTTNAGGNSLLCVCEVFIGNLL 161

```

Pedant information for DKFZphfk2_4m11, frame 3

Report for DKFZphfkd2_4m11.3

```

[LENGTH]      159
[MW]           17282.92
[pI]           9.06
[HOMOL]        PIR:S53951 probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae)
5e-12
[FUNCAT]       99 unclassified proteins          [S. cerevisiae, YMR034c] 2e-13
[PROSITE]      MYRISTYL      2
[PROSITE]      PKC_PHOSPHO_SITE      1
[KW]           TRANSMEMBRANE  4

```

```
SEQ      MRLLERMRKDWFMVGIVLAIAGAKLEPSIGVNGGPKPEITVSYIAVATIFNSGLSLKT
PRD      cccchhhhhhhhhhhhhhhhhhhhhcccceccccccccceeeeeccccccccccchhhh
MEM      . . . . . MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM . . . . .

SEQ      ELTALSALVHLKLHFLFIQIFTLAFFPATIWLQLLSITPINEWLLKGLQTVCMPPPVSS
PRD      hhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhcccchhhhhhhhhheeecccccccc
MEM      . . . . . MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM . . . . .

SEQ      AVILTKAVGGNEAAAFNFAFGSFLVSKHSLTCLLQLLL
PRD      ceeeeeccccchhhhhhhhhcccceecceeeeeeeccccc
MEM      . . . . . MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM
```

Prosites for DKFZphfkd2 4m11.3

PS00005	57->60	PKC_PHOSPHO_SITE	PDOC00005
PS00008	15->21	MYRISTYL	PDOC00008
PS00008	129->135	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfk2 4m11.3)

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DKFZphutel_17k7

group: uterus derived

DKFZphutel_17k7 encodes a novel 520 amino acid protein with weak similarity to *S. Cerevisiae* Fipl.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

similarity to *S.cerevisiae* Fipl

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 1914 bp

Poly A stretch at pos. 1897, polyadenylation signal at pos. 1867

```
1 CGGACGCGTG GCGGGACGCG TGGGGCCTTC CTGGGATTGG AGTCTCGAGC
51 TTTCTTCGTT CGTTCGCCGG CGGGTTCGCG CCCTTCTCGC GCCTCGGGGC
101 TGCGAGGCTG GGAAGGGGT TGGAGGGGGC TGTGATCGC CGCGTTAAG
151 TTGCGCTCGG GCGGCCATG TCGGCCGCG AGGTCGAGCG CCTAGTGTCG
201 GAGCTGAGCG GCGGGACCGG AGGGGATGAG GAGGAAGAGT GGCTCTATGG
251 CGATGAAAAT GAAGTTGAAA GGCCAGAAGA AGAAAATGCC AGTGCTAATC
301 CTCCATCTGG AATTGAAGAT GAAACTGCTG AAAATGGTGT ACCAAAACCG
351 AAAGTGACTG AGACCGAAGA TGATAGTGAT AGTGACAGCG ATGATGATGA
401 AGATGATGTT CATGTCACTA TAGGAGACAT TAAACGGGA GCACCACAGT
451 ATGGGAGTTA TGGTACAGCA CCTGTAAATC TTAACATCAA GACAGGGGGA
501 AGAGTTTATG GAACTACAGG GACAAAAGTC AAAGGAGTAG ACCTTGATGC
551 ACCTGGAAGC ATTAATGGAG TTCCACTCTT AGAGGTAGAT TTGGATTCTT
601 TTGAAGATAA ACCATGGCGT AAACCTGGTG CTGATCTTTC TGATTATTTT
651 AATTATGGGT TTAATGAAGA TACCTGGAAA GCTTACTGTG AAAAAACAAA
701 GAGGATACGA ATGGGACTTG AAGTTATACC AGTAACCTCT ACTACAAATA
751 AAATTACGGT ACAGCAGGGA AGAACTGGAA ACTCAGAGAA AGAACTGCC
801 CTTCCATCTA CAAAAGCTGA GTTACTTCT CCTCCTTCTT TGTTCAGAC
851 TGGGCTTCCA CCGAGCAGGA GATTACCTGG GGCAATTGAT GTTATCGGTC
901 AGACTATAAC TATCAGCCGA GTAGAAGGCA GCGGACGGGC AAATGAGAAC
951 AGCAACATAC AGGTCCTTTC TGAAAGATCT GCTACTGAAG TAGACAACAA
1001 TTTTAGCAAA CCACCTCCGT TTTCCCTCC AGGAGCTCCT CCCACTCACC
1051 TTCCACCTCC TCCATTTCTT CCACCTCCTC CGACTGTCAG CACTGCTCCA
1101 CCTCTGATTC CACCACCGGG TTTCTCTCCT CCACCAGGCG CTCCACCTCC
1151 ATCTCTTATA CCAACAATAG AAAGTGGACA TTCTCTGGT TATGATAGTC
1201 GTTCTGCACG TGCATTTCCA TATGGCAATG TTGCCTTTCC CCATCTTCCT
1251 GGTCTGCTC CTTCGTGGCC TAGTCTTGTG GACACCAGCA AGCAGTGGGA
1301 CTATTATGCC AGAAGAGAGA AAGACCGAGA TAGAGAGAGA GACAGAGACA
1351 GAGAGCGAGA CCGTGATCGG GACAGAGAAA GAGAACGCAC CAGAGAGACA
1401 GAGAGGGAGC GTGATCACAG TCCTACACCA AGTGTTTCA ACAGCGATGA
1451 AGAACGATAC AGATACAGGG AATATGCAGA AAGAGGTTAT GAGCGTCACA
1501 GAGCAAGTCG AGAAAAAGAA GAACGACATA GAGAAAGACG ACACAGGGAG
1551 AAAGAGGAAA CCAGACATAA GTCTTCTCGA AGTAATAGTA GACGTCGCCA
1601 TGAAAGTGAA GAAGGAGATA GTCACAGGAG ACACAAACAC AAAAAATCTA
1651 AAAGAAGCAA AGAAGGAAAA GAAGCGGGCA GTGAGCCTGC CCTGAACAG
1701 GAGAGCACC GAGCTACACC TGCAGAATAG GCATGGTTT GGCCTTTTGT
1751 GTATATTAGT ACCAGAAGTA GATACTATAA ATCTTGTTAT TTTCTGGAT
1801 AATGTTTAAG AAATTTACCT TAAATCTTGT TCTGTTTGT AGTATGAAAA
1851 GTTAACTTTT TTTCCAAAAT AAAAGAGTGA ATTTTTCATG TTAAGTTAAA
1901 AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

100 200 300 400 500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 3500 3600 3700 3800 3900 4000 4100 4200 4300 4400 4500 4600 4700 4800 4900 5000 5100 5200 5300 5400 5500 5600 5700 5800 5900 6000 6100 6200 6300 6400 6500 6600 6700 6800 6900 7000 7100 7200 7300 7400 7500 7600 7700 7800 7900 8000 8100 8200 8300 8400 8500 8600 8700 8800 8900 9000 9100 9200 9300 9400 9500 9600 9700 9800 9900 10000

ORF from 168 bp to 1727 bp; peptide length: 520
Category: similarity to known protein

1	MSAGEVERLV	SELSSGGTGGD	EEEEWLYGDE	NEVERPEEEN	ASANPPSGIE
51	DETAENVGPK	PKVTEDEDS	DDSDDDDEDD	VHVTIGDIKT	GALDQSYSGT
101	APVNLNKTG	GRVYGTGTGK	GVGVLDADPG	SINGVPLLEV	LDPDSFEDPK
151	RKPGADLSDY	FNYGFNEDTW	KAYCEKQKRI	RMGLEVIPVT	STTNKITVQQ
201	GRTGNSEKET	ALPSTKAEFT	SPPSLFKTLG	KPSRRLPGA	DVIGQITQIS
251	RVEGRRRANE	NSNIQVLRS	SATERVDNFS	PPPPFFPPAI	PPTHLPPIPP
301	LPPPPVTSTA	PPLIPPPGPF	PPPGAPPDYL	IPTIESGHSS	GYDSRSARAF
351	PYGNVAFPHL	RGSAPOWPSL	VDTSKQWDYR	ARREKDRRE	RDRDRERDRD
401	RDRERERTRE	PERERDHSV	PSVNSDEER	YRYREYAERG	YERHRASREK
451	EEHRHRERRH	EKEETHRKS	RSNSRRRHES	EEGDSHRRHK	HKKSRSKSEG
501	KEAGSEPAPE	OESTEATPAE			

BLASTP hits

Entry AF016427.4 from database TREMBL:
gene: "F32D1.9"; *Caenorhabditis elegans* cosmid F32D1.
Score = 392, P = 1.8e-36, identities = 156/519, positives = 212/519

Entry S62454 from database PIR:
hypothetical protein SPAC22G7.10 - fission yeast (Schizosaccharomyces pombe)
Score = 246, E = 2.0e-22, identities = 62/163, positives = 91/163

Entry A56545 from database PIR:
FIP1 protein - yeast (*Saccharomyces cerevisiae*)
Score = 186. P = 2.9e-16. identities = 56/206. positives = 92/206

Alert BLASTP hits for DKFZphut1 17k7, frame 3

TREMBLNEW:AF109907_1 product: "S164"; Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.. N = 2. Score = 236. P = 1.5e-16

```
>TREMBLNEW:AF109907_1 product: "S164"; Homo sapiens S164 gene, partial cds;  
PS1 and hypothetical protein genes, complete cds; and S171 gene, partial  
cds
```

Length = 735

HSPs :

Score = 236 (35.4 bits), Expect = 1.5e-16, Sum P(2) = 1.5e-16
Identities = 51/120 (42%), Positives = 76/120 (63%)

Query: 383 REKDRDRERDRDRERDRDRDRERERTREERERERDHSPTSPVFSNDEERYRYREYA---ER 439
REK+++RER+R+R+RDRDR +ER+R R+RER+RD S + + + + R RE + ER
Sbjct: 227 REKEKERERERERDRDRDRDKTEKERERDRDRDRDRDRDRERSS-DRNKDRSRSREKS RDRER 285

Query: 440 GYERHRASREKEERHRRER-RHREKEETRHKKSSRSNSRRRHESEEGDSHRRHKHKKSRSK 498
ER R + ER RER R RE+E R + + + R E+E D+ + R K ++ R K
Sbjct: 286 EREREREREREREREREREREREREKERERKKDRDEEDAYERRKLRLKREK 345

Query: 499 E 499
E
Sbjct: 346 E 346

Score = 214 (32.1 bits), -Expect = 4.4e-14, Sum P(2) = 4.4e-14
Identities = 50/133 (37%), Positives = 75/133 (56%)

Query: 383 REKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTSPVFN-DEERYRYREYAERG 440
RE++R+R ER+R+RCR+R+R++E+ER RERER+RD T D ER R R+ ER
Sbjct: 208 RERERERERERERERERERERERERERERERDRDRTKERDRDRERDRDR-RERS 266

Query: 441 YERHRASREKEERHRRERHREKEETRHKSSRSNSRRRHESEEGDSHRRHKHKKSRSKEG 500
+R++ E+ R+R RE+E R + R R R E + R + ++ K K
Sbjct: 267 SDRNKDRSRSREKRDRE-REERERERER-REEREREREREREREREREKDKKR 324

```
Query: 501 KEAGSEPAPEQESTE 515
      +E E A E+ E
Spict: 325 REEDEEDAYERRKLE 339
```

Score = 214 (32.1 bits), Expect = 4.4e-14, Sum P(2) = 4.4e-14
Identities = 55/141 (39%), Positives = 80/141 (56%)

Query: 383 REKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPSVENS-DEERYRYREYAERG 440
RE++R+R ER+R+RER+R+R++E+ER RERER+RD T D ER R R+ ER
Sbjct: 208 REREREREREREREREREREKEKEKERERERERDRDRDRTKERDRDRDRERDRDRD-RERS 266

Query: 441 YERHR-ASREKEE-RHRER-RHREKEETRHKSSRSNSRRRHESEEGDSHRRHKHKKSRS 497
+R++ SR +E+ R RER R RE+E R + R E E R K K K R
Sbjct: 267 SDRNKDRSRSREKSRDREREREREREREREREREREREREREREREKDKKRDRE 326

Query: 498 KEGKEAGSEPAPEQESTATPA 519
++ ++A E++ E A
Sbjct: 327 EDEEDAYERKKLERKLEKEAA 348

Score = 210 (31.5 bits), Expect = 1.2e-13, Sum P(2) = 1.2e-13
Identities = 59/142 (41%), Positives = 78/142 (54%)

Query: 383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVENS---DEERYRYREYAER 439
RE++RDR+RDR +ERDRDRDRER+R R+RER D + S D ER R RE ER
Sbjct: 235 RERERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKDRSRSREKSRDRERERERE-RER 293

Query: 440 GYERHRA-SREKE-ERHRER-RHREKEETRHKSS-----RSNSRRRHESEEGDSHRRH 489
ER R RE+E ER RER R REK++ R + R R+ +E R
Sbjct: 294 EREREREREREREREREREREREREKDKKRDREDEEDAYERKKLERKLEKEAAYQERL 353

Query: 490 KHKKSRSKEGKEAGSEPAPEQE 512
K+ + + K+ +E E E+E
Sbjct: 354 KNWEIRERKKTREYEKEAEREEE 376

Score = 205 (30.8 bits), Expect = 4.4e-13, Sum P(2) = 4.4e-13
Identities = 59/149 (39%), Positives = 83/149 (55%)

Query: 372 DTSKQWDYYARREKDRDR--ERDRDRERDRDRDRERERTRERERERDHSPTPSVENSDEE 429
+ K+ + R++DRDR ERDRDR+R+RDRDR+RER+ +R ++R S S D E
Sbjct: 228 EKEKERERERERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKDRSRSREKS---RDRE 284

Query: 430 RYRYREYAERG YERHRA-SREKE-ERHRER-RHREKEETRHKSS-----RSNSRRRHE 479
R R RE ER ER R RE+E ER RER R REK++ R + R R+
Sbjct: 285 RERERE-REREREREREREREREREREREREREKDKKRDREDEEDAYERKKLERKLR 343

Query: 480 SEEGDSHRRHKHKKSRSKEGKEAGSEPAPEQE 512
+E R K+ + + K+ +E E E+E
Sbjct: 344 EKEAAYQERLKNWEIRERKKTREYEKEAEREEE 376

Score = 202 (30.3 bits), Expect = 9.6e-13, Sum P(2) = 9.6e-13
Identities = 49/117 (41%), Positives = 70/117 (59%)

Query: 383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVENSDEERYRYREYAERGYE 442
REK RDRER+R+RER+R+R+RERER RERERER+ D++R R E E YE
Sbjct: 277 REKSRDRER-EKDKKDR-EEDEEDAYE 334

Query: 443 RHRSREKEERHRERRHREKEETRHKSSRSNSRR-RHESEEGDSHRRHKHKKSRSKE 499
R + E++ R +E ++E+ + R +R E+E + RR K++KR KE
Sbjct: 335 RRKL--ERKLEKEAAYQERLKNWEIRERKKTREYEKEAEREERREMAKEAKRLKE 390

Score = 183 (27.5 bits), Expect = 1.2e-10, Sum P(2) = 1.2e-10
Identities = 52/141 (36%), Positives = 79/141 (56%)

Query: 372 DTSKQWDYY-ARREKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPSVENSDEE 429
DT K+ + ++EK+R E++R RER+R+R+RERER RERERER+ ++E
Sbjct: 178 DTHKKLEEEKGKKKEKERQEIEKER-RERERERERERER-RERERERERER-----EREKE 230

Query: 430 RYRYREYAERG YERHRASREKEERHRER---RHREKEETRHKSSRSNSRRRHESEEGDSH 486
+ R RE ER +R R +R RER R RE+ R+K RS SR + E +
Sbjct: 231 KERERE-RERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKO-RSRSREKSRDRERERE 288

Query: 487 RRHKHKKSRSKEGKEAGSEPAPEQE 512
R + +++ + +E E E+E
Sbjct: 289 RERERERERERERERERERERERERE 314

Score = 171 (25.7 bits), Expect = 2.5e-09, Sum P(2) = 2.5e-09
Identities = 49/150 (32%), Positives = 78/150 (52%)

Query: 383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVENSDEERYRYREYAERGYE 442
RE++R+RER+R+RER+R+R+RERER RERERER+ +E+ Y R+ + E
Sbjct: 285 REREREREREREREREREREREREREREREREREREKDKKRDREDEEDAYERKKLERKLE 344

Query: 443 RHRSREK-----EERHRERRH---EKEETRHKSSRSNSRRRHESEEGDSHRRH-KH 491
+ A +E+ ER + R + E+EE R + ++R E E+ D R K+
Sbjct: 345 KEAAYQERLKNWEIRERKKTREYEKEAEREERREMAKEAKRLKEFLEDYDDDRDDPKY 404

Identities = 25/73 (34%), Positives = 33/73 (45%)

Query: 428 EERYRYREYAERGERHRASREKE-ERHRERRHREKEETRHKSSRSNSRRRHESEEGDSH 486
 EE +E + E+R RE+E ER RERR RE+E R + R E E
 Sbjct: 184 EEEKGKKEKERQEIEKERREREREREREREREREREREREREKEKERERERERDRDR 243

Query: 487 RRHKHKKSKRSKE 499

R K + R +E
 Sbjct: 244 DRTKERDRDRDRE 256

Score = 105 (15.8 bits), Expect = 3.1e-02, Sum P(2) = 3.1e-02

Identities = 31/87 (35%), Positives = 45/87 (51%)

Query: 382 RREKDRDRERDRDRDRDRDRER-ERTREERERERDHSPTPSVFNSEERYRYREYAERG 440

+R +DR++E + D ERDR R++E E R+R H P P D E R + AER
 Sbjct: 412 KRLRDREKEMEAD-ERDRKREKEELEIRQRLLAEGH-PDP-----DAELQRMQEQAERR 464

Query: 441 YERHRASREKEERHRERRHREKEETRHK 468

+ + +E E E +EKEE R +
 Sbjct: 465 -RQPQIKQEPESEEEEEEKQEKEEKREE 491

Score = 46 (6.9 bits), Expect = 1.5e-16, Sum P(2) = 1.5e-16

Identities = 13/49 (26%), Positives = 21/49 (42%)

Query: 54 AENGVPKPKVTETEDSDSDSDDDDDVHVTIGDIKTGAPQYGSYGTAP 102

A NG +P+ +D+ D + D + G I+ +Y S AP
 Sbjct: 70 ASNGNARPETVTNDDDEALDEETKRDRQMIK-GAIEVLIREYSSELNAP 117

Score = 46 (6.9 bits), Expect = 1.8e-04, Sum P(2) = 1.8e-04

Identities = 14/53 (26%), Positives = 21/53 (39%)

Query: 30 ENEVERPEEENASANPPSGIEDETAENGVPKPKVTETEDSDSDSDDDDDVH 82

+ E ER E E E E + + E E D D ++DE+D +
 Sbjct: 282 DREREREREREREREREREREREREREREREREREKDKKRDREDEEDAY 333

Score = 44 (6.6 bits), Expect = 2.0e-13, Sum P(2) = 2.0e-13

Identities = 13/60 (21%), Positives = 21/60 (35%)

Query: 20 DEEEEWLYGDENEVERPEEENASANPPSGIEDETAENGVPKPKVTETEDSDSDSDDDDED 79

++E + + + E ER E + E K + E E D D D + D
 Sbjct: 191 EKERQEIEKERREREREREREREREREREREREREKEKERERERERDRDRDRTKERD 250

Pedant information for DKFZphutel_17k7, frame 3

Report for DKFZphutel_17k7.3

[LENGTH] 520
 [MW] 58375.30
 [pI] 5.41
 [HOMOL] PIR:S62454 hypothetical protein SPAC22G7.10 - fission yeast
 (Schizosaccharomyces pombe) 3e-18
 [FUNCAT] 04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S.
 cerevisiae, YJR093c] 2e-13
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YJR093c] 2e-13
 [PROSITE] MYRISTYL 9
 [PROSITE] AMIDATION 1
 [PROSITE] CK2_PHOSPHO_SITE 18
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 12
 [PROSITE] ASN_GLYCOSYLATION 2
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 35.00 %

SEQ MSAGEVERLVSELGGTGGDEEEEWLYGDENEVERPEEENASANPPSGIEDETAENGVPK
 SEGXXXXXXXXXXXXXXXXXXXX
 PRD cccchhhhhhhhhcc

SEQ PKVTETEDSDSDSDDDDDVHVTIGDIKTGAPQYGSYGTAPVNLNIKTGGRVYGTGTGK
 SEGXXXXXXXXXXXXXXXXXXXX
 PRD cceeecc

SEQ VKGVDLDAPGSINGVPLLEVLDLSFEDKPWRKPGADLSDFNYGFNEDTWKAYCEKQKRI
 SEG
 PRD ceecc

SEQ RMGLEVIPVTSTTNKITVQGRGTGNSEKETALPSTKAEFTSPPSLFKTGLPPSRRLPGAI
 SEG
 PRD ccc

Prosites for DKFZphut1_17k7.3

(No Pfam data available for DKFZphut1_17k7.3)

DKFZphutel_18c12

group: uterus derived

DKFZphutel_18c12 encodes a novel 378 amino acid protein nearly identical to human WUGSC:H_DJ0872F07.1 protein.

The novel protein has an additional N-terminal domain, which is not present in WUGSC:H_DJ0872F07.1.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

nearly identical to human WUGSC:H_DJ0872F07.1 protein

on genomic level encoded by AC004537, 10 exons the predicted protein sequence AC004537_1 is only partially o.k. first exon wasn't predicted there are additional exons predicted (BLASTX/EST-BLAST shows that the cDNA is only partly spliced) intron -1216-3540/-3577-5059

Sequenced by AGOWA

Locus: map="7q31"

Insert length: 6005 bp

Poly A stretch at pos. 5980, polyadenylation signal at pos. 5968

```
1 AGCGGGTGCT GCTAGCGGAG GCGCCATATT GGAGGGGACA AAACCTCCGGC
51 GACAGCGAGT GACACAAATA AACCCCTGGA CCCCTTGTT CCCTCAGCTC
101 TAAGGGCCGC GATGTTGTAC CTAGAAGACT ATCTGGAAAT GATTGAGCAG
151 CTCCTATGG ATCTGCGGGA CCGCTTCACG GAAATGCGCG AGATGGACCT
201 GCAAGTGCAG AATGCAATGG ATCAACTAGA ACAAAGAGTC AGTGAATTCT
251 TTATGAATGC AAAGAAAAAT AAACCTGAGT GGAGGGAAGA GCAATGGCA
301 TCCATCAAAA AAGACTACTA TAAAGCTTTG GAAGATGCAG ATGACAAGGT
351 TCAGTTGGCA AACCAAGATAT ATGACTTGGT AGATCGACAC TTGAGAAAAGC
401 TGGATCAGGA ACTGGCTAAG TTTAAATAGG AGCTGGAAGC TGATAATGCT
451 GGAATTACAG AAATATTAGA GAGGCGATCT TTGGAATTAG ACACCTCCTTC
501 ACAGCCAGTG AACAAATCACC ATGCTCATTG ACATACTCCA GTGGAAAAAAA
551 GGAATATATA TCCAACTTCT CACCATACGA CAACAGATCA TATTCCTGAA
601 AAGAAATTTA AATCTGAAGC TCTTCTATCC ACCCTACGT CAGATGCCCT
651 TAAGGAAAT ACACAGGTT GTCGAATAA TAATCCACA GCCTCTTCTA
701 ACAATGCCTA CAATGTGAAT TCCTCCCAAC CTCTGGGATC CTATAACATT
751 GGCTCGTTAT CATTAGGAAC TGGTGCAGGG GCAATTACCA TGGCAGCTGC
801 TCAAGCAGTT CAGGCTACAG CTCAGATGAA GGAGGGACGA AGAACATCAA
851 GTTTAAAAGC CAGTTATGAA GCATTTAAGA ATAATGACTT TCAGTTGGGA
901 AAAGAATTTT CAATGGCCAG GGAACAGTT GGCTATTCAT CATCTTCGGC
951 ACTTATGACA ACATTAACAC AGAATGCCAG TTCATCAGCA GCCGACTCAC
1001 GGAGTGGTCG AAAGAGCAAA AACAAACAAC AGTCTTCAAG CCAGCAGTCA
1051 TCATCTTCCT CCTCCTCTTC TTCTTATCA TCGTGTCTT CATCATCAAC
1101 TGTTGTACAA GAAATCTCTC AACAAACAAC TGTAGTGCCA GAATCTGATT
1151 CAAATAGTCA GGTGATTGG ACTTACGACC CAAATGAACC TCGATACTGC
1201 ATTTGTAATC AGGTAAAAGT CTGTTATATC TATAAAAAGTA TAATCTGAAT
1251 AAAC TAGAAG GAAGAGAACT ATTTCAATTT TAAGCACTTT TTTAAACTCA
1301 CTTAAAATAC CTTTGCTTTA TTTGTATACT TTTCTCCCC TTCTTACAAA
1351 AGTGACATTT GCTGTAAAATA CTGAGTATAA AGAAAAATGT TACCCATAAT
1401 CCTAGCCCTC AGATACAACC TGTAACATAA CATTTTGGT ATACCACTAC
1451 CATATACCTC ATGTGCACAT TGGCTGCCTT AATAAAATAC AACAGACTGG
1501 GTAGCTTAAA CAACAGAAAA TAATTTCTCT ACAGGTATGA AGGCTGGGAA
1551 GTCCAAGATC AAGGTGTCCA CTGACTCAGT TCTGGAGGAG GGCTCCCTTC
1601 CTAGATGGAG ACTGCTGCCT TCTACCGGG TCCTCACATG ATAGAGGGAG
1651 AAAGAGTGTG CTCTGGTGTC TTTTCTTATA AGGGCACCAG CCTTGTGAGA
1701 GTAGGACCCC ACTCTATGAC CTCATTTAAC CTTTACCACC TCCTCACAGG
1751 CCCTGTTTCC AATTATAGTC ACGTTGGGGG TTAGGCTTC AACATATGAT
1801 TTTGAGACAT AAGCTTGCAT TTCATAACAC GTGTCTATGC AGATTGACAC
1851 ATGCATGTGT GTATAAGTTT GTCAGTAGGA ACCACAGTGT ATACTTTCTT
1901 GTTACTGGCT ATTTTCTCTA AATCAGGTAT ACCGAACATG ATTTTCTTTT
1951 AAGATCATAT TTTTAATTTT CACATAGTTA TCTCTTATGC CATCCAGTGT
2001 AGTTTCTTTA ACCAATACCT AGCTATAGAT TATATTAGTG GTTTTAATTT
2051 GTTTGAAATT AAGGATAATA TTACGATAGG CATTTTTTAA ATGTAATCCA
2101 TTTTATACAT CTAATTTCTT GGATAATCTT TTAGAAATAA AATTAGGCTG
2151 TAAATATTTG ACAGACACCA AAATATATTT TCTAGAAATT TATTACCAAA
2201 AATTAAATAA CATACCGGTT TACTAAACCC TGTCCAACAC TGGATATTAT
2251 TTTCTTTTAA AAAC TAAGTA CCAATTTGGT AGTTTATAT TATGATTGTT
2301 TTAATACAC TAGTATTATT GAAGTTGGAC ATTTTGTGAC CATTTTGTGTT
2351 TTTTACATTA TGAATCGACT CTAATGGTG TCGGCTGATT TTTCTATTGT
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2401 TTTTGGTTATG TACTCTAAAT ATTTGCTTGA TTTAGTTTTT TAAAAATAAT
2451 TCTAAAAATT TAATTTTATG TAGTTATGAC TGTTAATTTT TTTTATGAA
2501 GCAAGCCATG GATTATATAC TTAGAAGGGC TTTCTCTTTG GCTCTTCTTT
2551 CTACAAAAAA TTGTCTTGTA TAATATTTTC TCCTAGTTTT TATATGGTTT
2601 TGTCTAGTTC TTTGCATGCT TCAGTTTCTT CACATTTAAG ACTTAGTCTA
2651 TCAGCAGATT ATTTGTGCTA ACAGTATGAG TTGCCAGTCT GATTTTTTAA
2701 AATTTTAAACA ATTTGTTAGC TGTTCACATA TCACCCGATA AACATTTTTC
2751 AGTACAAATG ATAGAAAAAGC ATATCCTGTA TCCTGACAAC AAAAGTAGAT
2801 TACTTGCAAA AGAACAAAAT CAGACTGAAC CTAGAGTTTT CCTCTGTAAC
2851 ACTAAAAAAC TAGAAGGTGA TGGAAATATG CTGTAGAGCT TTCAGGGA
2901 AATTAAAGAG CCCCAAAAAC TTGATATTCA GAGAAGTTAT TTCTCTGCAT
2951 AGGACCATGT AAATATATTT TCACCTCATG AGAGAATCAG AAGATATGCC
3001 ATCTAGTTAA TCCTGTCTGA AAAATTATTC AATCCACTGA GAACTTCAGT
3051 GAACTCAAGA ATTAGCAAGT TATGCCCTAA AGTGCTGGTG ATGAAGAGCA
3101 AAAGAAAAAT GAGAAAGGAC ATAAATAGA TAAGTTTAGA AGTTTCAAGG
3151 AAGGAGACTA TTAATTGCAA AAATATATAT GACCTAATGT GACCCAAGAA
3201 GTAAAAAATT TCAGTAAGTA AATAATCAAG AAAGGAACCT AAAATTTTAA
3251 CAATAAGAAC TACCCAGAAA GATGACTCCT TCATCCGGGT GATTTATATG
3301 TCAAGTTCTT CCAGACTTCT GAAGGGCAGA TAATCTCTGT GCATTTCTTC
3351 CCACCCTTGC CCCACCCTGC CCAAAAGAGT ATTTCAGGAA AAAATTATTA
3401 TACCTTGATT CTCAATGTAA TTGTATATTC AGTGATTTTC CCTTTATTTT
3451 CCAGCAGTAT CATACATAAA CAGTTAATTG GTATCTAGGT GTTGTGTTACA
3501 TAGTCATAAT AAAGACATTT AATTTTTTTT AACTAGGTAT CTTATGGTGA
3551 GATGGTGGGA TGTGATAACC AAGATGTAAG TATTACATTT TTCTATTTAG
3601 GAATGAAAAA AATCACAGGT TGTATTACT TGAATATTG TCTTATTTGC
3651 TGTATGGTTT GGTCTAAGAA AACAGGTTTG CAGGTATATT AGTTATGTGA
3701 TGCTAATGCT AGAATATTTCC TCTTCAAAAT AGGGTAGTGT CCCTTAATGT
3751 GTTCCCTATT TTAATTTTAA AAGCTAATTT TATGGTTTTA TGTGCAGATT
3801 GTCTCAGAAG TGTATGTTG TATGAAAATT ATAAATACCC TCCTTTCCCT
3851 TTAATAAAAA ATACTGTGTT TACTAGAATC CAGTTTATTT ATCACATTGA
3901 AGAAATGGAA TTTTAAAAACA ATTCATTCTT TCAGGCTGCA CCGTGCTAAA
3951 GTGAAGGGTG GGATAATTGA GGATCTAATG TGAGATTATC TTCTCTCAT
4001 GAGTATAATA TTTTTCCTG TACTCTGCAG GTGTCAGCTG ATAAGAGCCA
4051 CCCTGATCTT AAAAAGTAAA GGAAATTTGA AAGGAAGGAA TTCTTGTTT
4101 TTAGGAGACT TAATTTTAGT TAGAGATACG TTTTATTATC AATACTGAGA
4151 ATATTGTTGT CTAGTAATTT TGAATTTTCT CTTATTTAGT AGTGACAGGA
4201 TCTTAAGATT AACAAAGAGT TTAATTTTGT AAAACAATCT GAAGATTGAG
4251 GGAGCTGGGT AGGTGCATTA AAATGTGTAC TTTTCTTAGA CCTGATAGGG
4301 TTACAGCAAC ATGCTCACGT AGATTGGGAC AGAGCTCTCT TCTGTTTCCC
4351 TGTCTAGAAT CCCTTGTAGG CTGTTTGTTG TTGTTGCAAA AACAATATTG
4401 CCCAACCATT TCAAGAACAT CACTGTAAAC TCTTCTGGGG CAGTTAGTGA
4451 AAATGATGAA TGAGATTTCT ATGAGTACCA GCATCATGCT TCTCTGATC
4501 TTCTTATTTCC CAGTTGTGCT CTTCTGAGTG CTAAGACTTT CATGAAAGAG
4551 TTTTCTGCTT AATATGTTTC AAAGAGGAAT AATTTTCTC TACATTTCAA
4601 GGAATGGAAG CACCCACGTA GGAAATGCAG GGCATAAGAC ATAAATTAAT
4651 GTCTTTAATT ACAATCAGCT TATTTCTACT TATGAGACAG CAAATAAGGC
4701 TGACTATTAA ATAAATCTT AAGTTATATT TACCTTCTAC ATAGAAGATT
4751 CATCCCACTT CTTTGTGCC TTGAAAGCTG AAAACTAGTG AATTTTCATT
4801 CATTAGGATG AGGGGACTAG ATTACATGGA CCTCAGGATT CTTGAAGATG
4851 CATAATTTTT CTGTGCCCTC ATTTCCCTCAT TCCTGAAGCT TATCATTTAG
4901 TCTAAATGAT GTCTAAATAA TCTAGATCTA AAAATTCTGA TGTACACAT
4951 CTAATTATTG TTAATTTAAA TGGATTATTC AGTCTCCTGA GCATATTTTA
5001 ATATACTCTC TTGTCTTCAG AAGTACTGAA AACTTGTTTT TTGCAATTTT
5051 GCTTCTTAGT GCCCTATAGA ATGGTTCCAT TATGGCTGCG TTGGATTGAC
5101 AGAGGCACCA AAAGGCAAAT GGTACTGTCC ACAGTGCATC GCTGCAATGA
5151 AGAGAAGAGG CAGCAGACAC AAATAAAGGT GGTCTTTTG TTTGATGAAG
5201 AAATAAACTT CAGCTGAAGA TTTTATATAG GACTTTAAAA AGAAGAGAAG
5251 AGAAGAAGAA AACAATGCAT TTCCAGGCAA CCACTTAAAG GATTACATA
5301 GACAATCCTA TAAGATCTTG AACTTGAATT TTATGGGTTG TATTTAATA
5351 ATGTAAGTAA ATTATTTATG CACTCTGGT GTGCTATGAA TATTATTCCA
5401 GTTAGCCTTG GATTATTTCA GTGGCCAACA TATGCAGACA TTTGTAATCC
5451 TCAACCATTT TCTCAAAGTA ATGGGCATT TATGATTAG ACTTCAAGGA
5501 ATTCCAATGA TGAAGATTTT AAGGAAAGTA TTTTATATTC AACACGTATA
5551 TTCTGCTGCA TGTACTGTAC TCCAGAGCTG TTATGTAACA CTGTATATAA
5601 ATGGTTGCAA AAAAAAAGAA AAGTCAGTGC TTCTAAAAAG AATTTAAGAT
5651 AATGGTTTTT AAAATGCCTT TATAATAAGC TTTGTTTCTT TGTGAACTA
5701 ATTCAGCAGG CTGAAGGAAA TGGTTCATGT GATAATGTGG GCTGGTATCC
5751 TCTAGAGTAC CTGGGTACAT AAACAGAAAC TCCTGTAGGT AAAAAGTAAT
5801 TTGTGCCATT AGTCTTCTA TGTCTCTGCA TCCAGATAGA GTGCAGTTCA
5851 TGAGGGAGGG GGGGGGGGAC TGAAGGGGAA AGGGCGTTAA AGTGATACAT
5901 TTTTATACCA AATGTGTTTA TTTTGTGTG CAAGTAATCC TTAATAATGC
5951 AATTGTATTA GGTGTTAAAA TAAAGTTTTT AAAAAATTA AAAAAAAGAA
6001 AAAAA
```

BLAST Results

Entry HSG20547 from database EMBL:
HSG20547| human STS A005W09.
Length = 154

Minus Strand HSPs:
 Score = 770 (115.5 bits), Expect = 2.9e-26, P = 2.9e-26
 Identities = 154/154 (100%)

Medline entries

98101645:
 The candidate tumour suppressor p33ING1 cooperates with p53 in cell growth control.

Peptide information for frame 1

ORF from 112 bp to 1245 bp; peptide length: 378
 Category: similarity to known protein

```

1  MLYLEDYLEM IEQLPMDLRD RFTEMREMDL QVQNAMDQLE QRVSEFFMNA
51 KKNKPEWREE QMASIKKDYI KALEDADEKV QLANQIYDLV DRHLRKLDQE
101 LAKFKMELEA DNAGITEILE RRSLELDTPS QPVNNHHAHS HTPVEKRKYN
151 PTSHTTTTDH IPEKKFKSEA LLSTLTSDAS KENTLGCRNN NSTASSNNAY
201 NVNSSQPLGS YNIGSLSSGT GAGAITMAAA QAVQATAQMK EGRTSSLKA
251 SYEAFKNNDF QLGKEFSMAR ETVGYSSSSA LMTTLTQNAS SSAADSRSGR
301 KSKNNKSSSS QSSSSSSSSS SLSSCSSSST VVQEISQOTT VVPESDSNSQ
351 VDWTYDPNEP RYCICNQKV CYIYKSII

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BLASTP hits

Entry AF044076_1 from database TREMBL:
 "ING1"; product: "candidate tumor suppressor p33ING1"; Homo sapiens candidate tumor suppressor p33ING1 (ING1) mRNA, complete cds. Homo sapiens (human)
 Length = 279
 Score = 162 (57.0 bits), Expect = 1.1e-09, P = 1.1e-09
 Identities = 48/183 (26%), Positives = 92/183 (50%)

Entry AC004537_1 from database TREMBL:
 gene: "WUGSC:H_DJ0872F07.1"; Homo sapiens PAC clone DJ0872F07 from 7q31, complete sequence.
 Score = 1814, P = 3.7e-187, identities = 358/358, positives = 358/358

Entry CEY51H1A_1 from database TREMBL:
 gene: "Y51H1A.4"; Caenorhabditis elegans cosmid Y51H1A
 Score = 213, P = 3.7e-15, identities = 37/123, positives = 82/123

Alert BLASTP hits for DKFZphut1_18c12, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphut1_18c12, frame 1

Report for DKFZphut1_18c12.1

```

[LENGTH]      378
[MW]           42275.72
[pI]           5.72
[HOMOL]        TREMBL:AC004537_1 gene: "WUGSC:H_DJ0872F07.1"; Homo sapiens PAC clone DJ0872F07
from 7q31, complete sequence. 1e-157
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YHR090c] 8e-05
[FUNCAT]       04.05.01.04 transcriptional control [S. cerevisiae, YNL097c] 2e-04
[PROSITE]      MYRISTYL 3
[PROSITE]      AMIDATION 2
[PROSITE]      CAMP_PHOSPHO_SITE 1
[PROSITE]      CK2_PHOSPHO_SITE 4
[PROSITE]      PROKAR_LIPOPROTEIN 1
[PROSITE]      GLYCOSAMINOGLYCAN 1
[PROSITE]      PKC_PHOSPHO_SITE 3
[PROSITE]      ASN_GLYCOSYLATION 5
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY 20.63 %

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Prosite for DKFZphute1 18c12.1

(No Pfam data available for DKFZphutel 18c12.1)

DKFZphutel_18i19

group: transcription factors

DKFZphutel_18i19 encodes a novel 759 amino acid protein with similarity to the SREBP-2 mutant sterol regulatory element binding protein-2 of *Cricetulus griseus*.

The SREBP-2 protein is embedded in the membranes of the nucleus and endoplasmic reticulum. In cholesterol-depleted cells the proteins are cleaved to release soluble NH₂-terminal fragments that enter the nucleus and activate genes encoding the low density lipoprotein receptor and enzymes of cholesterol synthesis. The new protein is a putative transcription factor capable of protein-protein interaction via a lim domain and additionally shows similarity to the common sunflower transcription factor SF3.

The new protein can find application in modulating/blocking the expression of genes involved in lipid metabolism.

similarity to transcription factor SF3

complete cDNA, complete cds, EST hits
strong similarity to mutated SREBP-2 of hamster,
similarity is not to SREP-2 part of protein but to the unknown part of
the fusion protein

Sequenced by AGOWA

Locus: /map=12

Insert length: 3664 bp

Poly A stretch at pos. 3647, polyadenylation signal at pos. 3636

```
1 GCGCTAGGTA GAGCGCCGGG ACCTGTGACA GGGCTGGTAG CAGCGCAGAG
51 GAAAGGCGGC TTTTAGCCAG GTATTTTCAGT GTCTGTAGAC AAGATGGAAT
101 CATCTCCATT TAATAGACGG CAATGGACCT CACTATCATT GAGGGAACA
151 GCCAAAGAAC TTTCTCTGT CAACAAGAAC AAGTCATCGG CTATTGTGGA
201 AATATTCTCC AAGTACCAGA AAGCAGCTGA AGAAACAAAC ATGGAGAAGA
251 AGAGAAGTAA CACCGAAAA CTCTCCAGC ACTTTAGAAA GGGGACCCTG
301 ACTGTGTTAA AGAAGAAGTG GGAGAACCCA GGGCTGGGAG CAGAGTCTCA
351 CACAGACTCT CTACGGAACA GCAGCACTGA GATTAGGCAC AGAGCAGACC
401 ATCCTCCTGC TGAAGTGACA AGCCACGCTG CTCTGGAGC CAAAGCTGAC
451 CAAGAAGAAC AATCCACCC CAGATCTAGA CTCAGGTCAC CTCCTGAAGC
501 CCTCGTTTCA GGTGATATC CCCACATCAA GGACGGTGAG GATCTTAAAG
551 ACCACTCAAC AGAAAGTAAA AAAATGGAAA ATTGTCTAGG AGAATCCAGG
601 CATGAAGTAG AAAATCAGA AATCAGTGAA AACACAGATG CTCGGGGCAA
651 AATAGAGAAA TATAATGTTT CGCTGAACAG GCTTAAGATG ATGTTTGAGA
701 AAGGTGAACC AACTCAAAC AAGATTCTCC GGGCCCAAAG CCGAAGTGCA
751 AGTGAAGGA AGATCTCTGA AAACAGCTAT TCTCTAGATG ACCTGGAAT
801 AGGCCCAGGT CAGTTGTCTT CTCTACATT TGACTCGGAG AAAATGAGA
851 GTAGACGAAA TCTGGAACCT CCACGCCCTC CAGAAACCTC TATAAAGGAT
901 CGAATGGCCA AGTACCAGGC AGCTGTGTCC AAACAAAGCA GCTCAACCAA
951 CTATACAAAT GAGCTGAAAG CCAGTGGTGG CGAAATCAA ATTCTATAAA
1001 TGGAGCAAAA GGAGAAATGT CCCCAGGTC CTGAGGTCG CATCACCCAT
1051 CAGGAAGGGG AAAAGATTTC TGCAAATGAG AATAGCCTGG CAGTCCGTTC
1101 CACCCCTGCC GAAGATGACT CCCGTGACTC CCAGGTTAAG AGTGAGGTTT
1151 AACAGCCTGT CCATCCCAAG CCCTAAGTC CAGATTCCAG AGCCTCCAGT
1201 CTTTCTGAAA GTTCTCCTCC CAAAGCAATG AAGAAGTTT AGGCACCTGC
1251 AAGAGAGACC TGCGTGGAA GTGAGAAGAC AGTCTATCCA ATGGAGCGTC
1301 TCTTGGCCAA CAGCAGGTTG TTTACATCA GCTGCTCCG TTGCTCCTAT
1351 TGTAACAACA AACTCAGTCT AGGAACATAT GCATCTTTAC ATGGAAGAAT
1401 CTATTGTAAG CCTCACTTCA ATCAACTCTT TAAATCTAAG GGCAACTATG
1451 ATGAAGGCTT TGGGCACAGA CCACACAAGG ATCTATGGGC AAGCAAAAAT
1501 GAAAACGAAG AGATTTTGGG GAGACCAGCC CAGCTTGCAA ATGCAAGGGA
1551 GACCCCTCAC AGCCGAGGGG TAGAAGATGC CCCTATTGCT AAGGTGGGTG
1601 TCCTGGCTGC AAGTATGGAA GCCAAGGCCT CCTCTCAGCA GGAGAAGGAA
1651 GACAAGCCAG CTGAAACCAA GAAGCTGAGG ATCGCCTGGC CACCCCCCAC
1701 TGAACCTTGA AGTTCAAGGA GTGCCCTTGA GGAAGGGATC AAAATGTCAA
1751 AGCCCAATG GCCTCCTGAA GACGAAATCA GCAAGCCCGA AGTTCCTGAG
1801 GATGTGATC TAGATCTGAA GAAGCTAAGA CGATCTTCTT CACTGAAGGA
1851 AAGAAAGCCG CCATTCACCTG TAGCAGCTTC ATTTCAAAGC ACCTCTGTCA
1901 AGAGCCCAAA AACTGTGTCC CCACCTATCA GGAAGGGCTG GAGCATGTCA
1951 GAGCAGAGTG AAGAGTCTGT GGGTGGGAAG GTTGCAAAA GGAACAAGT
2001 GGAAAATGCC AAGGCTTCTA AGAAGAATGG GAATGTGGGA AAAACAACCT
2051 GGCAAAACAA AGAATCTAAA GGAGAGACAG GGAAGAGAAG TAAGGAAGGT
2101 CATAGTTTGG AGATGGAGAA TGAGAATCTT GTAGAAAATG GTGCAGACTC
2151 CGATGAAGAT GATAACAGCT TCCTCAAACA ACAATCTCCA CAAGAACCCA
2201 AGTCTCTGAA TTGGTCGAGT TTTGTAGACA ACACCTTTGC TGAAGAATTC
2251 ACTACTCAGA ATCAGAAATC CCAGGATGTG GAACTCTGGG AGGGAGAAGT
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2301 GGTCAAAGAG CTCTCTGTGG AAGAACAGAT AAAGAGAAAT CGGTATTATG
2351 ATGAGGATGA GGATGAAGAG TGACAAATG CAATGATGCT GGGCCTTAAA
2401 TTCATGTTAG TGTTAGCGAG CCACTGCCCT TTGTCAAAT GTGATGCACA
2451 TAAGCAGGTA TCCCAGCATG AAATGTAATT TACTTGGAAG TAACCTTGGA
2501 AAAGAATTCC TTCTTAAAT CAAAAACAAA AAAAAAAC AAAAAACA
2551 CATTCTAAAT ACTAGAGATA ACTTTACTTA AATTCTTCAT TTTAGCAGTG
2601 ATGATATGCG TAAGTGCTGT AAGGCTTGTA ACTGGGAAA TATCCACCT
2651 GATAATAGCC CAGATTCTAC TGTATCCCA AAAGGCAATA TTAAGGTAGA
2701 TAGATGATTA GTAGTATATT GTTACACACT ATTTTGAAT TAGAGAACAT
2751 ACAGAAGGAA TTAGGGGCT TAAACATTAC GACTGAATGC ACTTTAGTAT
2801 AAAGGGCACA GTTTGTATAT TTTTAAATGA ATACCAATTT AATTTTTTAG
2851 TATTTACCTG TTAAGAGATT ATTTAGTCTT TAAATTTTT AGGTAAATTT
2901 TCTTGCTGTG ATATATATGA GGAATTTACT ACTTTATGTC CTGCTCTCTA
2951 AACTACATCC TGAACGAC GTCTGAGGT ATAATACAAC AGAGCACTTT
3001 TTGAGGCAAT TGAAAAACCA ACCTACACTC TTCGGTGCTT AGAGAGATCT
3051 GCTGTCTCC AAATAAGCTT TTGTATCTGC CAGTGAATTT ACTGTACTCC
3101 AAATGATTGC TTTCTTTCT GGTGATATCT GTGCTTCTCA TAATTACTGA
3151 AAGCTGCAAT ATTTTAGTAA TACCTTCGGG ATCACTGTCC CCCATCTTCC
3201 GTGTTAGAGC AAAGTGAAGA GTTTAAAGGA GGAAGAAGAA AGAACTGTCT
3251 TACACCACTT GAGCTCAGAC CTCTAAACCC TGTATTTCCC TTATGATGTC
3301 CCCTTTTGA GACACTAATT TTTAAATACT TACTAGTCT GAAATATATT
3351 GATTTTATC ACAGTATTCT CAGGGTGAAA TTAACCAAC TATAGGCCTT
3401 TTTCTTGGA TGATTTTCTA GTCTTAAGGT TTGGGGACAT TATAAACTTG
3451 AGTACATTTG TTGTACACAG TTGATATTCC AAATTGTATG GATGGGAGG
3501 AGAGGTGCTT TAAGCTGTAG GCTTTTCTTT GTACTGCATT TATAGAGATT
3551 TAGCTTAAAT ATTTTTFAGA GATGTAAAAC ATTCTGCTTT CTTAGTCTTA
3601 CCTAGTCTGA AACATTTTTA TTCAATAAAG ATTTTAATTA AAATTTGAAA
3651 AAAAAAAAAA AAAA

```

BLAST Results

Entry HS512217 from database EMBL:

human STS SHGC-14654.

Length = 250

Minus Strand HSPs:

Score = 1202 (180.3 bits), Expect = 1.8e-46, P = 1.8e-46

Identities = 242/244 (99%)

Medline entries

95263566:

Three different rearrangements in a single intron truncate sterol regulatory element binding protein-2 and produce sterol-resistant phenotype in three cell lines. Role of introns in protein evolution.

93258417:

Characterization of a pollen-specific cDNA from sunflower encoding a zinc finger protein.

Peptide information for frame 1

ORF from 94 bp to 2370 bp; peptide length: 759

Category: similarity to known protein

```

1 MESSPFNRRQ WTSLSLRVTA KESLVNKNK SSAIVEIFSK YQKAAEETNM
51 EKKRSNTENL SQHFRKGLT VLKKKWENPG LGAESHTDSL RNSSTEIRHR
101 ADHPPAEVTS HAASGAKADQ EEQIHPRSR LSPPEALVQG RYPHIKDGED
151 LKDHSTESKK MENCLGESRH EVEKSEISEN TDASGKIEKY NVPLNRLKMM
201 FEKGEPTQTK ILRAQSRAS GRKISENSYS LDDLEIGPGQ LSSSTFDSEK
251 NESRRNLELP RLSETSIKDR MAKYQAAVSK QSSSTNYTNE LKASGGEIKI
301 HKMEQKENVP PGPEVCITHQ EGEKISANEN SLAVRSTPAE DDSRDSQVKS
351 EVQQPVHPKP LSPDSRASSL SESSPPKAMK KFAQAPARETC VECQKTVYPM
401 ERLLANQQVF HISCFCRSYC NNKLSLGYA SLHGRIYCKP HFNQLFKSKG
451 NYDEGFGHRP HKDLWASKNE NEEILERPAQ LANARETPHS PGVEDAPIAK
501 VGVLAASMEA KASSOQEKED KPAETKKLRI AWPPPTLGS SGSALEEGIK
551 MSKPKWPPED EISKPEVPED VDLDLKKLRR SSSLKERSRP FTVAASFQST
601 SVKSPKTVSP PIRKGWMSSE QSEESVGGRV AERKQVENAK ASKKNNGNVGK
651 TTWQNKESKG ETGKRSKEGH SLEMENENLV ENGADSDDED NSFLKQSQSQ
701 EPKSLNWSSF VDNTFAEEFT TQNKQSQDVE LWEGEVVKEL SVEEQIKRNR

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751 YYDEDEDEE

BLASTP hits

Entry CG22818_1 from database TREMBL:
 "SREBP-2"; product: "mutant sterol regulatory element binding protein-2"; Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds. Cricetulus griseus (Chinese hamster)
 Length = 839
 Score = 1502 (528.7 bits), Expect = 3.9e-154, P = 3.9e-154
 Identities = 290/380 (76%), Positives = 322/380 (84%)

Entry S28507 from database PIR:
 transcription factor SF3 - common sunflower
 Length = 219
 Score = 212 (74.6 bits), Expect = 6.3e-18, Sum P(2) = 6.3e-18
 Identities = 36/82 (43%), Positives = 55/82 (67%)

Entry NTLIMDOM_1 from database TREMBL:
 "SF3"; product: "LIM-domain SF3 protein"; N.tabacum mRNA for LIM-domain protein Nicotiana tabacum (common tobacco)
 Length = 189
 Score = 216 (76.0 bits), Expect = 1.0e-16, P = 1.0e-16
 Identities = 42/94 (44%), Positives = 57/94 (60%)

Alert BLASTP hits for DKFZphut1_18i19, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphut1_18i19, frame 1

Report for DKFZphut1_18i19.1

[LENGTH] 759
 [MW] 85225.57
 [pI] 6.41
 [HOMOL] TREMBL:CG22818_1 gene: "SREBP-2"; product: "mutant sterol regulatory element binding protein-2"; Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds. 1e-151
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR257w] 3e-05
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YGR162w TIF4631 - mRNA cap-binding protein] 1e-04
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YGR162w TIF4631 - mRNA cap-binding protein] 1e-04
 [BLOCKS] BL00478B
 [PIRKW] zinc finger 9e-16
 [PIRKW] DNA binding 9e-16
 [SUPFAM] LIM metal-binding repeat homology 9e-16
 [PROSITE] MYRISTYL 6
 [PROSITE] LIM DOMAIN_1 1
 [PROSITE] AMIDATION 2
 [PROSITE] CAMP_PHOSPHO_SITE 4
 [PROSITE] CK2_PHOSPHO_SITE 28
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 15
 [PROSITE] ASN_GLYCOSYLATION 6
 [PFAM] LIM_domain containing proteins
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 5.53 %

SEQ MESSPFNRRQWTSLSLRVTAKELSLVNKNKSSAIVEIFSKYQKAAEETNMEKKRSNTENL
 SEG
 lctl-
 SEQ SQHFRKGTLTVLKKKWNPGGLGAESHTDSLRNSSTEIRHRADHPPAEVTSAAAGAKADQ
 SEG
 lctl-
 SEQ EEQIHPRSLRSPPEALVQGRYPHIKDGEDLDKHSTESKKMENCLGESRHEVEKSEISEN
 SEG
 lctl-
 SEQ TDASGKIEKYNVPLNRLKMMFEKGEPQTQTKILRAQSRASGRKISENSYSLDDLEIGPGQ
 SEG

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lctl- .....
SEQ  LSSSTFDSEKNESRRNLELPRLSETSIKDRMAKYQAAVSKQSSSTNYTNELKASGGEIKI
SEG  .....
lctl- .....
SEQ  HKMEQKENVPPGPEVCITHQEGEKISANENSLAVRSTPAEDDSRDSQVKSEVQQPVHPKP
SEG  .....x
lctl- .....
SEQ  LSPDSRASSLSESSPPKAMKKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYC
SEG  xxxxxxxxxxxxxxxx.....
lctl- .....ETTTTEEETTTCEEEETEEEEETTTTBTBT
SEQ  NNKLSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWASKNENEEILERPAQ
SEG  .....
lctl- TCBCBTBEEEEETEEEEETTTTTTTTTTCTTTTTTCTTT.....
SEQ  LANARETPHSPGVEDAPIAKVGVLAASMEAKASSQKEKEDKPAETKKLRIAWPPPTLG
SEG  .....
lctl- .....
SEQ  SGSALEEGIKMSKPKWPPPEDEISKPEVPEDVDLDLKKLRRSSSLKERSRPFTVAASFQST
SEG  .....xxxxxxxxxxxxxxxxxxxxx.....
lctl- .....
SEQ  SVKSPKTVSPPIRKGWSMSEQSEESVGGRVAERKQVENAKASKKNGNVGKTTWQNKESKG
SEG  .....
lctl- .....
SEQ  ETGKRKSEGHSLMENENLVENGADSDDDNSFLKQSPQEPKSLNWSSFVDNTFAEEFT
SEG  .....
lctl- .....
SEQ  TQNKQSQDVELWEGEVVKELSVVEEQIKRNRYYDEDEDEE
SEG  .....xxxxxxx
lctl- .....

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Prosites for DKF2phutel_18i19.1

PS00001	29->33	ASN_GLYCOSYLATION	PDOC00001
PS00001	59->63	ASN_GLYCOSYLATION	PDOC00001
PS00001	92->96	ASN_GLYCOSYLATION	PDOC00001
PS00001	251->255	ASN_GLYCOSYLATION	PDOC00001
PS00001	286->290	ASN_GLYCOSYLATION	PDOC00001
PS00001	706->710	ASN_GLYCOSYLATION	PDOC00001
PS00004	52->56	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	65->69	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	222->226	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	579->583	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	15->18	PKC_PHOSPHO_SITE	PDOC00005
PS00005	19->22	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00005	184->187	PKC_PHOSPHO_SITE	PDOC00005
PS00005	220->223	PKC_PHOSPHO_SITE	PDOC00005
PS00005	248->251	PKC_PHOSPHO_SITE	PDOC00005
PS00005	253->256	PKC_PHOSPHO_SITE	PDOC00005
PS00005	266->269	PKC_PHOSPHO_SITE	PDOC00005
PS00005	525->528	PKC_PHOSPHO_SITE	PDOC00005
PS00005	583->586	PKC_PHOSPHO_SITE	PDOC00005
PS00005	601->604	PKC_PHOSPHO_SITE	PDOC00005
PS00005	604->607	PKC_PHOSPHO_SITE	PDOC00005
PS00005	642->645	PKC_PHOSPHO_SITE	PDOC00005
PS00005	662->665	PKC_PHOSPHO_SITE	PDOC00005
PS00006	19->23	CK2_PHOSPHO_SITE	PDOC00006
PS00006	48->52	CK2_PHOSPHO_SITE	PDOC00006
PS00006	55->59	CK2_PHOSPHO_SITE	PDOC00006
PS00006	85->89	CK2_PHOSPHO_SITE	PDOC00006
PS00006	93->97	CK2_PHOSPHO_SITE	PDOC00006
PS00006	132->136	CK2_PHOSPHO_SITE	PDOC00006
PS00006	168->172	CK2_PHOSPHO_SITE	PDOC00006
PS00006	230->234	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00006	266->270	CK2_PHOSPHO_SITE	PDOC00006
PS00006	294->298	CK2_PHOSPHO_SITE	PDOC00006
PS00006	318->322	CK2_PHOSPHO_SITE	PDOC00006
PS00006	326->330	CK2_PHOSPHO_SITE	PDOC00006
PS00006	337->341	CK2_PHOSPHO_SITE	PDOC00006

PS00006	369->373	CK2_PHOSPHO_SITE	PDOC00006
PS00006	389->393	CK2_PHOSPHO_SITE	PDOC00006
PS00006	467->471	CK2_PHOSPHO_SITE	PDOC00006
PS00006	514->518	CK2_PHOSPHO_SITE	PDOC00006
PS00006	543->547	CK2_PHOSPHO_SITE	PDOC00006
PS00006	563->567	CK2_PHOSPHO_SITE	PDOC00006
PS00006	583->587	CK2_PHOSPHO_SITE	PDOC00006
PS00006	617->621	CK2_PHOSPHO_SITE	PDOC00006
PS00006	658->662	CK2_PHOSPHO_SITE	PDOC00006
PS00006	686->690	CK2_PHOSPHO_SITE	PDOC00006
PS00006	698->702	CK2_PHOSPHO_SITE	PDOC00006
PS00006	709->713	CK2_PHOSPHO_SITE	PDOC00006
PS00006	714->718	CK2_PHOSPHO_SITE	PDOC00006
PS00006	741->745	CK2_PHOSPHO_SITE	PDOC00006
PS00007	223->230	TYR_PHOSPHO_SITE	PDOC00007
PS00007	222->230	TYR_PHOSPHO_SITE	PDOC00007
PS00008	239->245	MYRISTYL	PDOC00008
PS00008	427->433	MYRISTYL	PDOC00008
PS00008	502->508	MYRISTYL	PDOC00008
PS00008	539->545	MYRISTYL	PDOC00008
PS00008	548->554	MYRISTYL	PDOC00008
PS00008	627->633	MYRISTYL	PDOC00008
PS00009	220->224	AMIDATION	PDOC00009
PS00009	662->666	AMIDATION	PDOC00009
PS00478	390->425	LIM_DOMAIN_1	PDOC00382

Pfam for DKFZphutel_18i19.1

HMM_NAME	LIM domain containing proteins		
HMM	*CagCNrpIyDREivMRAMNKvWHpECFrCcdCqqPLtegdeFYErDGRI		
	C	C++++Y+ E++ A+ V+H++CFRC+ C+ L+ G+ + ++ GRI	
Query	390	CVECQKTVYPMERLL-ANQQVFHISCFRCSYCNKLSLGT-YASLHGRI	436
HMM	YCKhDYYrrFg*		
	YCK+++ ++F+		
Query	437	YCKPHFNQLFK	447

DKFZphutel_1814

group: uterus derived

DKFZphutel_1814 encodes a novel 220 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of uterus-specific genes.

weak similarity to C.elegans D2085.2

complete cDNA, complete cds, few EST hits

Sequenced by AGOWA

Locus: /map="7q31"

Insert length: 1568 bp

Poly A stretch at pos. 1551, polyadenylation signal at pos. 1523

```
1  GCCGAGCGGA GAGGGTAGAG ACGGGGTTTC ACCGTGTTAG CCAAGATGGT
51 CTCGATCTCC TGACCTCGTG ATCCGCCCCG CTGGGCTCC CAAAGTGCTG
101 GGATTACAGG CGTGAGCCAC TCGGCCCGGC CTGTTGTACA GTTATTAAAG
151 TTATCATTTA ACATGGAAGA AGATGAGTTC ATTGGAGAAA AAACATTCCA
201 ACGTTATTGT GCAGAATCA TTAACATTTC ACAACAGATA GGTGATAGTT
251 GGGAAATGGAG ACCATCAAAG GACTGTTCTG ATGGCTACAT GTGCAAAATA
301 CACTTTCAAA TTAAGAATGG GTCTGTGATG TCACATCTAG GAGCATCTAC
351 CCATGGACAG ACATGTCTTC CCATGGAGGA GGCTTTCCAG CTACCCTTGG
401 ATGATTGTGA AGTGATTGAA ACTGCAGCAG CGTCCGAAGT GATTAAATAT
451 GAGTATCATG TCTTATATTC CTGTAGCTAC CAAGTGCCTG TACTTTACTT
501 TAGGGCAAGC TTTTAGATG GGAGACCTTT AACTCTGAAG GACATATGGG
551 AAGGAGTTCA TGAGTGCTAT AAGATGCGAC TGCTACAGGG ACCATGGGAC
601 ACTATTACGC AACAGGAACA TCCAATACTT GGGCAACCCCT TTTTGTACT
651 TCATCCCTGC AAGACGAATG AATTCATGAC TCCTGTATTA AAGAATTCTC
701 AGAAAATCAA TAAGAATGTC AACTATATCA CATCATGGCT GAGCATTGTA
751 GGGCCAGTTG TTGGGCTGAA TCTACCTCTG AGTTATGCCA AAGCAACGTC
801 TCAGGATGAA CGAAATGTCC CTTAACAAGA TTCTTCTATT GAGTTTAGGA
851 ATTGCGGCAC GAAGAATGCC AAGAGTTTAC CTGGCCAGCC CTGGCTTTAA
901 TAGGACTGAT ACCATGGAAT ATTCATCTC ACCAAGATGT GACATGGATT
951 ATTTTCCCT TGGACACAAA TGTCTACAGC AACTGATGTT TGATAGGCTG
1001 AATGTTTAGA AGAAACACTT CAAAGGGATA CATCATGCC AGGCATGGTG
1051 GCTCACACCT GTAATCCAAG CACTTTGGGA GGCCAAGGTG GGAGCATCAC
1101 TTGATCCTGG GAGTTCGAGA CCAGCCTGGG CAACATGGTG AAACCCGTGC
1151 GGTACAAAAA AATACAAAAA TTTGCCTGTT TATGGTGGTG TGTTCCTGTA
1201 GTCCAGCTC CCCAGGAGGC TGAGGTGGGA GGTGGCTTT AACCCAGGAG
1251 GCAGAGTTG CAGTGAGCTG AGACTGTGCC ACTGCAGTCC AGCCTGGGTG
1301 ACAGAGCCAG AACTGTCTC GGGAAAAAAA AAAAAAAA AAAGACACAT
1351 CATATAAAT AGCAAAAAA CAAATCTAAC TTATTAATAC TAGGAATACC
1401 AACATTATTA GGGCACTTGC AGGTATTCT TTTCTAGGCC AAGTACTTCA
1451 CTTCCATTG TCTGACATGG AGATTGAGGG AGAAATGTAT TTGTGTGTTT
1501 ATTTTAATGT AAGATATATA AAAATTAAAT TACTGGATTT ACCTGTCCCT
1551 GAAAAAAA AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 163 bp to 822 bp; peptide length: 220
Category: similarity to unknown protein

BLASTP hits

Alert BLASTP hits for DKFZphutet_18i4, frame 1

Pedant information for DKFZphutet1 18i4, frame 1

```
[LENGTH]          220
[MW]              25278.99
[pI]              5.34
[HOMOL]           TREMBL:CED2085_2 gene: "D2085.2"; Caenorhabditis elegans cosmid D2085 2e-11

[BLOCKS]          BL00221E
[PROSITE]         MYRISTYL          2
[PROSITE]         CK2_PHOSPHO_SITE    4
[PROSITE]         PKC_PHOSPHO_SITE    2
[PROSITE]         ASN_GLYCOSYLATION   1
[KW]              Alpha Beta
```

```

SEQ      MEEDFIGEIKTFORYCAEFIKHSQQIGDSEWRPSKDCSDGYMCKIHFIKNGSVMSHLG
PRD      cccccccchhhhhhhhhhhhhhhhhhhcccccceeeeeeeeeeeccceeeec

SEQ      ASTHGQTCLPNEEAFELPLDDCEVIETAAASEVIKYEYHVLVYSCSYQVPVLYFRASFLDG
PRD      cccccccchhhhhhhhhcccccceehhhhhchhhhhhhhhheeecccccceeeeeeeccccc

SEQ      RPLTLKDIWEGVHECYKMRLQLGPWDITIQEHPILGQPFVHLHPCKTNEFMTPLVKNLNSQ
PRD      cccccchhhhhhhhhhhhhhhhhhhcccccceccccccccccccceeecccccccccccccccccc

SEQ      KINKNVNYITSWLSIVGPVVLNLPLSYAKATSQDERNVP
PRD      cccccccccccccccccccccccccccccccccccccccccccccccccc

```

PS00001	52->56	ASN_GLYCOSYLATION	PDOC00001
PS00005	124->127	PKC_PHOSPHO_SITE	PDOC00005
PS00005	179->182	PKC_PHOSPHO_SITE	PDOC00005
PS00006	116->120	CK2_PHOSPHO_SITE	PDOC00006
PS00006	124->128	CK2_PHOSPHO_SITE	PDOC00006
PS00006	149->153	CK2_PHOSPHO_SITE	PDOC00006
PS00006	212->216	CK2_PHOSPHO_SITE	PDOC00006
PS00008	53->59	MYRISTYL	PDOC00008
PS00008	131->137	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphut1 18i4.1)

DKFZphut1_1811

group: nucleic acid management

DKFZphutes3_15j18 encodes a novel 184 amino acid protein with similarity to *S. cerevisiae* putative ribosomal protein YHR148w.

The novel protein is similar to several 40S ribosomal proteins and therefore seems to part of the corresponding ribosome subunit.

The new protein can find application in modulation of ribosome assembly, structure and function.

strong similarity to *S. cerevisiae* YHR148w

complete cDNA, complete cds, EST hits,
potential start at Bp 45 matches kozak consensus ANNatg
gene disruption of YHR148w is lethal!

Sequenced by AGOWA

Locus: unknown

Insert length: 1076 bp

Poly A stretch at pos. 1035, polyadenylation signal at pos. 1006

```
1 GCGCGCTCTC AGCTTCGGGT CCTGCGGCTG CGGCTGCCGC CATCATGGTG
51 CGGAAGCTTA AGTTCCACGA GCAGAAGCTG CTGAAGCAGG TGGACTTCCT
101 GAACTGGGAG GTCACCGACC ACAACCTGCA CGAGCTGCGC GTGCTGCGGC
151 GTTACCGGCT GCAGCGGCGG GAGGACTACA CGCGCTACAA CCAGCTGAGC
201 CGTGCCGTGC GTGAGCTGGC GCGGCGCCTG CGCGACCTGC CCGAACGCGA
251 CCAGTTCCGC GTGCGCGCTT CGGCCGCGCT GCTGGACAAG CTGTATGCTC
301 TCGGCTTGCT GCCCAGCGCG GGTTCGCTGG AGCTCTGCGA CTTTCGTACG
351 GCCTCGTCTT TCTGCGCGCG CCGCTCCTCC ACCGTGCTCC TCAAGCTGCG
401 CATGCGCGAG CACCTTCAGG CTGCCGTGGC CTTTGTGGAG CAAGGGCACG
451 TACGCGTGGG CCCTGACGTG GTTACCGACC CCGCTTCCTT TGTACGCGC
501 AGCATGGAGG ACTTTGTGAC TTGGGTGGAC TCGTCCAAGA TCAAGCGGCA
551 CGTGCTAGAG TACAATGAGG AGCGCGATGA CTTGATCTG GAAGCCTAGC
601 GGATCTCCCA CTTTGCATGG CTGTCTTTTA CAGATGGGAA AACTGAGGCC
651 TGATGCTGGA GATTCTATGA GGGTGCTCTC CTCAGGGGTA TCAGACGGTC
701 GTAGGTTCTT AAGAATTGGA TTCATCAGTG GCAGGCCATG CATAGAGCCA
751 CGGGAGGTGC GTCTTGTGTT TCCAGGAAAT GTTCTTAGAA CTTGGACTAC
801 TGATTATTAA TTGACTGTGC CTTGGGAAAC AGTGGGAAAT AACTTGGTGC
851 AGCACTGGGG TATTGTTGGA CTGGTTCAAT TCGTTAACT CGAATTCTTG
901 CTCCTGGCCC TGGTTAAGCT GTGTACAGAT GATGGAGAGT TTGGCCTCAA
951 GTTTTATATA ACTGAGCGAG ACTAGTGTT AGGATCTCCT CCCTTGTTTA
1001 AATGTCAATA AATGCCCCAA CTGCTTTGTA AGCTCAAAAA AAAAAAAAAA
1051 AAAAAAAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 45 bp to 596 bp; peptide length: 184
Category: strong similarity to known protein

```
1 MVRKLFHEQ KLLKQVDFLN WEVTDHNLHE LRVLRRLRLQ RREDYTRYNQ
51 LSRVRELAR RLRDLPERDQ FRVRASAALL DKLYALGLVP TRGSLELCDF
101 VTASSFCRRR LPTVLLKLRL AQHLQAAVAF VEQGHVRVGP DVVTDPAFLV
151 TRSMEDFTW VDSSKIKRHV LEYNEERDDF DLEA
```

BLASTP hits

Alert BLASTP hits for DKF2phutcl 1811, frame 3

Pedant information for DKFZphutel 1811, frame 3

Report for DKFZphutel 1811.3

[illegible]

Prosites for DKFZphute1 1811.3

PS00005	163->166	PKC_PHOSPHO_SITE	PDOC00005
PS00006	153->157	CK2_PHOSPHO_SITE	PDOC00006
PS00006	159->163	CK2_PHOSPHO_SITE	PDOC00006
PS00007	41->49	TYR_PHOSPHO_SITE	PDOC00007
PS00008	87->93	MYRISTYL	PDOC00008

Pfam for DKFZphutel 1811.3

HMM_NAME	Ribosomal protein S4		
HMM	*MSR.YRGPWKKIIRPGELPWLtNk....tklmrkYC..lRPgQHGW M+R ++ ++K++++++L W +++++ Y R+++ ++		
Query	1	MVRKLFKEQKLLKQVDFLNWEVTDHNLHELRLVLRRLRQRREDYTRYN	49
HMM	qrktLsKIRRMsqYrIRLQEKQKLRfMYGNiERQLRRYvriaEdKRKID Q + +R +++ + L+E + +R +++++L++++ + + L		
Query	50	QLSR--AVRELARRRLDLPERDQFRVRASAAALDKLYALGLVP-TRGSLE	96
HMM	YstGenLMQIEMLRLDNIVFRMGMAPIIHARQLINHRHIRVNDRIvNIP ++ + +++++RL++++ ++ MA ++A+ +++++H+RV++ +V++P		
Query	97	LCDFVTASSFCRRRLPTVLLKLRLMAOHLQAAVAFVEQGHVRVGPDDVVTDF	146
HMM	SYiCRPNDiISIRdkrMQSHikWnieSPegrmRPNHLerNnkkYeGtIN		


```
Query      147  ++++++ +      +++++W++ S+      ++R+ + Y+ +
AFLVTRS---M-----EDFVTWVDSSK-----IKRHVLEYNEERD 178
HMM
rIIERewiplkINELLVVEY+
+++ +
Query      179  DFDLE----- 183
```

DKFZphutel_19f19

group: transmembrane protein

DKFZphutel_19f19 encodes a novel 204 amino acid protein with similarity to murine p24 protein.

Murine p24 is expressed only in brain where it is localized exclusively in neurons. It seems to be a neuron-specific membrane protein localised in intracellular organelles of highly differentiated neural cells and may play a role in the neural organelle transport system. As p24, the novel protein contains 2 transmembrane regions, but it contains not the sequence homologous to the microtubule-binding domain of microtubule-associated proteins present in p24.

No informative BLAST results: No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes and as a new marker for uterine cells.

similarity to mouse P24 protein ;
membrane regions: 2

Summary DKFZphutel_19f19 encodes a novel 204 amino acid protein, with
similarity to mouse P24 protein.

similarity to mouse P24 protein

complete cDNA, complete cds, EST hits,
2 TM-domains

Sequenced by AGOWA

Locus: /map-14.8 cR from top of Chr20 linkage group

Insert length: 2042 bp

Poly A stretch at pos. 1958, polyadenylation signal at pos. 1940

```

1 GCAGGCAGAG AGATGAGGAA ACTGAGACCC AGAAAGGTGG AAGCACTTGT
51 CTAAGGTCAC GCCTCCAGGA AGCAGTGTGT CCACGACTCC AGTCCAAGTG
101 GTCAGGCTCC AGAGCCACACA GTCCCAGGGG TCCATGATGC CGAGCTGCAA
151 TCGTTCCTGC AGCTGCAGCC GCGGCCCCAG CGTGGAGGAT GGCAGTGGT
201 ATGGGGTCCG CTCCTACCTG CACCTCTTCT ATGAGGACTG TGCAGGCACT
251 GCTCTCAGCG ACGACCCTGA GGGACCTCCG GTCCTGTGCC CCCGCCGGCC
301 CTGGCCCTCA CTGTGTTGGA AGATCAGCCT GTCTCGGGG ACCCTGCTTC
351 TGCTGCTGGG TGTGGCGGCT CTGACCACTG GCTATGCAGT GCGCCCAAG
401 CTGGAGGGCA TCGGTGAGGG TGAGTTCCTG GTGTGGATC AGCGGGCAGC
451 CGACTACAAC CAGGCCCTGG GCACCTGTCT CCTGGCAGGC ACAGCGCTCT
501 GTGTGGCAGC TGGAGTTCTG CTCGCCATCT GCCTCTTCTG GGCCATGATA
551 GGCTGCTGTA GCCAGGACAC CAAGGCAGAG CCCTTGGACC CCGAAGCCGA
601 CAGCCACGTG GAGGTCTTCG GGGATGAGCC AGAGCAGCAG TTGTCAACCA
651 TAACCCCTTC TGCCAGTGGC CAGTCATGGT TCTCGCCACC CGCCAGCCCC
701 TTTGGGCAAT CTTCTGTGCA GACTATCCAG CCCAAGAGGG ACTCTGAGC
751 TGCCACATG GCCTAAGATG TGGGTCTTGG ATCCTTCCCC CTCTCAACCA
801 TAACCCCTTC TCAGTGTTC CCAACTTCT CCCTTAGAG CCCAACTCCA
851 GGTCAAATCT GGAGCTCAA TCCAGTGCT CCCTCCCCAG GAGTGGGGCC
901 CCAACTCTTC CAAGATACCA GCATTCTCTA AGTCCTCCCA AAACCTCTTA
951 CCCACACCCT CTTCCCAAGG CCTCAGGGG CAGAAAACAT CTCCTTCAAC
1001 CCGTCCCCAC TCCTTCCTCT GCATGACCTT GGGCAAACCC TTGCCCTTTC
1051 AAGCCATCAG CTCCTGCCTC TCTGCCATGA GGGCTTTGGA TCAGATTCTT
1101 CTTCTCGCCA GGATGAGGAC ACGCACTGCC CTCCATAGAC ACAGATGAAG
1151 GGGTGGGGGT CATTGAGCTC GAATGGGTCC CAGATGCTCA CTTGGCCTTT
1201 CCTTGACAGG TGAAGTGAAGA CGTTTGCTTC TCACAGTGTG TCTCTACCT
1251 GCATTTTGGC ATCAGAGCCC CCCAGCCCAC CCACCACAGG CAATTACTAG
1301 CCTAGTTTGA TAGGTGAGGT GGGTGAAGAA GGCTGGAGGT GACATGTCCG
1351 AGGTACACCA ACAAGCAGC ATGCAGGAAC TAGAAACACA TCTCAGCCT
1401 CCTCTGGGCC CAGCTCTTGT GCTACAGGTG GGGCGGAGCC AGCCCTCAC
1451 CTTCTTGGTT CCCTGAGGGT CCTCAGGGTG GAGGACAGGT TTGGCCACAG
1501 AAGACTAGCC AGAGGCCCTGA TGGTCCAGG TGGCTCTGGA TATACTTTGG
1551 ATATGATTTT AAATGGTCTC TAAGAGCCGG GGGTAGGGGG CAGGAAAAGT
1601 GGGTTGTCTT TGCCCTCAA AGTCCACCTA CCTAGAAACC AAGCCACGG
1651 TCTTGGCCGT GACCCTGATA ATAAATGGGC TCTCTCAGAG GCGCCAGCCC
1701 CTCCCTCCCC AGCCGGAGGC GTCATCTCTC TTCTGTACCA CTAGAGGGAG
1751 CTCTGATGCA GCTGGAGAGC AGCGCTCAAG GCTCTCGCCC CTCCCCTCCC
1801 TAACCTCTTC CTTGAGTCTC CACCAGCCTG AAGGGCCTCC TAGGGGATCC
1851 TCAGGCGGCC CCCACCAGG CACACCCTAC TGTCTTGTG CCTCAGCCCC
1901 CCTCTCATC CTGACCCCTT TCCATCCCAC CTTCCCTTTC AATAAACAGC
1951 TGGGATGGAA AAAAAAAAAA AGAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2001 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

```

BLAST Results

Entry HS417348 from database EMBL:
 human STS WI-14697.
 Length = 290
 Minus Strand HSPs:
 Score = 1254 (188.2 bits), Expect = 3.0e-50, P = 3.0e-50
 Identities = 262/273 (95%)

Medline entries

97334404:
 A newly identified membrane protein localized exclusively in
 intracellular organelles of neurons.

Peptide information for frame 2

ORF from 134 bp to 745 bp; peptide length: 204
 Category: similarity to known protein

1 MMPSNRSRCS CSRGPSVEDG KYGVRSYLH LFYEDCAGTA LSDDPEGPPV
 51 LCPRRPWPSL CWKISLSSGT LLLLLGVAAL TTGYAVPPKL EGIGEGEFLV
 101 LDQRAADYNQ ALGTCRLAGT ALCVAAGVLL AICLFWAMIG WLSQDTKAEP
 151 LDPEADSHVE VFGDEPEQQL SPIFRNASGQ SWFSPPASPF GQSSVQTIQP
 201 KRDS

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_19f19, frame 2

TREMBL:MMP2000_1 product: "P24 protein"; Mouse mRNA for P24 protein,
 complete cds., N = 1, Score = 295, P = 3.8e-26

>TREMBL:MMP2000_1 product: "P24 protein"; Mouse mRNA for P24 protein,
 complete cds.
 Length = 196

HSPs:

Score = 295 (44.3 bits), Expect = 3.8e-26, P = 3.8e-26
 Identities = 58/139 (41%), Positives = 81/139 (58%)

Query: 2 MPSCNRSRCS CSRGPSVEDGKW---YGVRSYLH LFYEDCAGTALSDDPEGPPVLCPRRPWP 58
 M SC+ +C R + +G + YGVRSYLH FYEDC + + + P R W
 Sbjct: 1 MTSCSNTCGSRRAQADTEGGYQQRGVRSYLHQFYEDCTASIWEYEDDFQIQRSPNR-WS 59
 Query: 59 SLCWKISLSSGTLLLLLGVAALTTGYAVPPKLEIGIGEGEFLVLDQRAADYNQALGTCRLA 118
 S+ WK+ L SGT+ ++LG+ L G+ VPPK+E GE +F+V+D A YN AL TC+LA
 Sbjct: 60 SVFWKVGILSGTVFVILGLTVLAVGLVPPKIEAFGEADFMVVDTHAVKYNGALDTCKLA 119
 Query: 119 GTALCVAAGVLLAICLFWAM 138
 G L G +A CL ++
 Sbjct: 120 GAVLFCIGGTSMAGCLLSV 139

Pedant information for DKFZphut1_19f19, frame 2

Report for DKFZphut1_19f19.2

[LENGTH] 204
 [MW] 21983.07
 [pI] 4.69
 [HOMOL] TREMBL:MMP2000_1 product: "P24 protein"; Mouse mRNA for P24 protein, complete
 cds. 7e-19
 [PROSITE] MYRISTYL 4

```

[PROSITE]    CAMP_PHOSPHO_SITE      1
[PROSITE]    CK2_PHOSPHO_SITE       3
[PROSITE]    PKC_PHOSPHO_SITE       1
[PROSITE]    ASN_GLYCOSYLATION      2
[KW]         TRANSMEMBRANE          2
[KW]         LOW_COMPLEXITY          10.29 %

```

```

SEQ  MMPSCNRSCSCSRGPSVEDGKWYGVRSYLHLFYEDCAGTALSDDPEGPPVLCPRRPWPSL
SEG  .....
PRD  cccccccccccccccccccccceehhhhhccccccccccccccccccccccccccccce
MEM  .....MM

```

```

SEQ  CWKISLSSGTL LLLGVAALT TGYAVPPKLEGIGEGEFLVLDQRAADYNQALGTCRLAGT
SEG  ....xxxxxxxxxxxxxxxxxxxxx.....
PRD  eeeeeccccceeeccccceeeccccccccccccccccceeeccccccccchhhhhhhchh
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

```

```

SEQ  ALCVAAGVLLAICLFWAMIGWLSQDTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQ
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccceeecccccccccccccccc
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

```

```

SEQ  SWFSPPASPFQSSVQTIQPKRDS
SEG  .....
PRD  cccccccccccccceeecccccccc
MEM  .....

```

Prosites for DKFZphutel_19f19.2

PS00001	6->10	ASN_GLYCOSYLATION	PDOC00001
PS00001	176->180	ASN_GLYCOSYLATION	PDOC00001
PS00004	201->205	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	114->117	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	157->161	CK2_PHOSPHO_SITE	PDOC00006
PS00008	38->44	MYRISTYL	PDOC00008
PS00008	92->98	MYRISTYL	PDOC00008
PS00008	119->125	MYRISTYL	PDOC00008
PS00008	127->133	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_19f19.2)

DKF2phutel_19g19

group: uterus derived

DKF2phutel_19g19 encodes a novel 400 amino acid protein, with strong but partial similarity to a bovine elastin-related protein expressed in fetal calf ligamentum nuchae.

The novel protein contains 2 RGD cell attachment sites.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of uterus-specific genes and as a new marker for uterine cells.

similarity to bovine elastin fragment

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: map=54.9 cR from top of Chr3 linkage group

Insert length: 3244 bp

Poly A stretch at pos. 3227, polyadenylation signal at pos. 3216

```
1  GTAAGTGCAG TAAGTCCCGC TTGGCCCTGG AGTCCACGCG GATTTTCGAA
51  GCTGGGGCTG GCAAGAGGCC GCTGGACACC ACGCTCCAGT CGTCAGCCCA
101 CTTCTAGACT GAACAGCGCG AGGCGGCGCG AGCGAGCCGG GTCCCACCAT
151 GGCCGCGAAT TATTCCAGTA CCAGTACCCG GAGAGAACAT GTCAAAGTTA
201 AAACCAGCTC CCAGCCAGGC TTCCTGGAAC GGCTGAGCGA GACCTCGGGT
251 GGGATGTTTG TGGGGCTCAT GGCCTTCCTG CTCTCCTTCT ACCTAATTTT
301 CACCAATGAG GGCCGCGCAT TGAAGACGGC AACCTCATTG GCTGAGGGGC
351 TCTCGCTTGT GGTGTCTCCT GACAGCATCC ACAGTGTGGC TCCGGAGAAT
401 GAAGGAAGGC TGGTGCACAT CATTGGCGCC TTACGGACAT CCAAGCTTTT
451 GTCTGATCCA AACTATGGGG TCCATCTTCC GGCTGTGAAA CTGCGGAGGC
501 ACGTGAGATG GTACCAATGG GTAGAACTG AGGAGTCCAG GGAGTACACC
551 GAGGATGGGC AGGTGAAGAA GGAGACGAGG TATTCTACA AACTGAATG
601 GAGGTGAGAA ATCATCAACA GCAAAAACCT CGACCAGAG ATTGGCCACA
651 ATAACCCGCA TGCCATGGCA GTGGAGTCAT TCACGGCAAC AGCCCCCTTT
701 GTCCAAATTG GCAAGT'TTTT CCTCTCGTCA GGCCTCATCG ACAAAGTCGA
751 CAACCTCAAG TCCCTGAGCC TATCCAAGCT GGAGGACCCT GATGTGGACA
801 TCATTGCGCG TGGAGACTTT TTCTACCACA GCGAAAATCC CAAGTATCCA
851 GAGGTGGGAG ACTTGGCTGT CTCCTTTTCC TATGCTGGAC TGAGCGGCGA
901 TGACCCTGAC CTGGGCCCCAG CTCACGTGGT CACTGTGATT GCCCGGCAGC
951 GGGGTGACCA GCTAGTCCCA TTCTCCACCA AGTCTGGGGA TACCTACTG
1001 CTCCTGCACC ACGGGGACTT CTCAGCAGAG GAGGTGTTTC ATAGAGAACT
1051 AAGGAGCAAC TCCATGAAGA CCTGGGGCCT GCGGGCAGCT GGCTGGATGG
1101 CCATGTTTAT GGGCCTCAAC CTTATGACAC GGATCCTCTA CACCTTGGTG
1151 GACTGGTTTC CTGTTTCCG AGACCTGGTC AACATTGGCC TGAAAGCCTT
1201 TGCCCTCTGT GTGGCCACCT CGCTGACCCT GCTGACCGTG GCGGCTGGCT
1251 GGCTCTTCTA CCGACCCCTG TGGGCCCTCC TCATTGCGCG CCTGGCCCTT
1301 GTGCCCATCC TTGTTGCTCG GACACGGGTG CCAGCCAAAA AGTTGGAGTG
1351 AAAAGACCCT GGCACCCGCC CGACACCTGC GTGAGCCCTA GGATCCAGGT
1401 CCTCTCTCAC CTCTGACCCA GCTCCATGCC AGAGCAGGAG CCCCCTGCAA
1451 TTTTGGACTC TGCACCCCTC CTCCTCTTCA GGGGCCAGAC TTGGCAGCAT
1501 GTGCACCAGG TTGGTGTTC AAGCTCATG TCTTCCCCAC ATCTCTCTT
1551 GCCAGTAAGC AGCTTTGGTG GGCAGCAGCA GCCATGAATG GCAAGCTGAC
1601 AGCTTCTCCT GCTGTTTCCT TCCTCTCTTG GACTGAGTGG GTACGGCCAG
1651 CCACTCAGCC CATTGGCAGC TGACAACGCA GACACGCTCT ACGGAGGCCT
1701 GCTGATAAAG GGCTCAGCCT TGCCGTGTGC TGCTTCTCAT CACTGCACAC
1751 AAGTGCCATG CTTTGGCACC ACCACCAAGC ACATCTGTGA TCCTGAAGGG
1801 CGGCCGTTAG TCATTACTGC TGAGTCTTGG GTCACCAGCA GACACACTGG
1851 GCATGGACCC CTCAAAGCAG GCACACCCAA AACACAAGTC TGTGGCTAGA
1901 ACCTGATGTG GTGTTTAAAA GAGAAGAAAC ACTGAAGATG TCCTGAGGAG
1951 AAAAGCTGGA CATATACTGG GCTTCACACT TATCTTATGG CTTGGCAGAA
2001 TCTTTGTAGT GTGTGGGATC TCTGAAGGCC CTATTTAAGT TTTTCTTCGT
2051 TACTTTGCTG CTTTCATGTG ACTTTCTTAC CCCAAGAGGA AGTTTCTGTA
2101 AATAAGATTT AAAAACAACA CAAAAAACA ACTTAATATT TCAGATGTT
2151 ACAGGAAACA CCGTTTAGTC TGTCAGTTGA ATTCAGAGCA CTGAAAGGTG
2201 TTAATTTGGG GTATGTGGTT TGATTGATAA AAAGTTACCT CTCAGTATT
2251 TGTGTCAGTG AGAAGCTTTA CAATGGATGC TTTTGAACA AGTATCAGCA
2301 AAAGGATTTG TTTTCACTCT GGGAGGAGAG GGTGGAGAAA GCACTTGCTT
2351 TCATCTCTCT GCATCGGAAA CTCCCTATG CACTTGAAGA TGGTTTAAAA
2401 GATTAAAGAA ACGATTAAAG GAAAAGTTG GAAGCTTTAT ACTAAATGGG
2451 CTCCTTCATG GTGACGCCCC GTCAACCACA ATCAAGAACT GAGGCCTGAG
2501 GCTGGTGTGA CAATGCCAC GCCTGCCTGG CTGCTTTTCA CTGGGAGTGC
2551 TTTTCGATGT GGCACCTGGG CTCCTAGGG CTGCTTCTGA GTGGTTCTTT
2601 CACGTGTTGT GTCCATAGCT TTAGTCTTCC TAAATAAGAT CCACCCACAC
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2651 CTAAGTCACA GAATTTCTAA GTTCCCAAC TACTCTCACA CCCTTTTAAA
2701 GATAAAGTAT GTTGTAACCA GGATGTCTTA AATGATTCTT TGTGTACCTT
2751 TTCTGTGATA TTCAGAAACC GTTTTGTGCC TGCTGGGAGT AATTCCTTTA
2801 GCAATTAAGT ATTTGGTAGC TGAATAAGGG GTCAGAACTT CTGAAACCAG
2851 AGATCTGTAA TCATCTCTAT TGGCCTGGGG TGCCTGTGCT ATAAATGAGT
2901 TTCTTCACAT GAAAAACACA GCCAGCCCAA GATGACTTAT CTGGGTTTAG
2951 GATTCAATAG TATTCATAA CTGCTTATTA CATGAGCAAT TTCATCAAAT
3001 CTCCAAACTC TTAAAGGATG CTTTCGGAAA ACACGCTGTA TACCTAGATG
3051 ATGACTAAAT GCAAAATCCT TGGGCTTGG TTTTCTTCTA GTAAGGATTT
3101 TAAATAACTG CCGACTTCAA AAGTGTCTT AAAACGAAAAG ATAATGTTAA
3151 GAAAAATTTG AAAGCTTTGG AAAACCAAAT TTGTAATATC ATTGTATTTT
3201 TTATTAAGAG TTTTGAATA AATTTCTAAA AAAAAAAAAA AAAA

```

BLAST Results

Entry HS545355 from database EMBL:

human STS WI-14815.

Length = 436

Minus Strand HSPs:

Score = 2040 (306.1 bits), Expect = 6.2e-86, P = 6.2e-86

Identities = 420/426 (98%)

Entry HS932147 from database EMBL:

human STS WI-8531.

Length = 341

Minus Strand HSPs:

Score = 1705 (255.8 bits), Expect = 4.7e-70, P = 4.7e-70

Identities = 341/341 (100%)

Medline entries

86051793:

Bovine elastin cDNA clones: evidence for the occurrence of a new elastin-related protein in fetal calf ligamentum nuchae.

Peptide information for frame 2

ORF from 149 bp to 1348 bp; peptide length: 400

Category: similarity to known protein

```

1 MAANYSSSTST RREHVKKVTS SQPGFLERLS ETSGGMFVGL MAFLLSFYLI
51 FTNEGRALKT ATSLAEGLSL VVSPDSIHSV APENEGRLVH IIGALRTSKL
101 LSDPNYGVHL PAVKLRRHVE MYQWVETES REYTEDGQVK KETRYSYNTE
151 WRSEIINSKN FDREIGHNPN SAMAVESFTA TAPFVQIGRF FLSSGLIDKV
201 DNFKSLSLSK LEDPHVDIIR RGDFFYHSEN PKYPEVGDLR VSFYAGLSG
251 DDPDLGPAHV VTVIARQRGD QLVPFSTRSG DTLILLHHGD FSAEEVFHRE
301 LRSNSMKTWG LRAAGWMAMF MGLNLMTRIL YTLVDWFPVF RDLVNIGLKA
351 FAFCVATSLT LLTVAAGWLF YRPLWALLIA GLALVPILVA RTRVPAKKLE

```

BLASTP hits

Entry I45887 from database PIR:

elastin - bovine (fragment)

Length = 40

Score = 131 (46.1 bits), Expect = 4.9e-08, P = 4.9e-08

Identities = 31/41 (75%), Positives = 34/41 (82%)

Alert BLASTP hits for DKFZphut1_19g19, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphut1_19g19, frame 2

Report for DKFZphut1_19g19.2

(LENGTH) 400

```

[MW]          44831.53
[pI]          7.23
[HOMOL]       PIR:I45887 elastin - bovine (fragment) 1e-06
[PROSITE]     RGD      2
[PROSITE]     MYRISTYL   3
[PROSITE]     CAMP_PHOSPHO_SITE 1
[PROSITE]     CK2_PHOSPHO_SITE  6
[PROSITE]     TYR_PHOSPHO_SITE  2
[PROSITE]     PKC_PHOSPHO_SITE  5
[PROSITE]     ASN_GLYCOSYLATION 1
[KW]          TRANSMEMBRANE 4

```

```

SEQ  MAANYSSSTSTREHVVKVTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ  ATSLAEGLSLVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPAVKLRRHVE
PRD  hhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  MYQWVETESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHNPNPSAMAVESFTA
PRD  hheehhhhhhecccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....M

SEQ  TAPFVQIGRFFLSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ  VFSYAGLSGDDPDGLPAHVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEVFHRE
PRD  ecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

SEQ  LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDILVNIGLKAFACVATSLT
PRD  hhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....MMM

SEQ  LLTVAAGWLFYRPLWALLIAGLALVPILVARTRPVPAKKE
PRD  hhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

```

Prosites for DKFZphut19g19.2.

PS00001	4->8	ASN_GLYCOSYLATION	PDOC00001
PS00004	140->144	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	9->12	PKC_PHOSPHO_SITE	PDOC00005
PS00005	10->13	PKC_PHOSPHO_SITE	PDOC00005
PS00005	97->100	PKC_PHOSPHO_SITE	PDOC00005
PS00005	276->279	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005
PS00006	10->14	CK2_PHOSPHO_SITE	PDOC00006
PS00006	63->67	CK2_PHOSPHO_SITE	PDOC00006
PS00006	209->213	CK2_PHOSPHO_SITE	PDOC00006
PS00006	249->253	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
PS00006	332->336	CK2_PHOSPHO_SITE	PDOC00006
PS00007	220->227	TYR_PHOSPHO_SITE	PDOC00007
PS00007	99->107	TYR_PHOSPHO_SITE	PDOC00007
PS00008	35->41	MYRISTYL	PDOC00008
PS00008	93->99	MYRISTYL	PDOC00008
PS00008	310->316	MYRISTYL	PDOC00008
PS00016	221->224	RGD	PDOC00016
PS00016	268->271	RGD	PDOC00016

(No Pfam data available for DKFZphut19g19.2)

DKFZphut1_19g22

group: cell structure and motility

DKFZphut1_19g22 encodes a novel 390 amino acid protein with very strong similarity to tuftelin/enamelin.

Tuftelin/enamelin are matrix proteins of the teeth. As other proteins involved in calcification, these proteins are also expressed in the uterus matrix.

The new protein can find application in modulation of tissue-calcification, especially the uterus.

complete cDNA, complete cds start at Bp 51, EST hits in 3' UTR, human homolog of mouse tuftelin
tuftelin is described as a matrix protein of teeth but it seems also to be present in the uterus matrix

Sequenced by AGOWA

Locus: unknown

Insert length: 3110 bp

Poly A stretch at pos. 3093, polyadenylation signal at pos. 3071

```
1 GCAGACAGCG GGGTGGACAA GTGGCGTGTG TGCTGCGACC CCGAGGGAAG
51 ATGAACGGGA CGCGGAACAT GTGTACCCTG GTGGACGTGC ACCCAGAGGA
101 CCAGGCGGCG GGCAGCGTGG ACATTCTCAG GCTGACTCTC CAGGGTGAAC
151 TGACAGGAGA TGAACCTGAA CACATAGCCC AGAAGGCGGG CAGGAAGACC
201 TATGCCATGG TGTCCAGCCA CTCAGCTGGT CATTCTCTGG CTTCAGAAGT
251 GGTGGAGTCC CATGATGGAC ATGAGGAGAT CATTAAGGTG TACTGAAGG
301 GGAGGTCTGG AGACAAGATG ATTACAGAGA AGAATATTAA CCAGCTGAAG
351 AGTGAAGTCC AGTACATCCA GGAGGCCAGG AACTGCCTAC AGAAGCTCCG
401 GGAGGATATA AGTAGCAAGC TTGACAGGAA CCTAGGAGAT TCTCTCCATC
451 GCACAGAGAT ACAGGTGGTG CTAGAAAAGC CAAATGGCTT TAGTCAGAGT
501 CCCACAGCCC TGTACAGCAG CCCACCTGAG GTGGACACCT GTATAAATGA
551 GGATGTTGAG AGCTTGAGGA AGACGGTGCA GGACTTGCTG GCCAAGCTTC
601 AGGAGGCCAA GCGGCAACAC CAGTCAGACT GTGTGGCTTT TGAGGTCACA
651 CTCAGCCGGT ACCAGAGGGA AGCAGAACAA AGTAATGTGG CCCTTCAGAG
701 AGAGGAGGAC AGAGTGGAGC AGAAAGAGGC AGAAGTCGGA GAGCTGCAGA
751 GGGCGTTGCT AGGGATGGAG ACGGAGCATC AGGCCTTACT GGGGAAAGTG
801 AGGGAAGGGG AGGTGGCCCT AGAGGAACTT CGGAGCAACA ATGCTGACTG
851 CCAAGCAGAA CGAGAAAAGG CTGCTACCCT GGAAAAGGAA GTGGCCGGGT
901 TGCGGGAGAA GATCCACCAC TTGGATGACA TGCTCAAGAG CCAGCAGCGG
951 AAAGTCCGGC AATGATAGA GCAGCTCCAG AATTCAAAAG CTGTGATCCA
1001 GTCAAAGGAC GCCACCATCC AGGAGCTCAA GGAGAAAATC GCCTATCTGG
1051 AGGCAGAGAA TTTAGAGATG CATGACCGGA TGGAACACCT GATAGAAAAA
1101 CAAATCAGTC ATGGCAACTT CAGCACCCAG GCCCGGGCCA AGACAGAGAA
1151 CCCGGGCAGT ATTAGGATAT CCAAGCCGCC TAGCCCGAAG CCCATGCCTG
1201 TCATCCGAGT GGTGGAAACC TGAGCTGCCT GGAGATGGTT GCTGCCATTG
1251 CTGCTGCCTC TGCTCGGAG AAGCCCACTG CCCCTGTTGG CTGTAAACAC
1301 TGCCCTTGAC TTCTGACTG TCCCCTGGCT GCACCCAGGA CTTGCGGCTC
1351 CTGTGTCTCA CCATTCCCAA GCCCTGGCC ACTCTAAGCT GGGCAGACGG
1401 AGCAGCAGCA CCTATTCAAG GCACCTGACG CCTTGGAAG ACATTGTCCT
1451 GCAAGCAGGA GCCAGGGCAA TATCTATATT CCTACAGTGA CTATTTTCT
1501 CTGTAGAGAG CCTCCCTTCT GTTGTAGACT GGAAGTGGC TGGCCATAA
1551 GCCAGGCCTT CATCAGATTG GGAGAGGTGA CAAGATTTCG CTCAGCCCTA
1601 AAAGCTGGAG ACACAGATGT CCAGAGTGAT TGGAGAATGT CCTGGGGGAA
1651 TGAAGTTCCT TCCACAAACA CAGCTCAGTT CTTAGCAACA AACTGTTTGT
1701 TTTTCTACTT GCTCCATCTG CAGCCTACGC TGCCCTGGCC TCCTGCAGAC
1751 AGATAGTGGG GTTACCTGGC AAGGCCTGGT GAGAGCCAGT GAACCTAAGC
1801 TTTGACTGGG TGGCCTTGTG TTTCTGGGGA GGAGGGAATG TACATTCAGG
1851 GAGTAGCCTT TTGCGGAAAA ATTCTCTAGG GCTACAGACA GTCATGTGTG
1901 ACTTCTCTCT GCTGTGAAAA CTCCCAGAGT CTCTTTAGGG ATTTTCCCTA
1951 AGGTGTACCA CCAGGCACAC CTCAGTCTTC TTGACCCAGA GCCTGAAAAC
2001 TGTTTTCAC TGGTTCACC AGTCCCAGCA AAATCCTCTT TGTATTTATT
2051 TTGCTAAGTT ATTGGTGGTT TTGCTTACAT CTCATGATTG ATATAATACC
2101 AAAGTCTTAT AGCCTTCTCT TGCAGTATTG GGATTGCTT GAAACCGGGA
2151 AAAGTGTTC CATTAGCCTT GTTAATCTCA GAGTGACACT ATTATGAATC
2201 TTTCTCTCCC TTTCTCTGCT CTGTTTCTTC TCTCTTCTC CTTCAAACCT
2251 GCTCTGCAGC TAAGGAAGGT GAGTCTACTT TCCCTGAGGC TTTGGGGTCA
2301 GAGTATATGT TGTTGGAGA AAGAGGSCAA TCAGGACTCT TCTGGGACCC
2351 AGATGAGTTC TTTACTAGCC CTCTGAACCC CCTTGCTCCA TAATTGGTCT
2401 TTTATCTCTG CTTGAATGA CCCTGCAGGT CATCATGGTT TTCTTTTTTT
2451 ATTGTTTTTT TTTTCTCTG AGACAGAGTC TCACTCTGTC ACCCAGGCTG
2501 GAGTGCAGTG GCSCGATCTC AGCTCACTGC AACCTCTGCC TCCCGGATTT
2551 AAGCGATTCT TCTGCCTCAG CCTCCCGAGT AGCTGGGACT ACAGGTGTGC
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2601 CACCACGCCT GGCTGATTTT TGTATTTTGA GTAGAGATGG GGTTTCACCA
2651 TACTGGCTAG GCTGGTCTCG AATTCCTGAC CTCAGGTGAT CCACCCACCT
2701 CGGCTTCCCA AAGTGCTAGG ATTATAGGCT TGAGCTACTG TGCCCGGCCC
2751 ATGGTGTTTT TCTTTAGGGC TCTCCTACA GCCTTGAGAA GTAGATAGGC
2801 ATCAGAGTAT GGTACTATAG GAATCAGAAA AATTCAAAAC AAATGTGGAT
2851 TAAGTGTTTA GGCTCTATGT GGCTCACGCA GCCAGAATCC TTAAGTCTGT
2901 GTGTTTCTGT GTCTCAAGAC TGGGCTCACA TTCTGGCTTT GTCCATAACA
2951 ATGCTCTGGG ATTTTCAGGA GTTCCCTCAT TTGTAAAATG AGGGGGTCAG
3001 AGCAGGTGAT ATCCATGTTT CTTCCCTTTC TGATATTGTT GTCTGTGGCA
3051 TATTCTTTGT ATGGCGAATT TAATAAATTA TATTAATGTG TCTAAAAAAA
3101 AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

98200312:
Tuftelin--aspects of protein and gene structure

97228909:
Timing of the expression of enamel gene products during mouse tooth development.

91340750:
Sequencing of bovine enamelin ("tuftelin") a novel acidic enamel protein.

Peptide information for frame 3

ORF from 51 bp to 1220 bp; peptide length: 390
Category: strong similarity to known protein

```

1  MNCTRNWCTL VDVHPEDQAA GSVDIRLRLTL QGELTGDELE HIAQKAGRKT
51 YAMVSSHAG HSLASELVES HDGHEEIIKV YLKGSRGDKM IHEKNINQLK
101 SEVQYIQEAR NCLQKLREDI SSKLDRLNGD SLHRQEIQV LEKPNFGFSQS
151 PTALYSSPPE VDTICINEDVE SLRKTVDLL AKLQEAQRQH QSDCVAFEV
201 LSRVQREAEQ SNVALQREED RVEQKEAFVG ELQRRLLGME TEHQALIAKV
251 REGEVALEEL RSNNADCOAE REKAATLEKE VAGLREKIHH LDDMLKSQQR
301 KVRQMIEQLQ NSKAVIQSKD ATIQELKEKI AYLEAENLEM HDRMEHLIEK
351 QISHGNFSTQ ARAKTENPGS IRISKPPSPK PMPVIRRVET

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_19g22, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphut1_19g22, frame 3

Report for DKFZphut1_19g22.3

```

[LENGTH]      390
[MW]           44264.09
[pI]           5.68
[HOMOL]        TREMBL:AF047704_1 product: "tuftelin"; Mus musculus tuftelin mRNA, complete
cds. 0.0
[FUNCAT]       08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w]
2e-11
[FUNCAT]       30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 2e-11
[FUNCAT]       1 genome replication, transcription, recombination and repair [M.
jannaschii, MJ1643] 7e-11
[FUNCAT]       09.13 biogenesis of chromosome structure [S. cerevisiae, YLR086w] 1e-08
[FUNCAT]       03.22.01 cell cycle check point proteins [S. cerevisiae, YGL086w] 6e-08
[FUNCAT]       30.10 nuclear organization [S. cerevisiae, YGL086w] 6e-08
[FUNCAT]       03.13 meiosis [S. cerevisiae, YNL250w] 7e-08

```

[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 7e-08
 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision
 repair) [S. cerevisiae, YKR095w] 1e-07
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR285w] 2e-07
 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 2e-07
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR216c] 1e-05
 [FUNCAT] 01.03.16 polynucleotide degradation [S. cerevisiae, YNL243w] 1e-04
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YNL243w]
 1e-04
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YNL243w] 1e-04
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins
 [S. cerevisiae, YNL243w] 1e-04
 [FUNCAT] 08.19 cellular import [S. cerevisiae, YNL243w] 1e-04
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YNL243w] 1e-04
 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 -
 myosin-1 isoform] 4e-04
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 4e-04
 [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 4e-04
 [FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YMR294w] 7e-04
 [EC] 3.6.1.32 Myosin ATPase 8e-09
 [PIRKW] blocked amino end 1e-07
 [PIRKW] nucleus 1e-06
 [PIRKW] citrulline 1e-07
 [PIRKW] tandem repeat 8e-09
 [PIRKW] heterodimer 3e-06
 [PIRKW] DNA repair 2e-06
 [PIRKW] heart 8e-09
 [PIRKW] endocytosis 3e-07
 [PIRKW] transmembrane protein 4e-10
 [PIRKW] zinc finger 3e-07
 [PIRKW] metal binding 3e-07
 [PIRKW] muscle contraction 8e-09
 [PIRKW] acetylated amino end 1e-06
 [PIRKW] actin binding 8e-09
 [PIRKW] microtubule binding 1e-06
 [PIRKW] cell division control 1e-06
 [PIRKW] ATP 8e-09
 [PIRKW] chromosomal protein 3e-06
 [PIRKW] thick filament 8e-09
 [PIRKW] phosphoprotein 1e-145
 [PIRKW] skeletal muscle 8e-09
 [PIRKW] calcium binding 1e-07
 [PIRKW] meiosis 2e-06
 [PIRKW] alternative splicing 7e-08
 [PIRKW] DNA condensation 3e-06
 [PIRKW] coiled coil 4e-10
 [PIRKW] P-loop 8e-09
 [PIRKW] heptad repeat 1e-07
 [PIRKW] methylated amino acid 8e-09
 [PIRKW] immunoglobulin receptor 2e-06
 [PIRKW] peripheral membrane protein 3e-07
 [PIRKW] cardiac muscle 8e-09
 [PIRKW] hydrolase 8e-09
 [PIRKW] muscle 7e-08
 [PIRKW] EF hand 1e-07
 [PIRKW] cytoskeleton 7e-08
 [PIRKW] hair 1e-07
 [PIRKW] smooth muscle 7e-08
 [PIRKW] calmodulin binding 3e-07
 [SUPFAM] conserved hypothetical P115 protein 2e-09
 [SUPFAM] myosin heavy chain 8e-09
 [SUPFAM] RAD50 protein 2e-06
 [SUPFAM] calmodulin repeat homology 1e-07
 [SUPFAM] myosin motor domain homology 8e-09
 [SUPFAM] alpha-actinin actin-binding domain homology 1e-06
 [SUPFAM] tropomyosin 7e-08
 [SUPFAM] protein-tyrosine kinase ret 3e-07
 [SUPFAM] plectin 1e-06
 [SUPFAM] trichohyalin 1e-07
 [SUPFAM] pleckstrin repeat homology 2e-06
 [SUPFAM] ribosomal protein S10 homology 1e-06
 [SUPFAM] protein kinase homology 3e-07
 [SUPFAM] protein kinase C zinc-binding repeat homology 2e-06
 [SUPFAM] giantin 4e-06
 [SUPFAM] kinesin-related protein KLPA 1e-06
 [SUPFAM] kinesin motor domain homology 1e-06
 [SUPFAM] human early endosome antigen 1 3e-07
 [SUPFAM] M5 protein 2e-06
 [PROSITE] MYRISTYL 1
 [PROSITE] AMIDATION 1
 [PROSITE] CK2_PHOSPHO_SITE 6

```

[PROSITE]      PKC_PHOSPHO_SITE      4
[PROSITE]      ASN_GLYCOSYLATION     2
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY         4.62 %
[KW]           COILED_COIL           35.13 %

SEQ      MNGTRNWCTLVDPEDQAAGSV DILRLTLQELTGDELEHIAQKAGRKYAMVSSH SAG
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....

SEQ      HSLASELVESHGHEEIIKVYLKGRSGDKMIHEKNINQLKSEVQYIQEARNCLQKLREDI
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    .....

SEQ      SSKLDRNLGDSLHRQEIQVVLEKPNGFSQSPTALYSSPPEVDTCTINEDVESLRKTVQDLL
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    .....cccccccccccccccccccc

SEQ      AKLQEAQRHQSDCVAFEVTL SRYQREAEQSNVALQREEDRVEQKEAEVGE LQRRLLGME
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      TEHQALLAKVREGEVALEELRSNNAD CQAEREKAATLEKEVAGLREKIHHLDMLKSQQR
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    CC.....cccccccccccccccccccccccccccccccccccccccccccc

SEQ      KVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEMHDRMEHLIERQISHGNFSTQ
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      ARAKTENPGSIRISKPPSPKPMFVIRVET
SEG      .....xxxxxxxxxxxxxxxxxxxxxx...
PRD      hhcccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....

```

Prosites for DKFZphut1_19g22.3

PS00001	2->6	ASN_GLYCOSYLATION	PDOC00001
PS00001	356->360	ASN_GLYCOSYLATION	PDOC00001
PS00005	121->124	PKC_PHOSPHO_SITE	PDOC00005
PS00005	171->174	PKC_PHOSPHO_SITE	PDOC00005
PS00005	370->373	PKC_PHOSPHO_SITE	PDOC00005
PS00005	378->381	PKC_PHOSPHO_SITE	PDOC00005
PS00006	9->13	CK2_PHOSPHO_SITE	PDOC00006
PS00006	35->39	CK2_PHOSPHO_SITE	PDOC00006
PS00006	122->126	CK2_PHOSPHO_SITE	PDOC00006
PS00006	157->161	CK2_PHOSPHO_SITE	PDOC00006
PS00006	175->179	CK2_PHOSPHO_SITE	PDOC00006
PS00006	322->326	CK2_PHOSPHO_SITE	PDOC00006
PS00003	355->361	MYRISTYL	PDOC00008
PS00003	46->50	AMIDATION	PDOC00009

(No Pfam data available for DKFZphut1_19g22.3)

DKFZphutel_19h17

group: intracellular transport and trafficking

DKFZphutel 19h17 encodes a novel 879 amino acid protein, with similarity to N.crassa osbP oxysterol-Binding protein.

The novel protein contains a oxysterol-binding protein family signature. Mammalian oxysterol-binding protein (OSBP) is a protein binds a variety of oxysterols (oxygenated derivatives of cholesterol). OSBP seems to play a complex role in the regulation of sterol metabolism. OSBP is a cytosolic/Golgi receptor for oxysterols such as 25-hydroxycholesterol, and thus a potential target of siphingomyelin turnover and cholesterol mobilization at the plasma membrane and/or Golgi apparatus. Therefore, the new protein seems to be involved in oxysterol metabolism.

The new protein can find application in modulating the response of cells to oxysterols. The protein can be used as marker for the golgi system. The Protein might be used to direct drugs to the golgi system in response to oxidative stress.

strong similarity to C.elegans ZK1086.1 and oxysterol-binding proteins

complete cDNA, complete cds, few EST hits
similarity to proteins involved in steroid biosynthesis

Sequenced by AGOWA

Locus: unknown

Insert length: 3828 bp

Poly A stretch at pos. 3811, polyadenylation signal at pos. 3784

```
1  GCCCGCGCGC  CCGGCCGGCC  CGGAGCACCG  AGCTCGCGGC  ACGGTAGGAG
51  AAGCCCCCGA  GCGCCACAG  CATGAAGGAG  GAGGCCTTCC  TCCGGCGCCG
101 CTTCTCCCTG  TGTCCACCTT  CCTCCACCCC  TCAGAAAGTC  GACCCCCGGA
151 AGCTCACCCG  GAACTTGCTC  CTCAGCGGAG  ACAATGAGCT  CTACCCACTC
201 AGCCCAAGGA  AGGACATGGA  GCCCAACGGC  CCGTCGCTGC  CCAGGGATGA
251 AGGGCCCCCG  ACCCAAGCT  CTGCCACGAA  GGTGCCACCG  GCAGAGTACA
301 GGTGTGTCAG  CCGGTCAGAC  AAGGAATGTG  TGTCCCCCAC  CGCCAGGGTC
351 ACCAAGAAGG  AGACTCTCAA  GGCGCAGAAG  GAGAACTACC  GGCAGGAGAA
401 GAAGCGCGCC  ACACGGCAGC  TGCTCAGCGC  TCTGACAGAC  CCCAGCGTGG
451 TCATCATGSC  TGACAGCCTG  AAGATCCGCG  GCACCCTGAA  GAGCTGGACC
501 AAGCTGTGGT  GCGTGCTGAA  GCCGGGGGTG  CTGCTCATCT  ACAAGACGCC
551 CAAGCTGGGC  CACTCGGTGG  GCACGGTGCT  GCTGCACTGC  TGGCAGCTCA
601 TCGAGCGGCC  CTCCAAGAAG  GACGGCTTCT  GCTTCAAGCT  CTTCACCCCG
651 CTGGATCACT  CCGTCTGGGC  CGTGAAGGGC  CCCAAAGGTG  AGAGCGTGGG
701 CTCCATCACA  CAGCCCTGTC  CCAGCAGCTA  CCTGATCTTC  AGGGCCGCTT
751 CCGAGTCAGA  TGGTCGCTGC  TGGCTGGACG  CCCTGGAGCT  GGCCTTGCGC
801 TGTCTTAGCC  TACTGAGACT  GGGCACCTGC  AAGCCGGGCG  GAGACGGGGA
851 GCCAGGGACC  TCGCCAGACG  CATCACCTTC  ATCGCTCTGT  GGGCTGCCAG
901 CCTCAGCCAC  TGTCCACCCA  GACCAAGACC  TGTTCCTACT  GAACGGGTCT
951 TCCTTGGAGA  ACGATGCATT  CTCAGACAG  TCGGAGAGAG  AGAACCTTGA
1001 GGAGTCAGAT  ACCGAGACCC  AGGACCATAG  CCGGAAGACG  GAGAGTGGCA
1051 GCGACCAATC  AGAGACCCCT  GGGCCCCCGG  TCGGAGAGAG  GACCACCTAT
1101 GTGGAGCAGC  TCCAGGAGGA  GCTGGGGGAG  CTGGGCGAGG  CGTCCCAGGT
1151 GGAGACAGTG  TCAGAGGAGA  ACAAGAGTCT  GATGTGGACC  CTGCTGAAGC
1201 AGCTACGGCC  AGGCATGGAC  CTGTCCCGCG  TGGTGCTACC  CACCTTCGTA
1251 CTGGAGCCGC  GCTCCTTCCT  GAACAAGCTC  TCCGACTACT  ACTACCACGC
1301 AGACCTGCTC  TCCAGGGCTG  CGGTGGAGGA  GGATGCCTAC  AGCCGCATGA
1351 AGCTGGTGCT  GCGGTGGTAC  CTGTCTGGCT  TCTACAAGAA  GCCCAAGGGA
1401 ATCAAGAAGC  CGTACAACCC  CATCCTGGGG  GAGACCTTCC  GCTGCTGCTG
1451 GTTCCACCCG  CAGACTGACA  GCCGCACATT  CTACATAGCA  GAGCAGGTGT
1501 CCCACCAACC  GCCCGTGTCT  GCCTTCCACG  TCAGCAACCG  GAAGGACGGC
1551 TTCTGCATCA  GTGGCAGCAT  CACAGCCAAG  TCCAGGTTTT  ATGGGAACCTC
1601 GCTGTGCGCG  CTGCTGGACG  GCAAAGCCAC  GCTCACCTTC  CTGAACCGAG
1651 CCGAGGATTA  CACCTTACC  ATGCCCTACG  CCCACTGCAA  AGGAATCCTG
1701 TATGGCACGA  TGACCTGGA  GCTGGGTGGG  AAGTCCACCA  TCGAGTGTGC
1751 GAAGAACAAC  TTCCAGGCCC  AGCTGGAATT  CAAACTCAAG  CCCTTCTTCG
1801 TCCGCTAGCA  CAGCATCAAC  CAGATCTCGG  GAAAGATCAC  GTCCGGAGAG
1851 GAAGTCCTGG  CGAGCCTCAG  TGGCCACTGG  GACAGGGACG  TGTATTATCAA
1901 GGAGGAAGGG  AGCGGAAGCA  GTGCGCTTTT  CTGGACCCCG  AGCCGGGAGG
1951 TCCGCAGACA  GAGGCTGAGG  CAGCACACGG  TGCCGCTGGA  GGAGCAGACG
2001 GAGCTGGAGT  CCGAGAGGCT  CTGGCAGCAC  GTCACCAGGG  CCATCAGCAA
2051 GCGCCACCA  CACAGGGCCA  CACAGGAGAA  GTTTGCACTG  GAGGAGGCAC
2101 AGCGGCAGCG  CGCCCTGAG  CGGCAGGAGA  GCCTCATGCC  CTGGAAGCCG
2151 CAGCTGTTCC  ACCTGGACCC  CATCACCCAG  GAGTGGCACT  ACCGATACGA
2201 GGACCACAGC  CCCTGGGACC  CCCTGAAGGA  CATCGCCACG  TTTGAGCAAG
2251 ACGGGATCCT  GCGGACCTTG  CAGCAGGAGG  CCGTGGCCCG  CCAGACCACC
```

```
2301 TTCCTGGGCA GCCCAGGGCC CAGGCACGAG AGGTCTGGCC CAGACCAGCG
2351 GCTTCGCAAG GCCAGCGACC AGCCTCCGG CCACAGCCAG GCCACGGAGA
2401 GCAGCGGATC CACGCCTGAG TCCTGCCCAG AGCTCTCAGA CGAGGAGCAG
2451 GATGGTGACT TTGTCCCTGG CGGTGAGAGC CCATGCCCTC GGTGCAGGAA
2501 GGAGGCGCGG CGGCTGCAGG CCCTGCACGA GGCCATCCTC TCCATCCGAG
2551 AGGCCCAGCA GGAGCTGCAC AGGCACCTCT CGGCCATGCT GAGCTCCACG
2601 GCACGGGCGAG CACAGGCACC GACCCCAGGC CTCCTGCAGA GCCCCGATC
2651 CTGTTTCTG CTCTGCGTGT TCCTGGCGTG TCAGCTGTTC ATTAACCACA
2701 TCCTCAAATA GGAGCCCTGG GGGCAGAGCT CCTGGCCAGT CCCGAGCCCT
2751 CCCTCCCAGG CACCCAGCAC TTTAAGCCTG CTCCTATGGAG GCAGAGAGGC
2801 CCGGCAAGCA CAGCCACTGT GACGGGGAGT CCAGGCGCAG GAGGGACCCG
2851 GGGCCACAAG GCGCTGCGGG CCCAGGTGTG CTGGGCCCTC CTCAGGGGCA
2901 CTGGCCTCTC TGCAGGGCCT TCCGCCAGC GCTGGCCTTA ATGCTAAAGC
2951 CAAATGCAGC TTCTGCTGTG CGACGCACTC CTGGCCATCT TGCCGTGTCA
3001 CCCCCTGTCC GGCTCCACT TGCCATGGGG GATGGATGGA TTTAGGGTGG
3051 GAGGGCCTGT GGGGGCCCTG GACAGTCACA CCCCAGCAGC AGTGAGTGGG
3101 CAGGTTTGA GAGCAGCCA GGGAGCCCCG AGTGGCCCAG GAGTCCCCC
3151 ACACACAGAT GCATAGGCCT GCCTTCCGGA GACCCTGTCC ACATTGCCGG
3201 GACCACCCGT GTGGGGCCAC TGGTGGGTGC CAGGGACAGG TTAGGGCCAC
3251 TGTGGGGAAG GCATTTTGGT TTTTATTCC ACGCTCTGCT GTTTGGATGG
3301 GAGCCCCACA GAGGCAGGTC CTGGAACCAC CCCACCCCCA CACCTGGACG
3351 CTCGCTCTG TGGGGGCACA CGCAGGTGGA GGTGGTGTG GGTGCAGGTG
3401 TGTGCAGGGG TGTGGGGGGC GCAGGGGTGT GGCTTAGCTG GCCCCGCACC
3451 CAGGCCGGGG AGGCTCAAGT TCGCCACTTT ACTCAGACCG ATGCACAGTC
3501 TTCCCATTTT ACACTTTTTT AATAAACATA ATTGCAATAT TTTAGGTGGG
3551 CTGCGAGCTG CAGTCAGCCT TCACGTCTGG CCTCAGTCCC CGTGTCAGTG
3601 CCGCTCTGCG TGTGCGTGTG CGCGTGTGTG AGCCTCTACA CATATATATA
3651 TGTACAGAGC CTTAAACCAC ATCGTGGCGG TGCCGTCTGA GCTGTAGCGG
3701 GTGGCTTTGT TTCCAGTTT TGTACCCGTG TCCTGTGCTC CCCTCCTCCC
3751 CCATCTGGGG ATGTGCTGT GTTCCACACC TTGAAATAAA CAGACACATA
3801 CGTGTTCTCT TAAAAAATA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

98315477:
The pleckstrin homology domain of oxysterol-binding protein recognises a determinant specific to Golgi membranes.

98146266:
A Drosophila homologue of oxysterol binding protein (OSBP)--implications for the role of OSBP.

98146266:
A Drosophila homologue of oxysterol binding protein (OSBP)--implications for the role of OSBP.

Peptide information for frame 3

ORF from 72 bp to 2708 bp; peptide length: 879
Category: strong similarity to known protein

```
1 MKEEAFRRR FSLCPPSSTP QKVDPRKLTR NLLSGDNEL YPLSPGKDME
51 PNGPSLPRDE GPPTPSSATK VPPAEYRLCN GSDKECVSPT ARVTKKETLK
101 AQKENYRQEK KRATRQLLSA LTDPSVVIMA DSLKIRGTLK SWTKLWCVLK
151 PGVLLIYKTP KVGQWVGTVL LHCCELIERP SKKDGFCFKL FHPLDQSVWA
201 VKGPKGESVG SITQPLPSSY LIFRAASESD GRCWLDAL EL ALRCSSLLRL
251 GTCKPGRDGE PGTS PDASPS SLCGLPASAT VHPDQDLFPL NGSSLEND AF
301 SDKSERENPE ESDTETQDHS RKTESGSDQS ETPGAPVRRG TTYVEQVQEE
351 LGELGEASQV ETVSEENKSL MWTL LKQLRP GMDLSRVVLP TFVLEPRSF L
401 NKLSDYYYHA DLLSRAAVEE DAYSRMKLV L RWYLSGFYKK PKGIKKPYNP
451 ILGETFRCCW FHPQTD SRTF YIAEQVSHHP PVSAFHVSNR KDGFCISGSI
501 TAKSRFYGNS LSALLDGKAT LTFLNRAEDY TLTMPYAHCK GILYGMTLE
551 LGGKVTIECA KNNFQAQLEF KLPFFGGST SINQISGKIT SGEEVLASLS
601 GHWDROVFIK EEGSGSSALF WTPSGEVRRQ RLRQHTVPLE EQTELESERL
```

```

651 WQHVTRAISK GDQHRATQEK FALEEAQRQR ARERQESLMP WKPQLFHLDLP
701 ITQEWYHYRYE DHSPWDPLKD IAQFEQDQIL RTLQOEAVAR QTTFLGSPGP
751 RHERSGPDQR LRKASDQPSG HSOATESSGS TPESCPQLSD EEQDGDVFG
801 GESPCPRCRK EARRLQALHE AILSIREAQ ELHRHLSAML SSTARAAQAP
851 TPGLLQSPRS WFLLCVFLAC QLFINHILK

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phutel_19h17, frame 3

TREMBL:CEZK1086_2 gene: "ZK1086.1"; *Caenorhabditis elegans* cosmid
ZK1086, N = 1, Score = 1495, P = 2.7e-153

PIR:S25324 hypothetical protein YKR003w - yeast (*Saccharomyces cerevisiae*), N = 2, Score = 574, P = 8.5e-57

TREMBL:CEAF195_7 gene: "C32F10.1"; *Caenorhabditis elegans* cosmid
C32F10., N = 1, Score = 588, P = 8.6e-57

PIR:S46796 hypothetical protein YKR003w homolog YHR001w - yeast
(*Saccharomyces cerevisiae*), N = 1, Score = 585, P = 1.9e-56

TREMBL:NCOSBP_1 gene: "osbP"; product: "oxysterol-binding protein";
N. crassa mRNA for putative oxysterol-binding protein, N = 1, Score =
571, P = 7e-55

TREMBL:AB017026_1 product: "oxysterol-binding protein"; *Mus musculus*
mRNA for oxysterol-binding protein, complete cds., N = 2, Score = 328,
P = 3e-35

>TREMBL:CEZK1086_2 gene: "ZK1086.1"; *Caenorhabditis elegans* cosmid ZK1086
Length = 751

HSPs:

Score = 1495 (224.3 bits), Expect = 2.7e-153, P = 2.7e-153
Identities = 327/663 (49%), Positives = 430/663 (64%)

```

Query:   129 MADSLKIRGTLKSWTKLWCVLKPGLLIYKTPKV--GQWVGTVLLHCCELIERPSKKDGF 186
          MAD+LKIRG LK W + +CVLKPGL++YK K G WVGTVLL+ CELIERPSKKDGF
Sbjct:   1 MADTLKIRGALKRWNRYCVLKPGLLILYKHKKADRGDVGTVLLNHCELIERSKKDGF 60

Query:   187 CFKLFHPLDQSVWAVKGPKGESVGSIT-QPLPSSYLIFRAASESDGRCWLDALELALRCS 245
          CFKLFHP+D S+W +GP G+S GS T PL +S+LI RA S+ GRCW+DALEL+ +C+
Sbjct:   61 CFKLFHFMDSIWGNRGLGQSFGSFTLNPLNTSFLICRAPSDQAGRCWMDALELSFKCT 120

Query:   246 SLLRLGTCKPGRDGEPTSPDASPSLLCGLPASATVHPDQDLFPLNGSSLENDAFSDK-S 304
          LL+ T D + G D+S + G + + D D G A S+ +
Sbjct:   121 GLLKK-TMNE-LDDKNG---DSSMND--GQRDESRMSRDS-----GDDTRELVASETDA 168

Query:   305 ERENPEESDTETQDHSRKTESGSDQSETPGAPVRRGTT---YVEQVQEELGELGEASQVE 361
          E+ E D + +DH E G SET +R T ++ +E G G S E
Sbjct:   169 EKHFEIDVQDEDH----EDGK-MSETSDT-IREAFTESAWIPSPKEVFGPDG--SLTE 220

Query:   362 TVSEENKSLMWTLKQLRPGMDLSRVVLPFTFVLEPRSFNLKLSDYHHADLLSRAAVEED 421
          V EENKSL+WTLKQ+RPGMDLS+VVLPTF+LEPRSF L KL+DYHHADL+S A E D
Sbjct:   221 EVGEENKSLIWTLLKQIRPGMDLSKVVLPFTFILEPRSFLEKLADYHHADLISEVAEPD 280

Query:   422 AYSRMKLVLIRWYLSGFYKKPKGKPKYPNPILGETFRCCWFHPQTDSTRFYIAEQVSHHPP 481
          + R+ V +++LSGFYKKPKG+KKYPNPILGETFRC W HP S TFY+AEQVSHHPP
Sbjct:   281 PFQIRIVKVTKFLLSGFYKKPKGLKPKYPNPILGETFRCKWEHPD-GSTTFYMAEQVSHHPP 339

Query:   482 VSAFHVSNRKGFCISGSITAKSRFYGNLSALLDGKATLTFLNRAEDYTLTMPYAHCKG 541
          VS+ ++NRK GF ISG+I AKS++YGNLSA+L GK LT LN E Y + +PYA+CKG
Sbjct:   340 VSSLFITNRKAGFNISGTILAKSKYYGNLSAILAGKLRLLTLNLGETYIVNLPYANCKG 399

Query:   542 ILYGTMTELGGKVITIEAKNNFQAQLEFKLPFFGGSTINQISGKITSGEEVLASLSG 601
          I+ GTMT+ELGG+V IEC K ++ L+FKLKP GG+ NQI G I G + LAS+ G
Sbjct:   400 IMIGTMTMELGGEVNIIECEKTGYRTTLDKLPKMLGGA--YNQIEGSIKYGSDRLASIEG 457

Query:   602 HWDNRDVFIEKEGSGSSALFWTPSGEVRRQRLRQHTVPLEEQTELESERLWQHVTRAISK 661
          WD + IK G W P+ EV + RL ++ + ++EQ E ES +LW+HVT AIS
Sbjct:   458 AWDGVIRIK--GPDGKKELWNPTPEVIKTRLPRIEINMDEQGEWESAKLWRHVTEAISNE 515

Query:   662 DQHRATQEKFALEEAQRQRARERQESLMPWKPQLFHLDLPITQEWYHYRYEDHSPWDPLKDI 721
          DQ++AT+EK ALE QR RA+ S +P + + F ++ Y + D+ PWD DI
Sbjct:   516 DQYKATEEKTALENDQARAK----SGIPHETKFFKKQH-GDDYVYIHADYRPNWNNNDI 570

```

```

Query:      722 AQFEQDGILRTLQQEAVAR--QTTFLGSPGPRHERSGPDQRLRKASDQPSGHSQATESSG 779
           Q E + +++T+ + + + + LGS      E S D+ + + +P + +
Sbjct:      571 QQIENNVVVKTISRHSKRKTGNSEQLGSDNTS-EASESDEEVI----EPKIKKKEIVPAK 625

Query:      780 STPESCPELSDE 791
           S P + PE++DE
Sbjct:      626 SKPIT-PEVADE 636

```

Pedant information for DKFZphutel_19h17, frame 3

Report for DKFZphute1_19h17.3

```

[LENGTH] 1879
[MW] 98616.79
[pI] 7.29
[HOMOL] TREMBL:CEZK1086_2 gene: "ZK1086.1"; Caenorhabditis elegans cosmid ZK1086 1e-157

[FUNCAT] 01.06.16 lipid and fatty-acid binding [S. cerevisiae, YHR001w] 3e-55
[FUNCAT] 01.06.01 lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YHR001w]
3e-55
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YPL145c] 3e-23
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YPL145c]
3e-23
[FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YAR044w] 5e-20
[BLOCKS] BL00168F
[BLOCKS] BL01013D Oxysterol-binding protein family proteins
[BLOCKS] BL01013C Oxysterol-binding protein family proteins
[BLOCKS] BL01013B Oxysterol-binding protein family proteins
[BLOCKS] BL01013A Oxysterol-binding protein family proteins
[PIRKW] transmembrane protein 1e-19
[SUPFAM] pleckstrin repeat homology 8e-18
[SUPFAM] ankyrin repeat homology 1e-19
[SUPFAM] unassigned ankyrin repeat proteins 1e-19
[PROSITE] MYRISTYL 12
[PROSITE] CAMP_PHOSPHO_SITE 6
[PROSITE] OSBP 1
[PROSITE] CK2_PHOSPHO_SITE 21
[PROSITE] PROKAR_LIPOPROTEIN 1
[PROSITE] TYR_PHOSPHO_SITE 2
[PROSITE] PKC_PHOSPHO_SITE 20
[PROSITE] ASN_GLYCOSYLATION 3
[PFAM] PH (pleckstrin homology) domain
[KW] TRANSMEMBRANE 1
[KW] LOW_COMPLEXITY 2.96 %
[KW] COILED_COIL 3.53 %

```

```

SEQ      MKEEAFLRRRFLCPPSSSTPQKVDPRLKLRNLLLSGDNELYPLSPGKDMPEPNGPSLPRDE
SEG
PRD      cccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc
COILS
MEM      .....

SEQ      GPPTPSSATKVPPAEYRLCNGSDKECVSPTARVTKKETLKAQKENYRQEKKRATRQLLSA
SEG
PRD      cccccccccccccceeeccccceeeeccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS
MEM      .....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ      LTDPSVIMADSLKIRGTLKSWTKLWCVLKPGVLLIYKTPKVGQWVGTVLLHCCELIERP
SEG
PRD      hccccceeeccccccccccccccccceeeeeeccccceeeccccccccceeecccccccccc
COILS
MEM      CCC.....

SEQ      SKKDGFCKFLFHPLDQSVWAVKGPKGESVGSITQPLPSSYLI FRAASESDGRCWLDALFL
SEG
PRD      cccccceeeccccccccceeeccccccceeeccccccccceeeeee hhhhhhhhhhhhhhhhh
COILS
MEM      .....

SEQ      ALRCSSLLRLGTCKPGRDGEPGTS PDASPSSLCGLPASATVHPDQDLFPLNGSSLENDAF
SEG
PRD      hhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc
COILS
MEM      .....

SEQ      SDKSERENPEESDTETQDHSRKTESGSDQSETPGAPVRRGTTYVEQVQEEELGELGEASQV

```

[illegible]

Prosite for DKFZphutel 19h17.3

PS000001	80->84	ASN_GLYCOSYLATION	PDOC000001
PS000001	291->295	ASN_GLYCOSYLATION	PDOC000001
PS000001	367->371	ASN_GLYCOSYLATION	PDOC000001
PS000004	9->13	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	26->30	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	95->99	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	111->115	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	338->342	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	762->766	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	82->85	PKC_PHOSPHO_SITE	PDOC000005
PS000005	90->93	PKC_PHOSPHO_SITE	PDOC000005
PS000005	94->97	PKC_PHOSPHO_SITE	PDOC000005
PS000005	98->101	PKC_PHOSPHO_SITE	PDOC000005
PS000005	132->135	PKC_PHOSPHO_SITE	PDOC000005
PS000005	138->141	PKC_PHOSPHO_SITE	PDOC000005
PS000005	159->162	PKC_PHOSPHO_SITE	PDOC000005
PS000005	181->184	PKC_PHOSPHO_SITE	PDOC000005
PS000005	252->255	PKC_PHOSPHO_SITE	PDOC000005

PS00005	301->304	PKC_PHOSPHO_SITE	PDOC00005
PS00005	304->307	PKC_PHOSPHO_SITE	PDOC00005
PS00005	320->323	PKC_PHOSPHO_SITE	PDOC00005
PS00005	455->458	PKC_PHOSPHO_SITE	PDOC00005
PS00005	488->491	PKC_PHOSPHO_SITE	PDOC00005
PS00005	501->504	PKC_PHOSPHO_SITE	PDOC00005
PS00005	586->589	PKC_PHOSPHO_SITE	PDOC00005
PS00005	647->650	PKC_PHOSPHO_SITE	PDOC00005
PS00005	824->827	PKC_PHOSPHO_SITE	PDOC00005
PS00005	843->846	PKC_PHOSPHO_SITE	PDOC00005
PS00005	857->860	PKC_PHOSPHO_SITE	PDOC00005
PS00006	82->86	CK2_PHOSPHO_SITE	PDOC00006
PS00006	94->98	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00006	227->231	CK2_PHOSPHO_SITE	PDOC00006
PS00006	263->267	CK2_PHOSPHO_SITE	PDOC00006
PS00006	293->297	CK2_PHOSPHO_SITE	PDOC00006
PS00006	304->308	CK2_PHOSPHO_SITE	PDOC00006
PS00006	312->316	CK2_PHOSPHO_SITE	PDOC00006
PS00006	325->329	CK2_PHOSPHO_SITE	PDOC00006
PS00006	342->346	CK2_PHOSPHO_SITE	PDOC00006
PS00006	358->362	CK2_PHOSPHO_SITE	PDOC00006
PS00006	362->366	CK2_PHOSPHO_SITE	PDOC00006
PS00006	590->594	CK2_PHOSPHO_SITE	PDOC00006
PS00006	643->647	CK2_PHOSPHO_SITE	PDOC00006
PS00006	659->663	CK2_PHOSPHO_SITE	PDOC00006
PS00006	713->717	CK2_PHOSPHO_SITE	PDOC00006
PS00006	755->759	CK2_PHOSPHO_SITE	PDOC00006
PS00006	780->784	CK2_PHOSPHO_SITE	PDOC00006
PS00006	784->788	CK2_PHOSPHO_SITE	PDOC00006
PS00006	789->793	CK2_PHOSPHO_SITE	PDOC00006
PS00006	824->828	CK2_PHOSPHO_SITE	PDOC00006
PS00007	402->409	TYR_PHOSPHO_SITE	PDOC00007
PS00007	415->424	TYR_PHOSPHO_SITE	PDOC00007
PS00008	137->143	MYRISTYL	PDOC00008
PS00008	163->169	MYRISTYL	PDOC00008
PS00008	274->280	MYRISTYL	PDOC00008
PS00008	326->332	MYRISTYL	PDOC00008
PS00008	381->387	MYRISTYL	PDOC00008
PS00008	498->504	MYRISTYL	PDOC00008
PS00008	508->514	MYRISTYL	PDOC00008
PS00008	541->547	MYRISTYL	PDOC00008
PS00008	552->558	MYRISTYL	PDOC00008
PS00008	577->583	MYRISTYL	PDOC00008
PS00008	613->619	MYRISTYL	PDOC00008
PS00008	728->734	MYRISTYL	PDOC00008
PS00013	860->871	PROKAR_LIPOPROTEIN	PDOC00013
PS01013	474->485	OSBP	PDOC00774

Pfam for DKFZphut1_19h17.3

HMM_NAME	PH (pleckstrin homology) domain		
HMM	*dvIREGWMYKWgswrkstgnWqrRWFvLrndpnrLiYYkddkdekPrYM		
	+VI+ +++++G + W + W+VL++ ++L+ YK + + + ++		
Query	126	VVIMADSLKIRGTLKS----WTKLWCVLKP--GVLLIYKTP-KVGQWVG	167
HMM	1IdldcWrMidVEidWmmdndHCFiIWtrq.....		
	L+C+ +I+ ++ ++ +CF+++ +		
Query	168	TVLLHCCELIERPSKDD---GFCFKLFHPLDQSVWAVKGPKGESVGSITQ	214
HMMrtYYFQAeNeEEMmeWMSaIrRaIw*		
	+ ++F+A++E++ + W++A++ A++		
Query	215	PLPSSYLIFRAASESDGRCWLDALALR	243

DKFZphutel_19j11

group: uterus derived

DKFZphutel_19j11 encodes a novel 708 amino acid protein with C-terminal similarity to several known proteins, such as human KIAA0231 or murine ras binding protein Sur8.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of uterus-specific genes.

Strong similarity to KIAA0231, similarity to ras binding protein Sur8

EST AA854189 extends the sequence (294 Bp), with this sequence complete cDNA,

Sequenced by AGOWA

Locus: unknown

Insert length: 2343 bp

Poly A stretch at pos. 2323, polyadenylation signal at pos. 2295

```
1 GCTCCTGCTA ACCCATCAC TGTGGAAATG AAAGGCCTGA AGACAGATTT
51 GGACCTTCAG CAGTACAGCT TTATAAATCA GATGTGTTAT GAGCGAGCCC
101 TCCACTGGTA TGCCAAGTAT TTCCCTTACC TTGTCTCAT CCATACCCTG
151 GTCTTTATGC TCTGCAGTAA CTTTGGTTC AAATTCCTG GTTCCAGCTC
201 CAAAATAGAA CATTTTCATCT CCATTCTGGG GAAGTGTTT GACTCTCCTT
251 GGACCACACG GGCTTTATCT GAAGTGTCTG GGGAGGACTC AGAAGAAAAG
301 GACAACAGGA AGAACAACAT GAACAGGTCC AACACCATCC AATCTGGTCC
351 AGAAGGCAGC CTGGTCAACT CTCAGTCTTT AAAGTCCATT CCTGAGAAGT
401 TTGTAGTTGA TAAATCCACT GCAGGGGCTC TGGATAAAAA GGAAGGTGAG
451 CAGGCTAAGG CTTTATTGGA GAAGGTGAAG AAGTTCAGGC TGCATGTGGA
501 AGAAGGTGAT ATTCTATATG CCATGTATGT TCGCCAGACT GTACTTAAAG
551 TTATCAAATT CCTAATCATC ATTGCATATA ATAGTGTCTT GGTTTCCAAG
601 GTCCAGTTTA CAGTGGACTG TAATGTGGAC ATTCAGGACA TGACTGGATA
651 TAAAAACTTT TCTTGCAATC ATACCATGGC ACACTTGTTT TCAAACTGT
701 CCTTTTGCTA TCTGTGCTTT GTTAGTATCT ATGGATTGAC GTGCCTTTAT
751 ACCTTATACT GGCTGTTCTA CCGTTCTCTA CGGGAATATT CCTTTGAGTA
801 TGCCCGTCAG GAGACTGGAA TTGATGATAT TCCAGATGTG AAAAATGACT
851 TTGCTTTTAT GCTTCATATG ATAGATCAGT ATGACCTCTT CTATTCCAAG
901 AGATTTGAGG TGTTCTCTG TGAAGTCAGT GAAAACAAAT TAAAGCAGCT
951 GAACCTAAAT AACGAATGGA CTCTGATAA ACTGAGGCAG AAGCTACAGA
1001 CAAATGCCCA TAATCGACTG GAATGCTCTT TTATCATGCT CTCTGGCCTT
1051 CCAGACACTG TTTTGAATC CACAGAGTTG CAATCTCTAA AACTTGAAAT
1101 CATTAAGAAC GTAATGATAC CAGCCACCAT TGCACAGCTA GACAATCTTC
1151 AAGAGCTCTC TCTGCACCAG TGTTCTGTCA AAATCCACAG TCGCGCGCTC
1201 TCTTTCCTGA AGGAAAACCT CAAGGTCTTG AGCGTCAAGT TTGATGACAT
1251 GAGGGAACCT CCCCCCTGGA TGTATGGGCT CCGAAATCTG GAAGAGCTGT
1301 ACCTAGTTGG CTCTCTAAGT CATGATATT CCAGAAATGT CACCCTTGAG
1351 TCTCTGCGGG ATCTCAAAAG CCTTAAATTT CTCTCTATCA AAAGCAACGT
1401 TTCCAAAATC CCTCAGGCAG TGGTTGATGT TTCCAGCCAT CTCCAGAAGA
1451 TGTGCATACA TAATGATGGC ACCAAGCTGG TGATGCTCAA CAACTTAAAG
1501 AAGATGACCA ATCTGACAGA GCTGGAGCTG GTCCACTGTG ACCTGGAGCG
1551 TATTCTCAT GCTGTGTTCA GCCTACTCAG CCTCCAGGAA TTGGACCTGA
1601 AGGAAAACAA TCTGAAATCT ATAGAAGAAA TCGTTAGCTT TCAGCACTTA
1651 AGAAAGTTGA CAGTGCTAAA ACTGTGGCAT AACAGCATCA CCTACATCCC
1701 AGAGCATATA AAGAAATCA CCAGCCTGGA ACGCCTGTCC TTTAGTCACA
1751 ATAAAATAGA GGTGCTGCCT TCCCACCTCT TCCTATGCAA CAAGATCCGA
1801 TACTTGGACT TATCGTACAA TGACATTCTG TTTATCCCCC CTGAAATTGG
1851 AGTTCTACAA AGTTTACACT ATTTTCCAT CACATGTAAC AAAGTGGAAA
1901 GCCTTCCAGA TGAACCTTAC TTCTGCAAGA AACTTAAAC TCTGAAGATT
1951 GGAAAAACA GCCTATCTGT ACTTTCACCG AAAATTGGAA ATTTGCTATT
2001 TCTTTCCTAC TTAGATGTAA AAGGTAATCA CTTTGAAATC CTCCCTCCTG
2051 AACTGGGTG CTGTCGGGCT CTGAAGCGAG CTGGTTTAGT TGTAGAAGAT
2101 GCTCTGTTTG AACTCTGCC TTCTGACGTC CGGGAGCAAA TGAAAAACAGA
2151 ATAACTTATT TTTCGTTAAA GTTTGACTGA AACACGCTTC TACCAATAC
2201 AGTATAAATA ATTAGGTAGT CTTAATGCCT TTCTATTTT TTTTTCCTTT
2251 TCACACAAA TGTACACAAA GATCGCGTAA GGAGTATGTA TTTTAAATAA
2301 AAATTTAATT GTATTTTTC AATATTAATA AAAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

96421675:
 Characterization of densin-180, a new brain-specific synaptic protein
 of the
 O-sialoglycoprotein family.

98337190:
 SUR-8, a conserved Ras-binding protein with leucine-rich
 repeats, positively regulates Ras-mediated signaling in *C.*
elegans.

Peptide information for frame 1

ORF from 28 bp to 2151 bp; peptide length: 708
 Category: similarity to known protein
 Classification: Cell signaling/communication

```

1 MKGLKTDLDL QQYSFINQMC YERALHWYAK YFPYLVLHT LVFMLCSNFW
51 FKFPGSSSKI EHFISILGKC FDSPWTTTRAL SEVSGEDSEE KDNRKNNMNR
101 SNTIQSGPEG SLVNSQSLKS IPEKFVVDKS TAGALDKKEG EQAKALFEKV
151 KKFRHLHVEEG DILYAMYVRQ TVLKVIKFLI IIAYSALVS KVQFTVDCNV
201 DIQDMTGYKN FSCNHTMAHL FSKLSFCYLC FVSIYGLTCL YTLYWLFYRS
251 LREYSFEYVR QETGIDDIPD VKNDFAFMLH MIDQYDPLYS KRFVFLSEV
301 SENKQLQNL NNEWTPDKLR QKLQTNANHR LELPLIMLSG LPDVFTEITE
351 LQSLKLEIK NVMIPATIAQ LDNLQELSLH QCSVKIHSAA LSFLKENLKV
401 LSVKFDMDRE LPPWMYGLRN LEELYLVGSL SHDISRNVTL ESLRDLKSLK
451 ILSIKSNVSK IPQAVVDVSS HLQKMCIHND GTKLVMLNNL KKMTNLTELE
501 LVHCDLERIP HAVFSLSLQ ELDLKENNLK SIEEIVSFQH LRKLTVLKLW
551 HNSITYIEH IKKLTSLERL SFSHNKLEVL PSHLFLCNKI RYLDLSYNDI
601 RFIPPEIGVL QSLQYFSITC NKVESLPDEL YFCKKLTCLK IGKNSLSVLS
651 PKIGNLLFLS YLDVKGNHFE ILPELGDCR ALKRAGLVVE DALFETLPSD
701 VREQMKTE
  
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_19j11, frame 1

TREMBL:HSD984_1 gene: "KIAA0231"; Human mRNA for KIAA0231 gene,
 partial cds., N = 1, Score = 1408, P = 4.5e-144

TREMBL:AF054827_1 gene: "soc-2"; product: "leucine-rich repeat protein
 SOC-2"; *Caenorhabditis elegans* leucine-rich repeat protein SOC-2
 (soc-2) mRNA, complete cds., N = 1, Score = 304, P = 5.7e-24

TREMBL:RNU66707_1 product: "densin-180"; *Rattus norvegicus* densin-180
 mRNA, complete cds., N = 1, Score = 311, P = 7.4e-24

TREMBL:AF068921_1 product: "Ras-binding protein SUR-8"; *Mus musculus*
 Ras-binding protein SUR-8 mRNA, complete cds., N = 1, Score = 302, P =
 1.1e-23

>TREMBL:HSD984_1 gene: "KIAA0231"; Human mRNA for KIAA0231 gene, partial
 cds.

Length = 476

HSPs:

Score = 1408 (211.3 bits), Expect = 4.5e-144, P = 4.5e-144
 Identities = 265/471 (56%), Positives = 361/471 (76%)

```

Query: 237 LTCLYTLWLFYRSREYSFEYVROETGIDDIPDVKNDFAFMLHMIDQYDPLYSKRFAVF 296
      LT Y+L+W+ SL++YSFE +R+++ DIPDVKNDFAF+LH+ DQYDPLYSKRFF+
Sbjct: 1 LTSSYSLWMLRSSLKQYSFEALREKSNYSIDIPDVKNDFAFILHLADQYDPLYSKRFSIF 60

Query: 297 LSEVSENKQLQNLNNEWTPDKLRQKLQTNANHRLELPLIMLSGLPDTVFEITELQSLKL 356
      LSEVSENKQLQ+NLNNEWTPDKLRQKLQTNANHRLELPLIMLSGLPDTVFEITELQSLKL
Sbjct: 61 LSEVSENKQLQINLNNEWTPDKLRQKLQTNANHRLELPLIMLSGLPDTVFEITELQSLKL 120
  
```

Query: 357 EIIKNVMIPATIAQLDNLQELSLHQCSVKIHSAAFLKLENKVLVSVKFDDMRELPPWY 416
 E+I V +P+ ++QL NL+EL ++ S+ + AL+FL+ENLK+L +KF +M ++P W++
 Sbjct: 121 ELIPEVKLPASVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTMGKIPRWVF 180

Query: 417 GLRNLEELYLVGSLSHDISRNVLTLESRLDKSLKILSIKSNVSKIPOAVVDVSSHLOKMC 476
 L+NL+ELYL G + + + LE +DLK+L+ L +KS++S+IPO V D+ LOK+
 Sbjct: 181 HLKKNLKEYLSCVLPQLSTMQLEGFQDLKNLRTLYLKSSLSRIPQVVTDLPSLQKLS 240

Query: 477 IHNDGTKLVMLNNLKKMTNLTELELVHCDLERIPHAVFSLSLQELDLKNNLKSIEETV 536
 + N+G+KLV+LNNLKKM NL LEL+ CDLERIPH++FSL +L ELDL+ENNLK++EEI+
 Sbjct: 241 LDNEGSKLVVLNNLKKMVNLKSLELISCDLERIPHSIFSLNNLHEDLDRENNLKTVEEII 300

Query: 537 SFQHLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPShLFLCNKIRYLDLS 596
 SFQHL+ L+ LKLWHN+I YIP I L++LE+LS HN IE LP LFLC K+ YLDLS
 Sbjct: 301 SFQHLQNLSCKLWHNNIAYIPAIGALSNLQSLDHNNIENLPQLQLFLCTKLHYLDLS 360

Query: 597 YNDIRFIPPEIGVLQSLQYFSITCNKVESLPDELYFCKKLTLLKIGKNSLSVLSPKIGNL 656
 YN + FIP EI L +LQYF++T N +E LPD L+ CKKL+ L +GKNSL LSP +G L
 Sbjct: 361 YNHLTFIPEEIQLYLSNLQYFAVTNNNIEMLPDGLFQCKKLQCLLLGKNSLMNLSPHVGEL 420

Query: 657 LFLSYLDVKGNHFEILPPELGDCRALKRAGLVVEDALFETLPDSDVREQMKT 707
 L++L++ GN+ E LPPEL C++LKR L+VE+ L TLP V E++T
 Sbjct: 421 SNLTHLELIGNYLETLPELEGCSQSLKRNCLIVEENLLNTLPLPVTERLQT 471

Pedant information for DKFZphut1_19j11, frame 1

Report for DKFZphut1_19j11.1

[LENGTH] 708
 [MW] 81812.82
 [pI] 7.55
 [HOMOL] TREMBL:HSD984_1 gene: "KIAA0231"; Human mRNA for KIAA0231 gene, partial cds.
 1e-149

[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YJL005w] 3e-17
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YJL005w] 3e-17
 [FUNCAT] 10.04.03 second messenger formation [S. cerevisiae, YJL005w] 3e-17
 [FUNCAT] 01.03.10 metabolism of cyclic and unusual nucleotides [S. cerevisiae, YJL005w] 3e-17
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YJL005w] 3e-17
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKL193c] 3e-09
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YKL193c] 3e-09
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YAL021c] 9e-08
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YAL021c] 9e-08
 [FUNCAT] 01.01.04 regulation of amino-acid metabolism [S. cerevisiae, YAL021c] 9e-08
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR353c] 3e-07
 [BLOCKS] BL00868F
 [BLOCKS] BL00985B Spermadhesins family proteins
 [EC] 3.4.17.3 Lysine carboxypeptidase 1e-08
 [EC] 4.6.1.1 Adenylate cyclase 3e-18
 [PIRKW] blocked amino end 1e-10
 [PIRKW] phosphotransferase 1e-09
 [PIRKW] nucleus 6e-08
 [PIRKW] duplication 3e-18
 [PIRKW] platelet 1e-10
 [PIRKW] tandem repeat 7e-16
 [PIRKW] keratan sulfate 7e-07
 [PIRKW] metallo-carboxypeptidase 1e-08
 [PIRKW] transmembrane protein 1e-10
 [PIRKW] serine/threonine-specific protein kinase 1e-09
 [PIRKW] autophosphorylation 1e-09
 [PIRKW] cartilage 7e-07
 [PIRKW] connective tissue 7e-07
 [PIRKW] magnesium 1e-09
 [PIRKW] cAMP biosynthesis 3e-18
 [PIRKW] ATP 1e-09
 [PIRKW] receptor 1e-09
 [PIRKW] leucine zipper 3e-13
 [PIRKW] glycoprotein 5e-12
 [PIRKW] extracellular matrix 7e-07
 [PIRKW] chondroitin sulfate proteoglycan 7e-07
 [PIRKW] cell adhesion 1e-08
 [PIRKW] hydrolase 1e-08
 [PIRKW] sulfoprotein 7e-07
 [PIRKW] membrane protein 1e-08
 [PIRKW] phosphorus-oxygen lyase 3e-18

```
[PIRKW] collagen binding 7e-07
[SUPFAM] leucine-rich alpha-2-glycoprotein repeat homology 3e-21
[SUPFAM] chaoptin 1e-08
[SUPFAM] gelsolin repeat homology 3e-21
[SUPFAM] protein kinase homology 1e-09
[SUPFAM] protein kinase Xa21 1e-09
[SUPFAM] fibromodulin 4e-12
[SUPFAM] yeast adenylate cyclase catalytic domain homology 3e-18
[SUPFAM] yeast adenylate cyclase 3e-18
[KW] TRANSMEMBRANE 3
[KW] LOW COMPLEXITY 1.41 %
```

```
SEQ      MKGLKTDLDLQQYSFINQMCYERALHWYAKYFPYLVIHTLVFMLCSNFWFKFPGSSSKI
SEG      .....
PRD      cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhcccceeeeccccccce
MEM      ..MMMMMMMMMMMMMMMMMMMMMM.....
```

```
SEQ      EHFISILGKCFDSPWTTTRALSEVSGEDSEEKDNRKNMNRSTNTIQSGPEGSLVNSQSLKS
SEG      . . . . .
PRD      eeeeeeeccccccccceeeeeccccccccccccccccccccccccccccccccceeecccccc
MEM
```

```
SEQ      IPEK FVVDKSTAGALDKKEGEQAKALFEKVKKFLRHVEEGDILYAMYVRQTVLKVIKFLI
SEG      .....
PRD      cccceeeccccccccchhhhhhhhhhhhhhhhhhhhhccccceehhhhhhhhhhhhhhhhh
MEM      MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM
```

[illegible]

```
SEQ      YTLYWLFYRSLREYSFEYVRQETGIDDIPDVKNDFAFMLHMIDQYDPLYSKRAVFLSEV
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhccccchhhhhhhhhhhhhhh
MEM      .....
```

```
SEQ      SENKCLKQLNLNNEWTPDKLRQKLQTAHNRLELPLIMLSGLPDTVFEITELQSLKLEIK
SEG      ..xxxxxxxxxx.....
PRD      hhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhh
MEM      .....
```

```

SEQ      NVMI PATT AQLDNLQELS LHQCSVKI HSAALS FLKENL KVL SVK FDDMREI LPW MYGLRN
SEG      . . . . .
PRD      hccccccchhhhhhhhhhhhhccccccccccccchhhhhhhhhccccccccccccchhh
MEM

```

```
SEQ      LEELYLVGSLSHDISRNVLTLESRLDKSLKILSIKSNVSKIQAQVVDVSSHLOKMCIHND
SEG
PRD      hhhhhhhccccccccccccccccchhhhhhhhhhhhhccccccccccccchhhhhhhhhhhcccc
MEM      .....
```

```

SEQ      GTKLVMLNNLKKMTNLTELELVHCDLERIPHAVFSLSLQELDLKNNLKSIEEIVSFOH
SEG      .....
PRD      ceeeeccccccchhhhhhhhhccccccccccchhhhhhhhhccccccccccccccch
MFM

```

```
SEQ      LRKLTVLKWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSHLFLCNKIRYLDLSYNDI
SEC
PRD      hhhhhhhccccceeeccccchhhhhheeeccccceeeccccchhhhhhhhcccc
MEM
```

```
SEQ      RFIPPEIGVLQSLQYFSITCNKVESLPDELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLS
SEG      .....
PRD      cccccccchhhhhhhhhhhhhccccccccccccchhhhhccccccccceccccccccchhh
MEM      .....
```

```
SEQ      YLDVKGNHFEILPPELGDCRALKRAGLVVEDALFETLPSDVREQMTE
SEC      .....
PRD      hhccccccccccccchhhhhhhheeecccccccccccccccccc
MEM      .....
```

(No Prosite data available for DKFZphut1_19j11.1)

(No Pfam data available for DKFZphut1_19j11.1)

DKFZphut1_li2

group: transcription factor

DKFZphut1_li2 encodes a novel 594 amino acid protein similar to signal transducing proteins.

The protein contains 2 WD-40 repeats, which is typical for the beta-transducin subunit of G-proteins. In addition, the protein contains a C3HC4 zinc finger and a leucine zipper. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. Due to the zinc finger the novel protein seems to be a new molecule involved in signal transduction and transcription.

The new protein can find application in modulating/blocking gene expression of genes controlled by this molecule.

similarity to Dictostelium myosin heavy chain kinase

complete cDNA, complete cds, EST hits
[PFAM] Zinc finger, C3HC4 type (RING finger)
[PFAM] WD domain, G-beta repeats
[SCOP] dltbpc_2.46.3.1.1 betal-subunit of the
signal-transducing G protei 3e-07

Sequenced by BMF2

Locus: /map="16p13.3"

Insert length: 3584 bp

Poly A stretch at pos. 3555, polyadenylation signal at pos. 3537

```
1 GGGCGGGAGG TGCTTCCCAA GGACCGTAGA TGCCTCTCTA GAGCATGAGC
51 TCAGGCAAGA GTGCCCCTCA CAACCGCTTC TCCGGGGGGC CCAGCAATCT
101 TCCCAACCCA GACGTCACCA CAGGGACACG AATGGAAACG ACCTTCGGAC
151 CCGCCTTTTC AGCCGTCACC ACCATCACA AAGCTGACGG GACCAAGACC
201 TACAAGCAGC ACTGCAGGAC AGCATGCCCC CCATCAGCAC TCCCCGCCGC
251 TCCGACTCCG CCATCTCTGT CCGCTCCCTG CACTCAGAGT CCAGCATGTC
301 TCTGCGCTCC ACATTCTCAC TGCCCGAGGA GGAGGAGGAG CCGGAGCCAC
351 TGGTGTTCGC GGAGCAGCCC TCGGTGAAGC TGTGCTGTCA GCTCTGTGTC
401 AGCGTCTTCA AAGACCCCGT GATCACCACG TGTGGGCACA CGTTCTGTAG
451 GAGATGCGCC TTGAAGTCAG AGAAGTGTC CGTGGACAAC GTCAAACTGA
501 CCGTGGTGGT GAACAACATC GCGGTGGCCG AGCAGATCGG GGAGCTCTTC
551 ATCCACTGCG GGCACGGCTG CCGGTAGCGG GGCAGCGGGA AGCCCCCAT
601 CTTTGAGCTG GACCCCGGAG GGTGCCCTT CACCATCAAG CTCAGCGCCC
651 GGAAGGACCA CGAGGGCAGC TGTGACTACA GGCTGTGCG GTGTCCCAAC
701 AACCCCAAGT GCCCCCCGCT GCTCAGGATG AACCTGGAGG CCCACCTCAA
751 GGAGTGCAG CACATCAAAT GCCCCACTC CAAGTACGGG TGCACGTTC
801 TCGGGAACCA GGACACTTAC GAGACCCACC TGAGACTTGG CCGCTTCGAG
851 GGCCTGAAGG AGTTTCTGCA GCAGACGGAT GACCGCTTCC ACGAGATGCA
901 CGTGGCTCTG GCCCAGAAGG ACCAGGAGAT CGCCTTCCTG CGCTCCATGC
951 TGGGAAAGCT CTCGGAGAAG ATCGACCAGC TAGAGAAGAG CCTGGAGCTC
1001 AAGTTTGAGC TCTGGACGA AAACCAAGAG AAGCTCAGCG AGGACCTCAT
1051 GGAGTTCCGG CGGGACGCAT CCATGTTAAA TGACGAGCTG TCCACATCA
1101 ACGCGCGGCT GAACATGGGC ATCCTAGGCT CCTACGACCC TCAGCAGATC
1151 TTCAAGTGCA AAGGGACCTT TGTGGGCCAC CAGGGGCCCTG TGTGGTGTCT
1201 CTGCGTCTAC TCCATGGGTG ACCTGCTCTT CAGTGGCTCC TCTGACAAGA
1251 CCATCAAGGT GTGGGACACA TGTACCACCT ACAAGTGTC GAAGACACTG
1301 GAGGGCCATG ATGGCATCGT GCTGGCTCTC TGCATCCAGG GGTGCAAACT
1351 CTACAGCGGC TCTGCAGACT GCACCATCAT TGTGTGGGAC ATCCAGAACC
1401 TGCAGAAGT GAACACCATC CGGGCCCATG ACAACCCGGT GTGCACGCTG
1451 GTCTCCTCAC ACAACGTGCT CTTACGCGG TCCCTGAAGG CCATCAAGGT
1501 CTGGGACATG GTGGGCACTG AGCTGAAGTT GAAGAAGGAG CTCACAGGCC
1551 TCAACCACTG GGTGCGGGCC CTGGTGGCTG CCCAGAGCTA CCTGTACAGC
1601 GGCTCCTACC AGACAATCAA GATCTGGGAC ATCCGAACCC TTGACTGCAT
1651 CCACGTCCTG CAGACGCTG GTGGCAGCGT CTAATCCATT GCTGTGACAA
1701 ATCACCACAT TGTCTGTGGC ACCTACGAGA ACCTCATCCA CGTGTGGGAC
1751 ATTGAGTCCA AGGAGCAGGT GCGGACCCCTC ACGGGCCACG TGGGCACCGT
1801 GTATGCCCTG GCGGTCTATC CGACGCCAGA CCAGACCAAA GTCTTCAGTG
1851 CATCCTACGA CCGGTCCCTC AGGGTCTGGA GTATGACAAA CATGATCTGC
1901 ACGCAGACCC TGCTGCGTCA CCAGGGCAGT GTCACCGCGC TGGCTGTGTC
1951 CCGGGGGCGA CTCTTCTCAG GGGCTGTGGA TAGCACTGTG AAGGTTTGGA
2001 CTTGCTAACA GGATCCAGGC CAGGCTGTGG TTTCCCTGA ACCAGCGCTG
2051 GACCTTTCTG AGCCAGGCTG GCCACATGGG GTGGTCTCGG GGTTCCTGCC
2101 TGCCCCGTGG GCATAGGTGG ACAGGCTCTG GCAGCCGGGC AGTGCCCTCC
2151 CCGTCCCTAG CTCGGCGAGC CTCCCTCTAC TCGGCACTGT CTTGCTGCCC
2201 CAGCCCCCTC CTGGGTGCCA GGTACGACGC TTGCCCCGGC CCACCTCTCA
2251 TCCCCACCTT CCATCCCCAC CCTAGATGGA GCGAGGGCCT TTTTACTCAC
2301 CTTTTCTACC GTTTTATAGC TGTATGTAGA TTTGGTTACC TCCTGGTTGA
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2351 AATAAATGCT CCACAGACTG TGGCTGTGAG TGGGGACAGC TCCTCGGGAC
2401 AAGGGGGCTG TGTGTGGCCT TGAGGTTGGT GTGCACAGGC ACTGGCTGCT
2451 GTGAGTGGGG GGGCATGGGG CAGTTTCCTT TGGTGGACCC CAGGACTTCG
2501 GCCCACTCCG GGGCCTCCCC TCCCTGCTAG GAGGCAACTC GTCACACCCA
2551 AGCTGCTGGC CTCCAGTCCC ATCTCCCCCA ACACATGTGC CCCCCAAAAG
2601 TGAGCCAGGC ACCTCTGTTT CCTGCTGTTT ATTGACAGCC GACGGCAGCG
2651 CCTTGCCCGC ACCTCCCTG CCCACCTGCT GGAGCCAGC CTGTGCCGCC
2701 CTCTGAGGAG AGGCCTGGGG GGACAGCTGG GCACGTCCAC TCGCAGGGAA
2751 ACACGGGGTG AGACAGCAGG AAGGGGCCCT GCACGCCGGG ACGCCACCTC
2801 CGCCAGCCGC CTCCACCCGC CCCACACCAC AATCGCTGGT TTTCCGCATT
2851 TTTTAAATTT TTTTTTTAAAG AAACGTCAAA GTTGTGCCCA ACACGTGTGA
2901 TCAGCAAACA CGATAGAGGA GACCAGTCAG TACTTCTTGG AGGGGGCAGG
2951 AGGAGAGAGG AAAAGGGAGG GCGAGAATGA CCACACAACA CAGCCTTGGA
3001 CCATGAGCAG AAGCGTCCGT GGGAACTCCA CTGGGGTGGA TGGGCTGCCT
3051 GCACAGCCCC TGGAGAGGGG GCCAGGCACA CCCTCAGAGG AGCTGCAAGC
3101 CCGTGGCCTG GCCTGCTACA TGCCCTGCTT CCACGTGGCT GCCACGCTGA
3151 CACACCCACA TTCACCAAAC CCACCCGCGC CCTGGGACGC AGCCACGCCA
3201 GGAGGAGGAC ACGGCCGCCG AGAGCAAGGC ACAACCTCGA GTTCTTGGGG
3251 CGCAGAGAAC TTAGGAGAGA AGCACGGAGG AGCCCCGGGC AGAGCACCCG
3301 CCCCCGGGCC CCAGCCTTCC ACCTGTGCTA GCAGCCTGGG GCCTCCACTC
3351 TGGCCGGAGG AAGGACCGCA GGCAGACAGC CTGGGCCTCT AACAGCTTTT
3401 GTCCGGAGCT AGACTTCGTG TCCTTTCAGT TGGTAAATGG TTTTCTATAG
3451 AATCAATAAT ATTTCTTTCT TTAATATAT ATTTGTAAAG GTTATACCTT
3501 TTTGTTTCTC TGGGGAATC CGCCTCAGCT CATTCCCAAT AAATTAATAC
3551 TCTTGATAAA AAAAAAAAAA AGAAAAAAAA AAAA

```

BLAST Results

Entry HSBE from database EMBL:

Homo sapiens (clone exon trap d5) chromosome 16p13.3 gene, exon.
Score = 2375, P = 7.1e-101, identities = 475/475

Entry HSBD from database EMBL:

Homo sapiens (clone exon trap d32) chromosome 16p13.3 gene, exon.
Score = 876, P = 3.0e-31, identities = 176/177

Medline entries

95122486:

Structural analysis of myosin heavy chain kinase A from Dictyostelium. Evidence for a highly divergent protein kinase domain, an amino-terminal coiled-coil domain, and a domain homologous to the beta-subunit of heterotrimeric G proteins.

96149460:

Dictyostelium myosin heavy chain kinase A regulates myosin localization during growth and development.

97277316:

Identification of a protein kinase from Dictyostelium with homology to the novel catalytic domain of myosin heavy chain kinase A.

96009891:

A gene responsible for vegetative incompatibility in the fungus Podospora anserina encodes a protein with a GTP-binding motif and G beta homologous domain.

Peptide information for frame 2

ORF from 224 bp to 2005 bp; peptide length: 594

Category: similarity to known protein

Prosites motifs: ZINC_FINGER_C3HC4 (70-80)

LEUCINE_ZIPPER (436-458)

LEUCINE_ZIPPER (436-458)

G_BETA_REPEATS (335-355)

G_BETA_REPEATS (376-391)

```

1 MPPISTPRRS OSAISVRSLSH SESSMSLRST FSLPEEEEEEP EPLVFAEQPS
51 VKLCCQLCCS VFKDPVITTC GHTFCRRCAL KSEKCPVDNV KLTVVVNNIA
101 VAEQIGELFI HCRHGCRVAG SGKPPIFEVD PRGCPFTIKL SARKDHEGSC
151 DYRPVRCFNN PSCPPLLRMN LEAHLKECEH IKCPHSKYGC TFIGNQDTYE
201 THLETCTREFG LKEFLQQTDD RFHEMHVALA QKDOEIAFLR SMLGKLSEKI
251 DQLEKSLELK FQVLDENQSK LSEDLMEFRR DASMLNDELH HINARLNMGI
301 LGSYDPQQIF KCKGTFVGHQ GPVWCLCVYS MGDLLFSGSS DKTIKVWDTG
351 TTYKCQKTLE GHGIVLALC IQGCKLYSGS ADCTIIVWDI QNLQKVNTIR
401 AHDNPVCTLV SSHNVLFSGS LKAIKVWDIV GTELKLKKEG TGLNHWVRAL
451 VAAQSYLYSG SYQTIKIWDI RTLDICHLVQ TSGGSVYSIA VTNHHIVCGT
501 YENLIHVWDI ESKEQVRLT GHVGTVYALA VISTPDQTKV FSASYDRSLR
551 VWSMDNMICT QTLRHQGSV TALAVSRGRL FSGAVDSTVK VWTG

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutcl_1i2, frame 2

SWISSPROT:KMHB_DICDI MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B)., N = 1, Score = 419, P = 3.6e-37

SWISSPROT:HET1_PODAN VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1., N = 1, Score = 392, P = 3.1e-33

SWISSPROT:YDJ5_SCHPO HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I., N = 1, Score = 357, P = 4.1e-30

TREMBL:AF032878_1 gene: "slimb"; product: "Slimb"; Drosophila melanogaster Slimb (slimb) mRNA, complete cds., N = 1, Score = 347, P = 1.7e-29

>SWISSPROT:KMHB_DICDI MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
Length = 732

HSPs:

Score = 419 (62.9 bits), Expect = 3.6e-37, P = 3.6e-37
Identities = 96/268 (35%), Positives = 158/268 (58%)

Query: 325 CLCVYSMGDLLFSGSSDKTIKVD-TCTTYKCQKTLEGHGIVLALCIQGCKLYSGSADC 383
C+C +LLF+G SD +I+V+D +C +TL+GH+G V ++C L+SGS+D
Sbjct: 467 CIC----DNLLFTGCSDNSIRVYDKSQNMCEVQTLKGHEGPVESICYNDQYLFSGSSDH 522

Query: 384 TIIVWDIQNLQKVNTIRAHNDNPVCTLVSSHNVLFSGSL-KAIKVDIVGTTELKLKKEGTC 442
+I VWD++ L+ + T+ HD PV T++ + LFSGS K IKVWD+ L+ K L
Sbjct: 523 SIKVWDLKLLRCIFTLEGHDKPVHTVLLNDKYLFGSSDKTIKVDL--KTLECKYTLES 580

Query: 443 LNHVVRALVAAQSYLYSGSY-QTIKIWDI RTLDICHLVQ TSGGSVYSIA VTNHHIVCGTY 501
V+ L + YL+SGS +TIK+WD++T C + L+ V +I + ++ G+Y
Sbjct: 581 HARAVKTLCSIGQYLFSGSNDKTIKVDLKTFRCNVTLKGHTKWVTTICILGTNLYSGSY 640

Query: 502 ENLIHVWDIESKEQVRLTGHVGTVYALAVISTPDQTKVFSASYDRSLRVWSMDNMICTQ 561
+ I VW+++S E TL GH V + + D+ +F+AS D +++W ++ + C
Sbjct: 641 DKTIRVWNLKSLECSATLRGHRWVEHVMVIC---DKL-LFTASDDNTIKIWDLETLCRNT 696

Query: 562 TLLRHQGSVTALAVSRGR--LFSGAVDSTVKVW 592
TL H +V LAV + + S + D +++VW
Sbjct: 697 TLEGHNATVQCLAVWEDKKCVISCSHDQSIRVW 729

Score = 415 (62.3 bits), Expect = 1.2e-36, P = 1.2e-36
Identities = 113/303 (37%), Positives = 166/303 (54%)

Query: 255 KSLEL-KFDVLDENQSKLSEDLMEFRRDASMLNDEL-SHINARLNMGILGS-----YD 305
KS++L K ++L N+ K S +L + ++ + SH+ N+ G YD
Sbjct: 427 KSIDLEKPEILINNKKKESINLETIKLIETIKGYHTSHLCICDNLLFTGCSDNSIRVYD 486

Query: 306 -PQIFKCKGTFVGHQGPVWCLCVYSMGDLLFSGSSDKTIKVDCTTYKCQKTLEGHG 364
Q +C T GH+GPV +C Y+ LFSGSSD +IKVD +C TLEGH
Sbjct: 487 YKSQNMCEVQTLKGHEGPVESIC-YN-DQYLFSGSSDHSIKVDL-KKLRICFTLEGHDK 543

Query: 365 IVLALCIQGCKLYSGSADCTIIVWDIQNLQKVNTIRAHNDNPVCTLVSSHNVLFSGSL-KA 423
V + + L+SGS+D TI VWD++ L+ T+ +H V TL S LFSGS K
Sbjct: 544 PVHTVLLNDKYLFGSSDKTIKVDLKTLECKYTLESHARAVKTLCSIGQYLFSGSNDKT 603

Query: 424 IKVWDIVGTTELKLKKEG TGLNHWVRALVAAQSYLYSGSY-QTIKIWDI RTLDICHLVQTS 482
IKVWD+ + L G WV + + LYSGSY +TI++W++++L+C L+
Sbjct: 604 IKVWDL--KTFRCNVTLKGHTKWVTTICILGTNLYSGSYDKTIRVWNLKSLECSATLRG 661

Query: 483 GGSVYSIAVTNHHIVCGTYENLIHVWDIESKEQVRTLTGHVGTVYALAVISTPDQTKVFS 542
 V + + + + + +N I +WD+E+ TL GH TV LAV D+ V S
 Sbjct: 662 DRWVEHVMICDKLLFTASDDNTIKIWDLETLCRNTTLEGHNATVQCLAVWE--DKKCVIS 719

Query: 543 ASYDRSLRVW 552
 S+D+S+RVW
 Sbjct: 720 CSHDQSIQIRVW 729

Score = 262 (39.3 bits), Expect = 3.2e-19, P = 3.2e-19
 Identities = 60/184 (32%), Positives = 109/184 (59%)

Query: 352 TYKCKTLEGHGDIVLALCIQGGCKLYSGSADCTIIVWDI--QNLQKVNTIRAHDNPNVCTL 409
 T K +T+G+ + LCI L++G +D +I V+D QN++ V T++ H+ PV ++
 Sbjct: 450 TIKLIETIKGYH-VTSHLCICDNLLFTGCSDNSIRVYDYKSONMECVQTLKGHEGPVESI 508

Query: 410 VSSHNVLFSGLK-AIKVWDIVGTELKLLKELTGLNHWVFEALVAAQSYLYSGSY-QTIKI 467
 + LFSGS +IKVWD+ +L+ L G + V ++ YL+SGS +TIK+
 Sbjct: 509 CYNDQYLFSGSSDHSIKVWDL--KKLRIFTLEGHDKPVETVLLNDKYLFSGSSDKTIKV 566

Query: 468 WDIRTLDCIHVLQTSGGSVYSIAVTNHHIVCGTYENLIHVWDIESKEQVRTLTGHVGTVY 527
 WD++TL+C + L++ +V ++ ++ ++ G+ + I VWD+++ TL GH V
 Sbjct: 567 WDLKTLECKYTLESHARAVKTLICISGQYLFSGSNDKTIKVWDLKTFRCNYTLKGHTKWVT 626

Query: 528 ALAVIST 534
 + ++ T
 Sbjct: 627 TICILGT 633

Score = 173 (26.0 bits), Expect = 1.7e-09, P = 1.7e-09
 Identities = 43/118 (36%), Positives = 65/113 (55%)

Query: 310 FKCKGTFVGHQGPVWCLCVYSMGDLLFSGSSDKTIKVWDTCTTYKCKTLEGHGDIVLAL 369
 F+C T GH V +C+ +G L+SGS DKTIVW+ + +C TL GHD V +
 Sbjct: 612 FRCNYTLKGHTKWVTTCICI--LGTNLYSGSYDKTIRVWNL-KSLECSATLRGHRWVEHM 668

Query: 370 CIQGGCKLYSGSADCTIIVWDIQLQKVNTIRAHDNPNV-CTLVSSHN--VLFSGSLKAIKV 426
 I L++ S D TI +WD++ L+ T+ H+ V C V V+ ++I+V
 Sbjct: 669 VICDKLLFTASDDNTIKIWDLETLCRNTTLEGHNATVQCLAVWEDKKCVISCSHDQSIQIRV 728

Query: 427 W 427
 W
 Sbjct: 729 W 729

Pedant information for DKFZphutel_1i2, frame 2

Report for DKFZphutel_1i2.2

[LENGTH] 594
 [MW] 66541.94
 [pI] 6.64
 [HOMOL] SWISSPROT:KMHB_DICDI MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B). 3e-37

[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YIL046w] 5e-21
 [FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YIL046w] 5e-21
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YIL046w] 5e-21
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YIL046w] 5e-21
 [FUNCAT] 01.01.04 regulation of amino-acid metabolism [S. cerevisiae, YIL046w] 5e-21
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YCR072c beta-transducin family] 2e-15
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YFL009w] 1e-14
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL009w] 1e-14
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YFL009w] 1e-14
 [FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YFL009w] 1e-14
 [FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YDL145c] 1e-13
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL145c] 1e-13
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPR178w] 2e-11
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR178w] 2e-11
 [FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YBR198c TAF90 - TFIID subunit] 3e-11
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YLR129w] 8e-09
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YCR057c] 2e-07
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YCR057c] 2e-07
 [FUNCAT] 02.16 fermentation [S. cerevisiae, YMR116c] 5e-07
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YMR116c] 5e-07

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[FUNCAT] 06.13 proteolysis [S. cerevisiae, YGL003c] 3e-06
[FUNCAT] 03.01 cell growth [S. cerevisiae, YKL021c] 2e-04
[FUNCAT] 01.03.07 deoxyribonucleotide metabolism [S. cerevisiae, YOR269w] 2e-04
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YOR212w] 0.001
[FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YOR212w] 0.001
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins
[S. cerevisiae, YOR212w] 0.001
[BLOCKS] BL00678
[BLOCKS] BL00518 Zinc finger, C3HC4 type, proteins
[SCOP] dltbgd_2.46.3.1.1 betal-subunit of the signal-transducing 3e-10
[EC] 2.7.1.129 Myosin-heavy-chain kinase 3e-26
[PIRKW] phosphotransferase 3e-26
[PIRKW] nucleus 1e-06
[PIRKW] plasma 9e-08
[PIRKW] duplication 3e-25
[PIRKW] hormone 9e-08
[PIRKW] zinc 3e-09
[PIRKW] cell cycle control 4e-13
[PIRKW] transmembrane protein 3e-12
[PIRKW] zinc finger 1e-08
[PIRKW] stomach 9e-08
[PIRKW] DNA binding 9e-06
[PIRKW] autophosphorylation 3e-26
[PIRKW] phosphoprotein 3e-26
[PIRKW] signal transduction 5e-08
[PIRKW] heterotrimer 5e-08
[PIRKW] coiled coil 3e-26
[PIRKW] multimer 3e-26
[PIRKW] transcription regulation 4e-10
[PIRKW] GTP binding 5e-08
[SUPFAM] chromobox homology 9e-06
[SUPFAM] RING finger homology 3e-09
[SUPFAM] coatamer complex beta' chain 1e-07
[SUPFAM] WD repeat homology 3e-26
[SUPFAM] yeast coatamer complex alpha chain 3e-12
[SUPFAM] GTP-binding regulatory protein beta chain 5e-08
[SUPFAM] PRL1 protein 2e-09
[PROSITE] WD_REPEATS 2
[PROSITE] LEUCINE_ZIPPER 1
[PROSITE] MYRISTYL 14
[PROSITE] CK2_PHOSPHO_SITE 4
[PROSITE] ZINC_FINGER_C3HC4 1
[PROSITE] PKC_PHOSPHO_SITE 18
[PROSITE] ASN_GLYCOSYLATION 1
[PFAM] Zinc finger, C3HC4 type (RING finger)
[PFAM] WD domain, G-beta repeats
[KW] Irregular
[KW] 3D
[KW] LOW_COMPLEXITY 6.23 %
[KW] COILED_COIL 6.73 %

```

```

SEQ MPPISTPRRSDAISVRLHSESSMSLRSTFSLPEEEEEPEPLVFAEQPSVKLCCQLCCS
SEG .....XXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXX.....
COILS .....
1gg2B .....

SEQ VFKDPVITTCGHTFCRRALKSEKCPVDNVKLTVVVNNIAVAEQIGELFIHCRHGCRVAG
SEG .....
COILS .....
1gg2B .....

SEQ SGKPPIFEVDPRGCPFTIKLSARKDHEGSCDYRPVRCPPNNPSCPPLLRNLEAHLKECEH
SEG .....
COILS .....
1gg2B .....

SEQ IKCPHISKYGCTFIGNQDTYETHLETCTRFEGLEFLQQTDDRFHEMHVALAQKDQEI AFLR
SEG .....
COILS .....CCCCCCCCCCCCCCCC
1gg2B .....

SEQ SMLGKLSEKIDQLEKSLELKFVDLDENQSKLSEDLMEFRDASMLNDELSHINARLNMG
SEG .....
COILS CCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....
1gg2B .....

SEQ LGSYDPQQIFKCKGTFVGHQGPVWCLCVYSMGDLLFSGSSDKTIKVWDTCTTYKCQKILE
SEG .....
COILS .....EECCCCCEEEEEETTTCEEEEETTTTEEEEEEG-GGCEEEEEEE
1gg2B .....

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SEQ      GHDGIVLALCIQGCKLYSGSADCTIIVWDIQNLQKVNTIRAHDPVCTLVSSHNVLFSGS
SEG      .....
COILS    .....
lgg2B    CCCCCEEEEETTCEEEEEETTTCEEEEEETTTTEEEEE-CTTTTCCCEE.....

SEQ      LKAIKVWDIVGTELKLLKELTGLNHWVRALVAAQSYLYSGSYQTIKIWDIRTLDCIHVLQ
SEG      .....XXXXXXXXXXXXX.....
COILS    .....
lgg2B    .....

SEQ      TSGGSVYSIAVTNNHIVCGTYENLIHVWDIESKEQVRTLTGHVGTVYALAVISTPDQTKV
SEG      .....
COILS    .....
lgg2B    .....

SEQ      FSASYDRSLRVWSDNMICTQTLLRHQGSVTALAVSRGRLFSGAVDSTVKVWTC
SEG      .....
COILS    .....
lgg2B    .....

```

Prosites for DKFZphut1_112.2

PS00001	267->271	ASN_GLYCOSYLATION	PDOC00001
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	15->18	PKC_PHOSPHO_SITE	PDOC00005
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	50->53	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	121->124	PKC_PHOSPHO_SITE	PDOC00005
PS00005	137->140	PKC_PHOSPHO_SITE	PDOC00005
PS00005	141->144	PKC_PHOSPHO_SITE	PDOC00005
PS00005	205->208	PKC_PHOSPHO_SITE	PDOC00005
PS00005	247->250	PKC_PHOSPHO_SITE	PDOC00005
PS00005	340->343	PKC_PHOSPHO_SITE	PDOC00005
PS00005	343->346	PKC_PHOSPHO_SITE	PDOC00005
PS00005	352->355	PKC_PHOSPHO_SITE	PDOC00005
PS00005	398->401	PKC_PHOSPHO_SITE	PDOC00005
PS00005	420->423	PKC_PHOSPHO_SITE	PDOC00005
PS00005	464->467	PKC_PHOSPHO_SITE	PDOC00005
PS00005	548->551	PKC_PHOSPHO_SITE	PDOC00005
PS00005	588->591	PKC_PHOSPHO_SITE	PDOC00005
PS00006	32->36	CK2_PHOSPHO_SITE	PDOC00006
PS00006	201->205	CK2_PHOSPHO_SITE	PDOC00006
PS00006	330->334	CK2_PHOSPHO_SITE	PDOC00006
PS00006	533->537	CK2_PHOSPHO_SITE	PDOC00006
PS00008	115->121	MYRISTYL	PDOC00008
PS00008	133->139	MYRISTYL	PDOC00008
PS00008	194->200	MYRISTYL	PDOC00008
PS00008	299->305	MYRISTYL	PDOC00008
PS00008	314->320	MYRISTYL	PDOC00008
PS00008	364->370	MYRISTYL	PDOC00008
PS00008	379->385	MYRISTYL	PDOC00008
PS00008	419->425	MYRISTYL	PDOC00008
PS00008	460->466	MYRISTYL	PDOC00008
PS00008	484->490	MYRISTYL	PDOC00008
PS00008	499->505	MYRISTYL	PDOC00008
PS00008	524->530	MYRISTYL	PDOC00008
PS00008	568->574	MYRISTYL	PDOC00008
PS00008	583->589	MYRISTYL	PDOC00008
PS00518	70->80	ZINC_FINGER_C3HC4	PDOC00449
PS00029	436->458	LEUCINE_ZIPPER	PDOC00029
PS00678	335->350	WD_REPEATS	PDOC00574
PS00678	376->391	WD_REPEATS	PDOC00574

Pfam for DKFZphut1_112.2

HMM_NAME WD domain, G-beta repeats

HMM *MGHnnWVWCvafSPDGGrWFIVSGSWDgtCRLWD*
 ++GH ++VWC+ + G + ++SGS D+T+++WD

Query 316 FVGHQGPVWCLCVYSMGDL-LFSGSSDKTIKVWD 348

22.93 519 553 1 34 dkfzphut1_112.2 similarity to Dictostelium myosin heavy chain kinase

Alignment to HMM consensus:

Query *MrGHnnWVWCvAF..SPDGzWFIVSGSWDgTCRLWD*
++GH ++V+++A+ +PD ++S+S D+++R+W+
dkFzphute1 519 LTGHVGTVYALAVISTPDQTK-VFSASYDRSLRVWS 553

HMM_NAME Zinc finger, C3HC4 type (RING finger)

HMM *CPICFctFQ1DyPWPFFdePmMlPCGhsFCypCIrrW..CPmC*
C++C + F++P++++CGH+FC+ C +++ CP+
Query 55 CQLC-----CSV---FKDPVITTCGHTFCRRCALKSEKCPVD 88

DKFZphut1_20b19

group: metabolism

DKFZphut1_20b19 encodes a novel 486 amino acid protein with similarity to bacterial sarcosine oxidases (EC 1.5.3.1.)

The novel protein seems to be a novel enzyme with sarcosine oxidase activity.

The new protein can find application in modulation of sarcosine metabolism and as a new enzyme for biotechnologic production processes.

similarity to sarcosine oxidases

membrane regions: 1

Summary DKFZphut1_20b19 encodes a novel 486 amino acid protein, with similarity to sarcosine oxidases.

similarity to sarcosine oxidases

complete cDNA?, complete cds potential start at Bp 48, EST hits,

Sequenced by AGOWA

Locus: unknown

Insert length: 1967 bp

Poly A stretch at pos. 1950, no polyadenylation signal found

```
1 AGCGAGGCAG CAGTGCAGCT TTCAGAGGGT CCGGGCTCAG AGGGGTTATG
51 ATTCGGAGGG TTCTGCCGCA CGGCATGGGC CGGGGCCTCT TGACCCGGAG
101 GCCAGGCACG CGCAGAGGAG GCTTTCTCTT GGAAGGAGT GGAAAGGTGT
151 CTGAGATTAA GAAGAAGATC AAGTCGATCC TGCCTGGAAG GTCCTGTGAT
201 CTACTGCAAG ACACCAGCCA CCTGCCCTCCC GAGCACTCGG ATGTGGTGAT
251 CGTGGGAGGT GGGGTGCTTG GCTTGTCTGT GGCCTATTGG CTGAAGAAGC
301 TGGAGAGCAG ACGAGGTGCT ATTCGAGTGC TAGTGGTGGA ACGGGACCAC
351 ACGTATTAC AGGCCTCCAC TGGGCTCTCA GTAGGTGGA TTTGTGAGCA
401 GTTCTCATTG CCTGAGAACA TCCAGCTCTC CCTCTTTTCA CCCAGCTTTC
451 TACGGAACAT CAATGAGTAC CTGGCCGTAG TCGATGCTCC TCCCCTGGAC
501 CTCCGGTTCA ACCCCTCGGG CTACCTCTTG CTGGCTTCAG AAAAGGATGC
551 TGCAGCCATG GAGAGCAACG TGAAAGTGCA GAGGCAGGAG GGAGCCAAAG
601 TTTCTCTGAT GTCTCTGAT CAGCTTCGGA ACAAGTTTCC CTGGATAAAC
651 ACAGAGGGAG TGGCTTTGGC GTCTTATGGG ATGGAGGACG AAGGTGGTT
701 TGACCCCTGG TGCTGTCTCC AGGGGCTTCG GCGAAAGGTC CAGTCCTTGG
751 GAGTCTTTTT CTGCCAGGGA GAGGTGACAC GTTTGTCTC TTCATCTCAA
801 CGCATGTTGA CCACAGATGA CAAAGCGGTG GTCTTGAAA GGATCCATGA
851 AGTCCATGTG AAGATGGACC GCAGCCTGGA GTACCAGCCT GTGGAATGCG
901 CCATTGTGAT CAACGCAGCC GGAGCCTGGT CTGCGCAAAT CGCAGCACTG
951 GCTGGTGTTG GAGAGGGGCC GCCTGGCACC CTGCAGGGCA CCAAGCTACC
1001 TGTGGAGCCG AGGAAAAGGT ATGTGTATGT GTGGCACTGC CCCCAGGGAC
1051 CAGGCCTAGA GACTCCGCTT GTTGACAGCA CCAAGTGAGC CTATTTTCGC
1101 CGGGAAGGAT TAGGTAGCAA CTACCTAGGT GGTCTGAGCC CCACTGAGCA
1151 GGAAGAACCG GACCCGGCGA ACCTGGAAGT GGACCATGAT TTCTTCCAGG
1201 ACAAGGTGTG GCCCATTGTT GCCCTGAGGG TCCCAGCTTT TGAGACTCTG
1251 AAGGTTTACA GCGCTGGGC CGGCTATTAC GACTACAACA CCTTTGACCA
1301 GAATGGCGTG GTGGGCCCCC ACCCGCTAGT TGTCAACATG TACTTTGCTA
1351 CTGGCTTCAG TGGTCACGGG CTCCAGCAGG CCCCTGGCAT TGGGCGAGCT
1401 GTAGCAGAGA TGGTACTGAA GGGCAGGTTT CAGACCATCC ACCTGAGCCC
1451 CTTCTCTTTT ACCCGCTTTT ACTTGGGAGA GAAGATCCAG GAGAACAACA
1501 TCATCTGAGC ATGTGTGCTC TGCCTGGCT CCACTGGCTT GCATCCTGGC
1551 TGTGTTTACA GCCTTGTTTG CTGCTTCCAT CTTCCCAGT ACTGTGCCAG
1601 GCCTTCTCCC CCTCCCAGT GTCCTCTCCT CTCAGGCAGG CCATTGCACC
1651 CATATGGCTG GGCAGGCACA GGCAGTGAGG CCGAGGCCAA TAGCGAGTGA
1701 TGAGCGGGAT CCTAGGACTG ATCTGTAGCC CATGCTGATG TCACCCACCA
1751 GGGCAATCCA TCTGGAGGCC TGAGCACCTT GGCCAGGAC TGGCTTCATC
1801 CTGGCACTGA CCAGGAAAGA CTGCCTCTGA CCCTCTTAGC AGACAGAGCC
1851 CAGGCATGGG AGCACTCTGG GGCAGCCTGG CTCAGGTTTA TTGATTTTCG
1901 TCTGTTTACC CTATCCATTA ATCAATACAT GTAATTAACCT CCTTCCCTCC
1951 AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 48 bp to 1505 bp; peptide length: 486
 Category: similarity to known protein

```

1 MIRRVLPFGM GRGLLTRRPG TRRGGSFLDW DGKVSEIKKK IKSILPGRSC
51 DLLQDTSGLP PEHSDVVIWG GGVGLSVAY WLKKLESRRG AIRVLVVERD
101 HTYSQASTGL SVGGICQQFS LPENIQLSLF SASFLRNINE YLAVVDAPPL
151 DLRFNPSGYL LLASEKDAAA MESNVKVQRQ EGAKVSLMSP DQLRNKFPWI
201 NTEGVALASY GMEDEGWFDW WCLLQGLRRK VQSLGVLFQV GEVTRFVSSS
251 QRMLTTDDKA VVLKRIHEVH VKMDRSLEYQ PVECAIVINA AGAWSAQIAA
301 LAGVGEGPPG TLQGTCLPVE PRKRYVYVWH CPQGPGLTLP LVADTSGAYF
351 RREGLGSNYL GGRSPTEQEE PDPANLEVDH DFFQDKVWPH LALRVPAFET
401 LKQSAWAGY YDYNFTDQNG VVGPHPLVWN MYFATGFSCH GLQQAPGIGR
451 AVAEMVLKGR FQIDLSPLF FTRFYLGEKI QENNII

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_20b19, frame 3

TREMBL:CEM04B2_4 gene: "M04B2.4"; *Caenorhabditis elegans* cosmid M04B2,
 N = 1, Score = 801, P = 9.2e-80

PIR:B71184 probable sarcosine oxidase - *Pyrococcus horikoshii*, N = 2,
 Score = 194, P = 2e-26

PIR:B69284 sarcosine oxidase, subunit beta (soxB) homolog -
Archaeoglobus fulgidus, N = 3, Score = 189, P = 8.2e-22

TREMBL:AF042732_1 gene: "Bb"; product: "unknown protein"; *Anopheles*
gambiae (Bb) gene, partial cds; and TU37B2 (TU37B2), and diphenol
 oxidase-A2 (Dox-A2) genes, complete cds., N = 1, Score = 386, P =
 8.7e-36

PIR:F71008 probable sarcosine oxidase - *Pyrococcus horikoshii*, N = 2,
 Score = 200, P = 4e-25

>TREMBL:CEM04B2_4 gene: "M04B2.4"; *Caenorhabditis elegans* cosmid M04B2
 Length = 527

HSPs:

Score = 801 (120.2 bits), Expect = 9.2e-80, P = 9.2e-80
 Identities = 171/433 (39%), Positives = 260/433 (60%)

```

Query:   61 PEHSDVVIWGGVGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQQFS 120
          P +++VI+GGG+ G S A+WLK+ R +V+VVE + ++++ST LS GGI QQFS
Sbjct:   91 PYRAEIVIIIGGLSGSSTAFLWKE-RFRDEDFKVVVVVENNDVFTKSSTMLSTGGITQQFS 149

Query:  121 LPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLLLA-SEKDAAMESNVKVQR 179
          +PE + +SLF+ FLR+ E+L ++D+ D+ F P+GYL LA ++++ M S KVQ
Sbjct:  150 IPEFVDMSLFTTEFLRHAGEHLRLDSEQPDINFPTGYLRLAKTDEEVEMMRSAAWKVQI 209

Query:  180 QEGAKVSLMSPDQLRNKFPWINTGVALASYGMEDEGWFDWCLLQGLRRKVQSLGVLF 239
          + GAKV L+S D+L ++P++N + V LAS G+E+EG D W LL +R K +LGV +
Sbjct:  210 ERGAKVQLLSKDELTKRYPYMNVDVLLASLGVENEGTIDTWQLLSAIREKNITLGVQYV 269

Query:  240 QGEVTRFVSSSQRM-----LTDDKAVVLKRIHEVHVKMDRS-LEYQPVECAIVI 288
          +GEV F R T D+ + +RI V V+ + +P+ +++
Sbjct:  270 KGEVEGFQFERHRASSEVHAFGGDATADENKLAQRISGLVLRPQMNDASARPIRAHLIV 329

Query:  289 NAAGAWSAQIAALAGVGEGPPGTQLQGTCLPVEPRKRYVYVWHCPQGPGLTLPVADTS-G 347
          NAAG W+ Q+A +AG+C+G G L +P++PRKR V+V P P + P + D S G
Sbjct:  330 NAAGFWAGQVAKMAGIGKGT-GLL-AVPVPIQPRKRDVVFIFAPDVPS-DLPFIIDPSTG 386

Query:  348 AYFRREGLSNYLGGRSPTEQEEP--DPANLEVDHDFQDKVWPHLALRVPAFETLKVQS 405
          + R+ G +L GR+P+++E+ D +NL+VD+D F K+WP L RVP F+T KV+S
Sbjct:  387 VFRCQTDSGQTFVLVGRTPSKEEADAKRDSNLDVDYDDFYQKIWPVLVDRVPGFQTAKVKS 446

```

Query: 406 AWAGYYDYNTFDQNGVVGPHPLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTID 465
 AW+GY D NTFD V+G HPL N++ GF G+ + RA AE + G + ++
 Sbjct: 447 AWSGYQDINTFDAPVIGEHPLYTNLHMMCGFGERGVMHSMARAYAEIRIFDGAYINVN 506

Query: 466 LSPFLFTRFYLGKEIQE 482
 L F R + I E
 Sbjct: 507 LRKFDMRIRIVKMDPITE 523

Pedant information for DKFZphutel_20b19, frame 3

Report for DKFZphutel_20b19.3

[LENGTH] 486
 [MW] 53811.85
 [pI] 7.66
 [HOMOL] TREMBL:CEM04B2_4 gene: "M04B2.4"; Caenorhabditis elegans cosmid M04B2 1e-78

[FUNCAT] c energy conversion [H. influenzae, HI0499] 8e-05
 [BLOCKS] BL00677A D-amino acid oxidases proteins
 [BLOCKS] BL00623A GMC oxidoreductases proteins
 [BLOCKS] BL01304A
 [EC] 1.5.99.2 Dimethylglycine dehydrogenase 2e-07
 [PIRKW] flavoprotein 2e-07
 [PIRKW] oxidoreductase 2e-07
 [PROSITE] MYRISTYL 12
 [PROSITE] CK2_PHOSPHO_SITE 5
 [PROSITE] GLYCOSAMINOGLYCAN 1
 [PROSITE] PKC_PHOSPHO_SITE 6
 [KW] TRANSMEMBRANE 1
 [KW] LOW_COMPLEXITY 7.00 %

SEQ MIRRVLPHGMRGLLTRPGTRRGGSFSLDWDGKVSSEIKKKIKSILPGRSCDLLQDTSHP
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ccc
 MEM

SEQ PEHSDVIVGGVGLGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQQFS
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ccc
 MEMMM

SEQ LPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLLASEKDAAAMESNVKVRQ
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ccchhh
 MEM

SEQ EGAKVSLMSPDQLRNKFPWINTGVALASYGMEDEGWFDWCLLQGLRRKVQSLGVLFQ
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ccc
 MEM

SEQ GEVTRFVSSSQRLTTDDKAVVLKRIHEVHVKNDRSLEYQPVCAIVINAAGAWSAQIAA
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ccc
 MEM

SEQ LAGVGEGPPGTLQGTLPVEPRKRYVYVWHCPQGPGLTLPVADTSGAYFRREGLSNYL
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD hhcc
 MEM

SEQ GGRSPTEQEEPDANLEVDHDFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNG
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ecc
 MEM

SEQ VVGPHPLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPLFTRFYLGKEI
 SEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 PRD ccc
 MEM

SEQ QENNII
 SEG
 PRD ccccccc
 MEM

Prosites for DKFZphute1_20b19.3

PS00002	438->442	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	16->19	PKC_PHOSPHO_SITE	PDOC00005
PS00005	21->24	PKC_PHOSPHO_SITE	PDOC00005
PS00005	87->90	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00005	250->253	PKC_PHOSPHO_SITE	PDOC00005
PS00005	400->403	PKC_PHOSPHO_SITE	PDOC00005
PS00006	120->124	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00006	255->259	CK2_PHOSPHO_SITE	PDOC00006
PS00006	364->368	CK2_PHOSPHO_SITE	PDOC00006
PS00006	366->370	CK2_PHOSPHO_SITE	PDOC00006
PS00008	9->15	MYRISTYL	PDOC00008
PS00008	20->26	MYRISTYL	PDOC00008
PS00008	71->77	MYRISTYL	PDOC00008
PS00008	75->81	MYRISTYL	PDOC00008
PS00008	109->115	MYRISTYL	PDOC00008
PS00008	182->188	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008
PS00008	235->241	MYRISTYL	PDOC00008
PS00008	292->298	MYRISTYL	PDOC00008
PS00008	310->316	MYRISTYL	PDOC00008
PS00008	354->360	MYRISTYL	PDOC00008
PS00008	447->453	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphute1_20b19.3)

DKFZphutel_20g21

group: signal transduction

DKFZphutel_20g21 encodes a novel 861 amino acid protein with partial similarity to human ras inhibitor and other ras inhibitor proteins.

Ras is a signal transducing molecule involved in the receptor tyrosine kinase/RAS/Map kinase signalling cascade. Ras proteins bind GDP/GTP and show intrinsic GTPase activity. Mutations in ras, which change aa 12, 13 or 61 activate the potential of ras to transform cultured cells and are implicated in a variety of human tumours. The novel protein seems to be a new ras inhibitor protein.

The new protein can find application in modulating/blocking ras dependent signal transduction pathways.

Ras inhibitor

additional 1188 Bp at 5' and 1107 at 3' end in comparison to I22483

Sequenced by AGOWA

Locus: unknown

Insert length: 4137 bp

Poly A stretch at pos. 4116, no polyadenylation signal found

```

1 GGGAGAACTG AAACAGGAGA TGGTCCGGAC AGATGTCAAC CTGGAAAATG
51 GCCTGGAACC CGCTGAAACC CACAGCATGG TAAGACACAA GGATGGTGGC
101 TATTCCGAGG AAGAGGACGT GAAGACCTGT GCCCGGGACT CAGGCTATGA
151 CAGCCTCTCC AACAGGCTCA GCATCTTGGA CCGGCTCCTC CACACCCACC
201 CCATATGGGT GCAGCTGAGT CTGAGTGAGG AGGAGGCAGC AGAGGTCCTG
251 CAGGCCACGC CTCCGGGGAT CTTCTGGGTT CATAAACTA CCAAGATGCA
301 GAAGAAAGTC CTCCTCCTCC GCCTGCCCTG TGAATTTGGG GCCCCACTCA
351 AGGAATTTGC CATAAAGGAA AGCACATACA CCTTTTCCCT GGAAGGCTCA
401 GGAATCAGTT TCGCAGATTT ATTCCGGCTC ATTGCTTTCT ACTGCATCAG
451 CAGGGATGTT CTACCATTTA CTTGAAGTT GCCTTATGCC ATTTCAACAG
501 CCAAGTCGGA GGCTCAGCTT GAAGAACTGG CCCAGATGGG ACTAAATTTT
551 TGGAGCTCCC CAGCTGACAG CAAACCCCGG AACCTTCCAC CTCCCCATAG
601 GCTCTCTTTC TCCGACGGTG TCTGTCCTGC CTCCTGCGT CAGCTCTGCC
651 TTATAATGG AGTGCATTCT ATCAAAACCA GGACGCCTTC AGAGCTGGAG
701 TGCAGCCAGA CCAACGGGGC CCTGTGCTTT ATTAATCCCC TTTTCTTGAA
751 AGTGCACAGC CAGGACCTCA GTGGAGGCCT GAAACGGCCG AGCACAAAGGA
801 CTCCCAACGC GAATGGCAGC GAGCGGACTC GGTCCCCCCC ACCCAGGCCC
851 CCGCCACCCG CTATTAATAG TCTCCACACA AGCCCTCGGC TGGCCAGGAC
901 TGAACCCAG ACGAGCATGC CAGAAACAGT CAACCATAAC AAACATGGGA
951 ACGTAGCTCT GCCTGGAACG AAACCAACTC CCATCCCTCC ACCCCGGCTG
1001 AAGAAGCAGG CTTCTTTTCT GGAAGCAGAG GGCGGTGCAA AGACCTTGAG
1051 CGCGGGCCGG CCGGCGCGAG GCCCGAGCT GGAGCTGGGC ACAGCTGGCA
1101 GCCCAGGTGG GGCCCCGCTT GAGGCGGCC CCGGGGATTG CACAAGGGCC
1151 CCGCCGCCCA GCTCTGAATC ACGGCCCCCG TGCCATGGAG GCCGGCACCG
1201 GCTGAGCGAC ATGAGCATTT CTACTTCCTC CTCGACTCG CTGGAGTTCTG
1251 ACCGGAGCAT GCCTCTGTTT GGCTACGAGG CGGACACCAA CAGCAGCCTG
1301 GAGGACTACG AGGGGGAAG TGACCAAGAG ACCATGGCGC CCCCCATCAA
1351 GTCCAAAAAG AAAAGGAGCA GCTCCTTCGT GCTGCCAAG CTCGTCAAGT
1401 CCCAGCTGCA GAAGGTGAGC GGGGTGTTCA GCTCCTTCAT GACCCCGGAG
1451 AAGCGGATGG TCCGAGGAT CGCCGAGCTT TCCCGGGACA AATGCACCTA
1501 CTTGGGTGTC TTAGTGCAGG ACTACGTGAG CTTCTGTCAG GAGAACAAGG
1551 AGTGCCACGT GTCCAGCACC GACATGCTGC AGACCATCCG GCAGTTCATG
1601 ACCCAGGTCA AGAACTATT GTCTCAGAGC TCGGAGCTGG ACCCCCCCAT
1651 CGAGCTCGTG ATCCCTGAAG ACCAAATAGA TGTGGTGCTG GAAAAAGCCA
1701 TGCACAAGTG CATCTGAAG CCCCTCAAGG GGCATGTGGA GGCCATGCTG
1751 AAGGACTTTC ACATGGCCGA TGGCTCATGG AAGCAACTCA AGGAGAACCT
1801 GCAGCTTTGT CGGCAGAGGA ATCCGAGGA GCTGGGGGTC TTCGCCCGA
1851 CCCTGATTT TGTGGATGTG GAGAAAATCA AAGTCAAGTT CATGACCATG
1901 CAGAAGATGT ATTCCGCCGA AAAGAAGGTC ATGCTGCTGC TGCGGGTCTG
1951 CAAGCTCATT TACACGGTCA TGGAGAACAA CTCAGGAGG ATGTATGGCG
2001 CTGATGACTT CTTGCCAGTC CTGACCTATG TCATAGCCCA GTGTGACATG
2051 CTTGAATTGG AACTGAAAT CGAGTACATG ATGGAGCTCC TAGACCCATC
2101 GCTGTTACAT AGAGAAGGAG GCTATTACTT GACAAGCGCA TATGGAGCAC
2151 TTTCTCTGAT AAAGAATTTT CAAGAAGAAC AAGCAGCGCG ACTGCTCAGC
2201 TCAGAAACCA GAGACCCCT GAGGCAGTGG CACAACCGGA GAACCACCAA
2251 CCGGACCATC CCCTCTGTGG ACGACTTCCA GAATTACCTC CGAGTTGCAT
2301 TTCAGGAGGT CAACAGTGGT TGCACAGGAA AGACCTCCT TGTGAGACCT
2351 TACATACCA CTGAGGATGT GTGTCAGATC TGCGCTGAGA AGTTCAAGGT
2401 GGGGGACCT GAGGAGTACA GCCTCTTTCT CTTGCTTGAC GAGACATGGC
2451 AGCAGCTGGC AGAGGACACT TACCCTCAAA AAATCAAGGC GGAGCTGCAC

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2501 AGCCGACCAC AGCCCCACAT CTTCCACTTT GTCTACAAAC GCATCAAGAA
2551 CGATCCTTAT GGCATCATT TCCAGAACGG GGAAGAAGAC CTCACCACCT
2601 CCTAGAAGAC AGGCGGGACT TCCAGTGGT GCATCCAAAG GGGAGCTGGA
2651 AGCCTTGCTT TCCCGCTTCT ACATGCTTGA GCTTGAAAAG CAGTCACCTC
2701 CTCGGGGACC CCTCAGTGTA GTGACTAAGC CATCCACAGG CCAACTCGGC
2751 CAAGGGCAAC TTTAGCCACG CAAGGTAGCT GAGGTTTGTG AAACAGTAGG
2801 ATTCTCTTTT GGCAATGGAG AATTGCATCT GATGGTTCAA GTGTCCTGAG
2851 ATTGTTTGCT ACCTACCCCC AGTCAGGTTT TAGGTTGGCT TACAGGTATG
2901 TATATGTGCA GAAGAAACAC TTAAGATACA AGTCTTTTG AATTCAACAG
2951 CAGATGCTTG CGATGCAGTG CGTCAGGTGA TTCTCACTCC TGTGGATGGC
3001 TTCATCCCTG CCTTCCTTCC TTTCTTTTTC CTTTTTTTTT TTTTTTTTTT
3051 TTTTACAAA GAGCCTTCAT GTTTTATAT ATTTCATAGA AATTTTATA
3101 GCAGTTGCAG GTAAACTGTC AGGATTGGTT TTAATAATT TTTGTAACCT
3151 TAAATATTG TATAATTATG CATGTGATT TAACATTAA TATTCAAAAA
3201 TAAATCTCTT GCTGGATTG AGAGTATTGC ATTTTAAAG TCTCTCTCT
3251 GTAACGGAT GTTTTGGCAA CTTGTGGGG AGAGACTGCT GGATTTCTTA
3301 AAGCAACGTA TTCCTGACAC TGGCCACAGA ATGCCTTTGG AAATCGGATG
3351 TACTGTCTC TTGTTACGCT TTAGTGGTGT TTTGCTGTT TGTTTTTTAA
3401 ACAATGATG CTGAGAATAA GGAGAGAAAT GAATGTAGAG AGAGGTAGAG
3451 AGAGAAATAT GAATCTAAT AAAGGACTGA GGAGTGCAGT CTGCTGGTTC
3501 AGGCTCTTCA AAGATGTAG AAAAAGAGAT AGAAGGAACC ACCTATGCTT
3551 AAAATACTGT AAATATGCAG TGAGGTTTGG CAAAATCTAT TCCATGTGTG
3601 ATTTGCTTGT AGAAACAATT TTGAAAGCCC CTTGAGGAAA ATAAAAATCA
3651 AGAAGAACAC TTTTCTCCCT TTCCATACA AATTAAACT TAACAGCATC
3701 AAATTATTGG GACCAGAAAC CAAGTAATGT ATAATGTGGC TTTTGTGAG
3751 TTAAATAAGA TGCTATATA TGGAGAAGAA TTTGAAATG CACAAAAAAA
3801 TCAATCTACA TTATCAGAAC CTGCAGTGAA ATTAAACTTA TGTAAATAA
3851 AACCAGTTTG CAGGTGCACA AACTATGAGG GTCTTGATC CACGTAACAC
3901 AGGTAGTTAC AAAAACATGT TATTGTACTG TGTAAGATG CATAGTCATC
3951 TCATTTGGTT GGCTTTGTAC CTTGTACCTT TTTAGCCTT GGCTTTTGT
4001 GAAC TAGAAC CCTCAGACA TACTGTGTT TACTTTTGT AATGATTTT
4051 TAAATGGAAT TTTGCACATA ATACATTGTA ATACTGTATG ATAATCATGT
4101 GTGAAATAA TTTTGAAT AAAAATAA AAAAAA

```

BLAST Results

Entry I22483 from database EMBL:
Sequence 15 from patent US 5527896.
Length = 1829
Plus Strand HSPs:
Score = 9097 (1364.9 bits), Expect = 0.0, P = 0.0
Identities = 1821/1823 (99%), Positives = 1821/1823 (99%),

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 20 bp to 2602 bp; peptide length: 861
Category: known protein
Classification: Cell signaling/communication

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1 MVRTDVNLEN GLEPAETHSM VRHKDGGYSE EEDVKT CARD SGYDSL SNRL
51 SILDRLLHTH PIWLQLSLSE EEAAEVLQAO PPGIFLVHKS TKMOKKVL SL
101 RLPCEFGAPL KEFAIKESTY TFSLESGSIS FADLFRLIAF YCISRDVLPF
151 TLKLPYAIST AKSEAQLEEL AQMGLNFWSS PADS KPPNLP PPHRPLSSDG
201 VCPASLRQLC LINGVHSIKT RTPSELECSQ TNGALCFINP LFLKVHSQDL
251 SGG LKRPSTR TPNANGTERT RSPPPRPPP AINS LHTSPR LARTETQ TSM
301 PETVNH NKHG NVALPGTKPT PIPPPRLKKQ ASFLEAEGGA KTLSGGRPGA
351 GPELELG TAG SPGGAPPEAA PGDCTRAPPP SSES RPPCHG GRQLSDMSI
401 STSSSDSLEF DRSMPLFGYE ADTNSSLEDY EGESDQETMA PPIKSKKRS
451 SSFVLPKLVK SQLQKVSGVF SSFMTPEKRM VRRIAELSRD KCTYFGCLVQ
501 DYVSFLQENK ECHVSSTDM L QTI RQFMTQV KNYLSQSSEL DPPIESLIPE
551 DQIDVVLEKA MHKCI LKPLK CHVEAM LKDF HMDGSGWKQL KENLQLVRQR
601 NPQELGVFAP TPDFVDVEKI KVKFMTMQKM YSPEKKVMLL LRVCKLIYTV
651 MENNSGRMYG ADDFLPVLT Y VIAQCDMLEL DTEI EYMMEL LDPSLLHGE
701 GYVLTSA YCA LSLIKNFQEE QAARLLSSET RDTLRQWHKR RTTNRTIPSV
751 DDFQNYLRVA FQEVNSGCTG KTL LV RPYIT TEDVCOICAE KFKVGDPEEY
801 SLFLFVDETW QQLAEDTY PQ KIKAE LHSRP QPHIFHFVYK RIKNDPYGII
851 FQNGEEDLT T S

```

No BLASTP hits available

TREMBL:RNU80076_1 product: "RIN1"; Rattus norvegicus RIN1 mRNA, complete cds., N = 3, Score = 606, P = 6.8e-97

PIR:A38637 Ras interactor RIN1 - human, N = 3, Score = 587, P = 1.9e-92

TREMBL:HSRASINL_1 product: "ras inhibitor"; Human ras inhibitor mRNA, 3' end., N = 2, Score = 592, P = 9.8e-61

SWISSPROT:RIN1_HUMAN RAS INTERACTION/INTERFERENCE PROTEIN 1 (RAS INHIBITOR JC99) (FRAGMENT)., N = 2, Score = 587, P = 4.1e-60

PIR:B38637 Ras inhibitor (clone JC265) - human (fragment), N = 1, Score = 2446, P = 4.6e-254

>PIR:B38637 Ras inhibitor (clone JC265) - human (fragment)
Length = 471

HSPs:

Score = 2446 (367.0 bits), Expect = 4.6e-254, P = 4.6e-254
Identities = 471/471 (100%), Positives = 471/471 (100%)

Query: 391 GRQRLSDMSISTSSSDSLEFDRSMPLFGYEADTNSSLEDYEGESDQETMAPPIKSKKKRS 450
GRQRLSDMSISTSSSDSLEFDRSMPLFGYEADTNSSLEDYEGESDQETMAPPIKSKKKRS
Sbjct: 1 GRQRLSDMSISTSSSDSLEFDRSMPLFGYEADTNSSLEDYEGESDQETMAPPIKSKKKRS 60

Query: 451 SSFVLPKLKVSQQLQKVSQVGFSSFMTPEKRMVRRIAELSRDKCTYFGCLVQDYVSFLQENK 510
 SSFVLPKLKVSQQLQKVSQVGFSSFMTPEKRMVRRIAELSRDKCTYFGCLVQDYVSFLQENK
 Sbjct: 61 SSFVLPKLKVSQQLQKVSQVGFSSFMTPEKRMVRRIAELSRDKCTYFGCLVQDYVSFLQENK 120

Query: 511 ECHVSSDMLQTIQRFMTQVKNYLSQSSELDPPIESLIPEDQIDVVLEKAMHKCILKPLK 570
ECHVSSDMLQTIQRFMTQVKNYLSQSSELDPPIESLIPEDQIDVVLEKAMHKCILKPLK
Sbjct: 121 ECHVSSDMLQTIQRFMTQVKNYLSQSSELDPPIESLIPEDQIDVVLEKAMHKCILKPLK 180

Query: 571 GHVEAMLKDFHMADGSKQLKENLQLVRQRNPQELGVFAPTPDFVDVEKIKVKFMTMQKM 630
GHVEAMLKDFHMADGSKQLKENLQLVRQRNPQELGVFAPTPDFVDVEKIKVKFMTMQKM
Sbjct: 181 GHVEAMLKDFHMADGSKQLKENLQLVRQRNPQELGVFAPTPDFVDVEKIKVKFMTMQKM 240

Query: 631 YSPEKKVMLLLRVCKLIYTVMENNSGRMYGADDFLPVLTYYIAQCMDLELDTEIEYMMEL 690
YSPEKKVMLLLRVCKLIYTVMENNSGRMYGADDFLPVLTYYIAQCMDLELDTEIEYMMEL
Sbjct: 241 YSPEKKVMLLLRVCKLIYTVMENNSGRMYGADDFLPVLTYYIAQCMDLELDTEIEYMMEL 300

Query: 691 LDPSLLHGECCYYLTSAYGALSLIKNFQEEQARLLSSETRDTLRQWHKRRRTTNRTPSV 750
LDPSLLHGECCYYLTSAYGALSLIKNFQEEQARLLSSETRDTLRQWHKRRRTTNRTPSV
Sbjct: 301 LDPSLLHGECCYYLTSAYGALSLIKNFQEEQARLLSSETRDTLRQWHKRRRTTNRTPSV 360

Query:	751	DDFQNYLRVAFQEVNSGCTGKTL	LLVRPYITTEDV	CQCAEKFVGDPEEYSLFLFVDET	810
		DDFQNYLRVAFQEVNSGCTGKTL	LLVRPYITTEDV	CQCAEKFVGDPEEYSLFLFVDET	
Sbjct:	361	DDFQNYLRVAFQEVNSGCTGKTL	LLVRPYITTEDV	CQCAEKFVGDPEEYSLFLFVDET	420

Query: 811 QQLAEDTYPQKIKAE LHSRPQPHI FHFVYKRIKNDPYGII FQNGEEDLTT 861
 Sbjct: 421 QQLAEDTYPQKIKAE LHSRPQPHI FHFVYKRIKNDPYGII FQNGEEDLTT 471

Pedant information for DKF2phutel_20g21, frame 2

Report for DKFZphute1-20g21.2

```
[LENGTH]      861
[MW]           96380.26
[pI]           6.15
[HOMOL]        PIR:B38637 Ras inhibitor (clone JC265) - human (fragment) 0.0
[FUNCAT]       08.13 vacuolar transport      [S. cerevisiae, YML097c] 3e-10
[FUNCAT]       06.04 protein targeting, sorting and translocation [S. cerevisiae, YML097c]
3e-10
[FUNCAT]       30.03 organization of cytoplasm [S. cerevisiae, YML097c] 3e-10
[FUNCAT]       08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YML097c]
3e-10
[PIRKW]        alternative splicing 3e-59
[SUPFAM]       Ras interactor RIN1 3e-59
```

(No Prosite data available for DKFZphut1_20g21.2)
(No Pfam data available for DKFZphut1_20g21.2)

DKFZphute1_20h13

group: intracellular transport and trafficking

DKFZphute1_20h13 encodes a novel 955 amino acid protein with similarity to alpha-adaptins.

Adaptins are components of the adaptor complexes which link clathrin to receptors in coated vesicles. The alpha-adaptins, which are found exclusively in endocytic coated vesicles, separate into two bands on SDS gels, designated A and C. The novel protein is very similar to both alpha adaptin A and C. The novel protein is a new human alpha-adaptin.

The new protein can find application in modulating endocytosis and vesicle trafficking in cells.

strong similarity to alpha-adaptins

complete cDNA, complete cds start at Bp 78, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 3352 bp

Poly A stretch at pos. 3297, polyadenylation signal at pos. 3279

```
1 GCGCCCGGTC CCGCTTGCC AGCCCCCGCT GCTCTGTGCC CTGTCCGGCC
51 AGGCCTGGAG CCGACACCAC CGCCATCATG CCGGCCGTGT CCAAGGGCGA
101 TGGGATGCGG GGGCTCGCGG TGTTTCATCTC CGACATCCGG AACTGTAAGA
151 GCAAAGAGGC GGAAATTAAG AGAATCAACA AGGAAGTGGC CAACATCCGC
201 TCCAAGTTCA AAGGAGACAA AGCCTTGGAT GGCTACAGTA AGAAAAAATA
251 TGTGTGTAAA CTGCTTTTCA TCTTCCTGCT TGGCCATGAC ATTGACTTTG
301 GGCACATGGA GGCTGTGAAT CTGTTGAGTT CCAATAAATA CACAGAGAAG
351 CAAATAGGTT ACCTGTTTCA TTCTGTGCTG GTGAAGTCGA ACTCGGAGCT
401 GATCCGCCTC ATCAACAACG CCATCAAGAA TGACCTGGCC AGCCGCAACC
451 CCACCTTCAT GTGCCCTGGC CTGCACTGCA TCGCCAACGT GGGCAGCCGG
501 GAGATGGGCG AGGCCTTTGC CGCTGACATC CCCCAGCATC TGGTGGCCGG
551 GGACAGCATG GACAGTGTC AAGCAGAGTG GGCCTGTGCT CTCCTTCGAC
601 TGTACAAGGC CTCGCCTGAC CTGGTGCCCA TGGCGGAGTG GACGGCGCGT
651 GTGGTACACC TGCTCAATGA CAGCACATG GGTGTGGTCA CGGCCGCCGT
701 CAGCCTCATC ACCTGTCTCT GCAAGAAGAA CCCAGATGAC TTCAAGACGT
751 GCGTCTCTCT GGCTGTGTCG CGCCTGAGCC GGATCGTCTC CTCTGCCTCC
801 ACCGACCTCC AGGACTACAC CTACTACTTC GTCCCAGCAC CCTGGCTCTC
851 CTGTAAGGTC TCGCGGCTGC TGCACTGCTA CCCCCTCCA GAGGATGCGG
901 CGTGAAGGCG GCGGCTGGTG GAATGTCTGG AGACTGTGCT CAACAAGGCC
951 CAGGAGCCCC CCAATCCAA GAAGGTGCAG CATTCACAC CCAAGAACGC
1001 CATCCTCTTC GAGACCATCA GCCTCATCAT CCACTATGAC AGTGAGCCCA
1051 ACCTCCTGGT TCGGGCCTGC AACCAGCTGG GCCAGTTCCT GCAGCACCAG
1101 GAGACCAACC TGCGCTACCT GGCCCTGGAG AGCATGTGCA CGCTGGCCAG
1151 CTCCGAGTTC TCCCATGAAG CCGTCAAGAC GCACATTGAC ACCGTCATCA
1201 ATGCCCTCAA GACGGAGCGG GACGTCAAGC TGCGGCAGCG GCGCGCTGAC
1251 CTCCTCTACG CCATGTGTGA CCGGAGCAAT GCCAAGCAGA TCGTGTCCGA
1301 GATGCTGCGG TACCTGGAGA CGGCAGACTA CGCCATCCGC GAGGAGATCG
1351 TCCTGAAGGT GGCCATCCTG GCCGAGAAAT ACGCCGTGGA CTACAGCTGG
1401 TACGTGGACA CCATCCTCAA CCTCATCCGC ATTGCGGGCG ACTACGTGAG
1451 TGAGGAGGTG TGGTACCGTG TGCTACAGAT CGTCACCAAC CGTGATGACG
1501 TCCAGGGCTA TGCCGCCAAG ACCGTCTTTG AGGCGCTCCA GGCCCTGCC
1551 TGTCACGAGA ACATGGTGAA GGTGCGCGC TACATCCTTG GGGAGTTTGG
1601 GAACCTGATT GCTGGGGACC CCGCTCCAG CCCCCAGTG CAGTTCTCCC
1651 TGCTCCACTC CAAGTTCCAT CTGTGCAGCG TGGCCACGCG GCGCTGCTG
1701 CTGTCCACTC ACATCAAGTT CATCAACCTC TTCCCGAGA CCAAGGCCAC
1751 CATCCAGGGC GTCCTGCGGG CCGCTCCCA GCTGCGCAAT GCTGACGTGG
1801 AGCTGCAGCA GCGAGCCGTG GAGTACCTCA CCTCAGCTC AGTGGCCAGC
1851 ACCGACGTCC TGGCCACGGT GCTGGAGGAG ATGCCGCCCT TCCCCGAGCG
1901 CGAGTCTGTC ATCCTGGCCA AGCTGAAACG CAAGAAGGGG CCAGGGGCGG
1951 GCAGCGCCCT GGACGATGGC CGGAGGGACC CCAGCAGCAA CGACATCAAC
2001 GGGGGCATGG AGCCCCCCCC CAGCACTGTG TCGACGCCCT CGCCCTCCGC
2051 CGACCTCCTG GGGCTGCGGG CAGCCCTCC CCGGCAGCA CCCCAGCTT
2101 CTGCAAGGAG AGGGAACCTT CTGGTGACG TCTTCGATGG CCGGCGCGCC
2151 CAGCCAGGCC TGGGGCCAC CCCCAGGAG GCCTTCCTCA GCCCAGGTCC
2201 TGAGGACATC GGCCCTCCCA TTCCGGAAGC CGATGAGTTG CTGAATAAGT
2251 TTGTGTGTAA GAACAACGGG GTCCTGTTCC AGAACCAGCT GCTGCAGATC
2301 GGAGTCAAGT CAGAGTTCGG ACAGAACCTG GGCCGATGT ATCTCTTCTA
2351 TGGCAACAAG ACCTCGGTGC AGTTCCAGAA TTTCTACCC ACTGTGTTT
2401 ACCCGGGAGA CCTCCAGACT CAGCTGGCTG TGCAGACCAA GCGGTGGCG
2451 GCGCAGGTGG ACGGCGGCGC GCAGGTGCAG CAGGTGCTCA ATATCAGTGT
2501 CCTGCGGGAC TTCCTGACGC CCCCCTGCT GTCCGTGCGC TTCCGGTACG
2551 GTGGCGCCCC CCAGGCCCTC ACCCTGAAGC TCCAGTGAC CATCAACAAG
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2601 TTCTTCCAGC CCACCGAGAT GGCGGCCAG GATTTCCTCC AGCGCTGGAA
2651 GCAGCTGAGC CTCCTCAAC AGGAGGCGCA GAAATCTTC AAAGCCAACC
2701 ACCCATGGA CGCAGAAGTT ACTAAGGCCA AGCTTCTGGG GTTTGGCTCT
2751 GCTCTCCTGG ACAATGTGGA CCCCAACCTT GAGAACTTCG TGGGGGCGGG
2801 GATCATCCAG ACTAAAGCCC TGCAGGTGGG CTGTCTGCTT CGGCTGGAGC
2851 CCAATGCCCA GSCCCAGATG TACCGGCTGA CCCTGCGCAC CAGCAAGGAG
2901 CCGTCTCTCC GTACCTGTG TGAGCTGCTG GCACAGCAGT TCTGAGCCCT
2951 GGACTCTGCC CCGGGGGATG TGGCCGGCAC TGGGCAGCCC CTTGGACTGA
3001 GGCAGTTTTG GTGGATGGGG GACCTCCACT GGTGACAGAG AAGACACCAG
3051 GGTGGGGG ATGCTGGGA CTTCCTCCG GCCTTTTGTA TTTTATTTT
3101 TGTTCATCTG CTGCTGTTTA CATTCTGGGG GGTAGGGGG AGTCCCCCTC
3151 CCTCCCTTTC CCCCCAAGC ACAGAGGGGA GAGGGGCCAG GGAAGTGGAT
3201 GTCTCCTCCC CTCCCACCCC ACCCTGTTGT AGCCCCCTCT ACCCCCTCCC
3251 CATCCAGGGG CTGTGTATTA TTGTGAGCGA ATAAACAGAG AGACGCTAAA
3301 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3351 AA

```

BLAST Results

No BLAST result

Medline entries

89155572:

Cloning of cDNAs encoding two related 100-kD coated vesicle proteins (alpha-adaptins).

97431776:

Alpha-adaptin, a marker for endocytosis, is expressed in complex patterns during Drosophila development.

Peptide information for frame 3

ORF from 78 bp to 2942 bp; peptide length: 955
 Category: strong similarity to known protein

```

1 MPAVSKGDGM RGLAVFISDI RNCKSKEAEI KRINKELANI RSKFKGDKAL
51 DGYSKKKYVC KLLFIFLLGH DIDFGHMEAV NLLSSNKYTE KQIGYLFISV
101 LVNSNSELIR LINNAIKNDL ASRNPTFMCL ALHCIAVGS REMGEAFAAD
151 IPRILVAGDS MOSVKQSAAL CLLRLYKASP DLVPMGEWTA RVVHLLNDQH
201 MGVVTAAVSL ITCLCKKNPD DFKTCVSLAV SRLSRIVSSA STDLDQDYTY
251 FVPAPWLSVK LLRLQCYPY PEDAAVKGR LVECLETVLNK AQEPPKSKKV
301 QHSNAKNAIL FETISLIHY DSEPNLLVRA CNQLGQFLQH RETNLRYLAL
351 ESMCTLASSE FSHEAVKTHI DTVINALKTE RDVSVRQRAA DLYAMCDRS
401 NAKQIVSEML RYLETADYAI REEIVLKVAI LAEKYAVDYS WYVDITLNL
451 RIAGDYSVEE VMYRVLQIVT NRDDVQGYAA KTVFEALQAP ACHENMVKVG
501 GYILGEFGNL IAGDPRSSPP VQFSLLSKF HLCSVATRAL LLSTYIKFIN
551 LFPETKATIO GVLRAQSRLR NADVELQORA VEYLTLSVA STDVLATVLE
601 EMPPFPERES SILAKLKRKK GPGAGSALDD GRDPSSNDI NGGMEPTPST
651 VSTPSPSADL LGLRAAPPPA APPASAGAGN LLVDVFDGPA AQPSLGPTPE
701 EAFLSPGPED IGPPPEADE LLNKFVCKNN GVLFENQLLQ IGVKSEFRQN
751 LGRMYLFYGN KTSVQFQNF SPTVVHPGDLQ TQLAVQTKRV AAQVDGGAQV
801 QQVLNIECLR DFLTPPLLSV RFRYGGAPQA LTLKLPVTIN KFFQPTMAA
851 QDFFQRWKQL SLPQQAQKI FKANHPMDAE VTKAKLLGFG SALLDNVDPN
901 PENFVGAGII QTKALQVGCL LRLEPNAAQAO MYRLTLRTSK EPVSRHLCEL
951 LAQQF

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_20h13, frame 3

PIR:B30111 alpha-adaptin C - mouse, N = 1, Score = 3990, P = 0

PIR:S11276 alpha-adaptin c - rat, N = 1, Score = 3987, P = 0

SWISSPROT:ADAC_RAT ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE
 ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).. N = 1, Score = 3982, P = 0

SWISSPROT:ADAC_MOUSE ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX
2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA
MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).., N = 1, Score =
3976, P = 0

TREMBL:AB020706_1 gene: "KIAA0899"; product: "KIAA0899 protein"; Homo
sapiens mRNA for KIAA0899 protein, partial cds., N = 1, Score = 3932, P
= 0

>PIR:B30111 alpha-adaptin C - mouse
Length = 938

HSPs:

Score = 3990 (598.6 bits), Expect = 0.0e+00, P = 0.0e+00
Identities = 787/955 (82%), Positives = 858/955 (89%)

```
Query:      1 MPAVSKGDMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC 60
            MPAVSKGDMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC 60
Sbjct:      1 MPAVSKGDMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC 60

Query:     61 KLLFIFLLGHDIDFGHMEAVNLLSSNKYTEKQIGYLFISVLVNSNSELIRLINNAIKNDL 120
            KLLFIFLLGHDIDFGHMEAVNLLSSN+YTEKQIGYLFISVLVNSNSELIRLINNAIKNDL
Sbjct:     61 KLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIGYLFISVLVNSNSELIRLINNAIKNDL 120

Query:    121 ASRNPTFMCLALHCIANVGSREMGEAFAADIPRILVAGDSMDSVKQSAALCLLRLYKASP 180
            ASRNPTFM LALHCIANVGSREM EAFA +IP+ILVAGD+MDSVKQSAALCLLRLY+ SP
Sbjct:    121 ASRNPTFMGLALHCIANVGSREMAEAFAGEIPKILVAGDTMDSVKQSAALCLLRLYRTSP 180

Query:    181 DLVPMGEWTA RVVHLLNDQHM GVVTAAVSLITCLCKKNPDDEKTCVSLAVSRLSRIVSSA 240
            DLVPMG+WT+RVVHLLNDQH+GVVTAA SLIT L +KNP++FKT VSLAVSRLSRIV+SA
Sbjct:    181 DLVPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSVSLAVSRLSRIVTSA 240

Query:    241 STDLQDYTYFYFVPAPWLSVKLLRLLOCYPPEDAAVKGRIVECLETVLNKAQEPKSKKV 300
            STDLQDYTYFYFVPAPWLSVKLLRLLOCYPPP D AV+GRL ECLET+LNKAQEPKSKKV
Sbjct:    241 STDLQDYTYFYFVPAPWLSVKLLRLLOCYPPP-DAVVRGRLTECLETILNKAQEPKSKKV 299

Query:    301 QHSNAKNAILFETISLIIHYDSEPNLLVRACNLGQFLQHRETNLRYLALESMTLASSE 360
            QHSNAKNA+LFE ISLIIH+DSEPNLLVRACNLGQFLQHRETNLRYLALESMTLASSE
Sbjct:    300 QHSNAKNAVLFEAISLIIHHDSEPNLLVRACNLGQFLQHRETNLRYLALESMTLASSE 359

Query:    361 FSHEAVKTHIDTVINALKTERDVSVRQRAADLLYAMCDRSNAQIVSEMLRYLETADYAI 420
            FSHEAVKTHI+TVINALKTERDVSVRQRA DLYAMCDRSNA+QIV+EML YLETADY+I
Sbjct:    360 FSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSNAQQIVAEMLSYLETADYSI 419

Query:    421 REEIVLKVAILAEKYAVDYSWYVDITILNLIRIAGDYVSEEVWYRVLQIVTNRDDVQGYAA 480
            REETVLKVAILAEKYAVDY+WYVDITILNLIRIAGDYVSEEVWYRV+QIV NRDDVQGYAA
Sbjct:    420 REEIVLKVAILAEKYAVDYTWYVDITILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAA 479

Query:    481 KTVFEALQAPACHENMVKVGYYILGEFGNLIAGDPRSSPPVQFSLHLSKFHLCSVATRAL 540
            KTVFEALQAPACHEN+VKVGYYILGEFGNLIAGDPRSSP +QF+LLHLSKFHLCSV TRAL
Sbjct:    480 KTVFEALQAPACHENLVKVGYYILGEFGNLIAGDPRSSPLIQFNLLHLSKFHLCSVPTRAL 539

Query:    541 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYLTLSVASTDVLATVLE 600
            LLSTYIKF+NLFPE KATIQ VLR+ SQL+NADVELQQRAVEYL LS+VASTD+LATVLE
Sbjct:    540 LLSTYIKFVNLFPEVKATIQDVLRSQSLKNADVELQQRAVEYLRSTVASTDILATVLE 599

Query:    601 EMPFFPERESSILAKLKKKGPGAGSALDDGRRDPSSNDINGGMEPTP---STVSTPSPS 657
            EMPFFPERESSILAKLK+KKGP + L-+ +R+ S D+NGG EP P S STPSPS
Sbjct:    600 EMPFFPERESSILAKLKKKKGPSTVTDLEETKRERSI-DVNGGPEPVPASTSAASTPSPS 658

Query:    658 ADLLGLRAAPP-PAAPPASAGAGNLLVDVFDGPAAPSLGPTPEEAFLSPGPEDIGPPIP 716
            ADLLGL A PP P PP S+G G LLVDVF A+ ++ P L+PG ED
Sbjct:    659 ADLLGLGAVPPAPTGPSSSGGG-LLVDVFSQSAS--AVAP-----LAPGSEDN----- 704

Query:    717 EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGNKTSVQFQNFSPVTVHP 776
            +FVCKNNGVLFENQLLQIG+KSEFRQNLGRM++FYGNKTS QF NF+PT++
Sbjct:    705 -----FAFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIYGNKTSQFLNFTPTLICA 759

Query:    777 GDLOTQLAVQTKRVAAQVDGGAQVQVNLNIECLRDFTLPPLLSVRFYGGAPQALTLKLP 836
            DLQT L +QTK V VDGAQVQV+NIEC+ DF P+L+++FRYGG Q +++KLP
Sbjct:    760 DDLQTNLNLQTKPVDPTVDGGAQVQVNVNIECISDFTEAPVLNIQFRYGGTFQNVSVKLP 819

Query:    837 VTINKFFQPTEMAAQDFQQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSALLDN 896
            +T+NKFFQPTEMA+QDEFQQRWKQLS PQQE Q IFKA HPMD E+TKAK++GFGSALL+
Sbjct:    820 ITLNKFFQPTEMASQDFQQRWKQLSNPQQEVQNIKAKHPMDTEITKAKIIGFGSALLEE 879

Query:    897 VDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRLCELLAQQF 955
            VDPNP NEVGAGII TK Q+GCLLRLEPN QAQMYRLTLRTSK+ VS+ LCELL++QF
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497

Prosites for DKF2phute1_20h13.3

(No Pfam data available for DKFZphut1_20h13.3)

DKFZphute1_20m11

group: cell cycle

DKFZphute1_20m11 encodes a novel 225 amino acid protein with similarity to yeast sds22 and protein phosphatase-1 regulatory subunits.

sds22 is a regulatory polypeptide of protein phosphatase-1 that is required for the completion of mitosis in both fission and budding yeast. The novel protein seems to be a new regulator protein for protein phosphatase-1.

The new protein can find application in modulating/blocking the activity of protein phosphatase-1 and in modulating the cell cycle.

similarity to suppressor protein sds22

complete cDNA, complete cds, EST hits
localisation? only a part of the STS matches

Sequenced by AGOWA

Locus: /map="17"?

Insert length: 5822 bp

Poly A stretch at pos. 5803, polyadenylation signal at pos. 5786

```
1 GGGCGCTTGG TTCCCCAGCA ACCGGGAGAC GCGTCTGCTG CGTGGAACCG
51 CCGAGTTCCTC AGCGCTTGAG AAGGAAAATT CTGGATCTGT TATCTGTGAG
101 GAGGCCACTC CGTTGACAGT TGTGTAAAC TCTGCTGCTT TCCCCAGCTC
151 CAACCTCTCT GGTCTTCAAC AACACTATCA TCAGGGAAAA CGTGGGGGAA
201 GATGAACCAAG CCGTGCAACT CGATGGAGCC GAGGGTGATG GACGATGACA
251 TGCTCAAGCT GGCCGTCGGG GACCAGGGCC CCCAGGAGGA GGCCGGGCAG
301 CTGGCCAAGC AGGAGGGCAT CCTCTTCAAG GATGTCTGT CCCTGCAGCT
351 GGACTTTCGG AACATCCTCC GCATAGACAA CCTCTGGCAG TTTGAGAAGT
401 TGAGGAAGCT GCAGCTGGAC AATAACATCA TTGAGAAGAT CGAGGGCCTG
451 GAGAACCTCG CACACCTGGT CTGGCTGGAT CTGTCTTTCA ACAACATTGA
501 GACCATCGAG GGGCTGGACA CACTGGTGAA CCTGGAGGAC CTGAGCTTGT
551 TCAACAACCG GATCTCCAAG ATCGACTCCC TGGACGCCCT CGTCAAGCTG
601 CAGGTGTGTG CGCTGGGCAA CAACCGGATT GACAACATGA TGAACATCAT
651 CTACCTCCGG CGGTTCAAGT GCCTGCGGAC GCTCAGCCTC TCTAGGAACC
701 CTATCTCTGA GGCAGAGGAT TACAAGATGT TCATCTGTGC CTACCTTCCT
751 GACCTCATGT ACCTGGACTA CCGGCGCATT GATGACCACA CAGCAAGTGT
801 CTCCCTCTCA GTCTCCAGC CCTGTGAGAC AGATTCTCTA AGCCCCCAGG
851 TTTCTTGGA AAGGGGCATT GAAGAGTAGC TTCCCTGCC CACAACATAGG
901 AGAGAAAGGG CAGCTCCCTC TTCCTAATCC CTTTACCTGA CTCTGTCAGA
951 GTGATTCCAG CAGCACCTT GTAAGTACTG TTTTGTGTGC GTTCCCAGGG
1001 GCCAGGCCTC TTCCACACAC TGTCCCAGGG CCACCTCACA GCCATCCTGC
1051 ACTGTCTAGT TTTCCAGATG AAGAAGCTGA GGAGGGCTGG GAGCAGTGGC
1101 TCACGCCTGT AATCCAGCA CTTTGAGAGG CTGAGCGGG AGGATCGCTT
1151 GAGCCAAGGA GTTCAAGACC AGCCTGGGCA ACATAGGGAG ACCCATCTC
1201 TACAGAAACT ACCAAAATTA GCCAGGTGTG GTGGCACACA CCAGTAATCC
1251 TGGTACTCA CAAGCCGAG GTAGAAGAA CGCTTGAGAC TAGGAGTTTG
1301 AGGCTGCAGT GAACTAAGAA GATGCCATTG CACTCCAGCC TGGGCAACAG
1351 AGTGAAAAAA TTAAAAAATT AGAAAAGAAA AGAAGTTGAG GAGGCCCAAG
1401 GAGGGCAAGC AGCCAGGATC ACTGGCTCAA GGCCAAGCCA GGATTACCCC
1451 TAAGTTGGTG TCATCCCAGG AGCAATATTA ACAGCTGAGC TCCAGAGGGA
1501 ACCAGGCCAT CAGAGGCTCA GGCTTGGCTC TCAGGGGCAG AGTCAGGGCT
1551 GGAGGTAGAG ACCTGAGTGT CATCTGAGGA TTGCCAATTG GCAGTAGTTG
1601 AAGCCATGGT ACAGGTGGGA TCACCTGGGG CACATGGAGT GAGCTGGGGG
1651 ACGGGGACTA AGTTCTAGAG GTGCCAGCAT TCCTGGCCAG GTACAGGGGG
1701 ATGAGCCAGT CGGCTGGAGA GAGCCAAGGG CCAGACCCTC GTGACCAGCC
1751 CTATGGCCTC ACTTACCTC TGTCTGTGTG TCCTCCTTCC CTAAAAGAGG
1801 GCCAGAAGGC CTGCTGAGGG CTGTTGGGAG TGAGAGAGCA AGTCCTCTGT
1851 GGAGAACACC CAGTCTGGGG CGAGGGGAGC GCTCCATTGC TGTGGCTCCT
1901 GCGCTGGAGA TGGCCCCGGG AACCCAGCAG TGCCACGCTG CCTCCGCTC
1951 CTCTGGTCT TTCCCTGATT TCCCTGCGCT CACAAAAACC TGGTGAGGGT
2001 CATCAGGAGA TGGGCATTCT CATCCACGAG ACCTCATGGC TTTACAGGCC
2051 TTTATGCAGG CCCCTGTGCA ACACCCCTGC CCATGCGCGG GAGGCTGCAG
2101 CATGGCAGAG GCGGCATGGC AGAGGCGGTG TGGCTCGGAG GAACCTCTGG
2151 TAACAATGCC ACTCCCGTTC CCTGGTCAGA AAAAGCTTGC GGAGGCTAAG
2201 CACCATGACA GCATCGACGA GCTGAAGCAC CAGGAGAACC TGATGCAGGC
2251 CCAGCTGGAG GACGAGCAGG CGCAGCGGGA GGAGCTAGAG AAGCACAAGA
2301 CTGCGTTTGT GGAACACCTG AATGGCTCCT TCCTGTTTGA CAGCATGTAC
2351 GCTGAGGACT CAGAGGGCAA CAATCTGTCC TACCTGCCTG GTGTCGGTGA
2401 GCTCCTTGAG ACCTACAAGG ACAAGTTTGT CATCATCTGC GTGAATATTT
2451 TTGAGTATGG CCTGAAACAG CAGGAGAAGC GGAAAACAGA GCTTGACACC
2501 TTCAGTGAAT GTGTCCGTGA GGCCATCCAG GAAAACCAGG AGCAGGGCAA
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2551 ACGCAAGATT GCCAAATTCG AGGAGAAGCA CTGTGCGAGT TTAAGTGCCA
2601 TTCGAGAGGA GTTGGAACTG CCCAACATTG AGAAGATGAT CCTAGAATGC
2651 AGTGCTGACA TCAGTGAGTT GTTCGATGCG CTCATGACGC TGGAGATGCA
2701 GCTGGTGGAG CAGCTGGAGG TAAGGCTGGG CCCTGGGCAC AAGTGCCAGA
2751 ATCTGGCGAT CAGCTGCAC ATCCATAGGT GAAGTGTAGC TTCTATGGGC
2801 ACGCCTCTGC TGGAAACGTC CAGCACGACT CAGCGTGGCA GGCTGTAGCT
2851 TTCTTGCTCA TCAGTCTGTG TTGCTTTTAT TACATTTTAA TCATTTACAT
2901 TGGAAAGTAT TCTTTGGGAA AATGACAGGT GAGCTCATTC TTCTGAAATG
2951 GTCCCCCTAT CTTGGAAATC AGTGGGGAGA GGTTTTTGAT TAGACCCCTG
3001 GAGCTATCCG GGTACTCTAA AGGCAAAGCG CACCCCTACT TGGGGACCAA
3051 ACAAAAGACC CTCCGCATTG CAGCCTGCAG TTGCCGCTTC TCAGGTGACG
3101 TGAGGAGGCT GCAACTCAGC ACTAAGTAGT GAAAATGAAA AGCGCCGCTG
3151 TCTGAAATTC ATTACAGGCC AGAGTATGTG TTACAAGGCA GCGGAGGCTG
3201 GGAGTCTGAA GTGGTGTGAT GAATTGAACC TCATCGGATG CTGCTGTGGC
3251 TGGGCCAAGT GATAGCACCT AATCAATTCC TCACACGTCA AGTGACACCT
3301 CAGACATGGG ATAGATTTCC CCATCACATC ACAGGGCAGG TGCTCCCTCC
3351 CTGCTGGAGC GCACAGGCAC TGCAGAAGCA GCGCACAGTG CCAGGGGCGA
3401 GTGAGGCAGC AGCTCCCAGC CTTTTCAGGC ACGGAGATTG CTTTTCAACA
3451 TCCAAACATT TCCAGAAACC CATGTGCCAT CCTACTTGTA TTAAGTGTGG
3501 CCAGAAAGCC ACAAGCGCAA TCATGCTTTT CAATGACCCT ATTTTTATTC
3551 ACGAGAACAG CACATACATG TGTTTTGAAA TTATGTGAGG TGCTCACTCT
3601 GCACAGAGTA CTCACATTCC TATAGATTCC ACCCCTGCCC ACCTTGCAGC
3651 CCTCGGAGT CTTAGCAGAT GGGAGTGGGG CACTCCGAGA GTGGCAGGCC
3701 TGGAGATCAC ATCTTCCATT GTTCTTCAA TCAACACTAA CTCCCATTG
3751 GGCCTTAGGT GCCTTGCTAA GCACCACAAA ACAGCAACTA ACTGAAAGAG
3801 ATCTGGAGTG CACGCCGCTT CCTACTGAGG GCCTCCTCTC TGTCAGGCAC
3851 CTTGCAAGGC ATTTTGTGTG AAGTGACTCA TTTAACCTCA CCACAAGGCC
3901 ACAACGCGAG GATTATGCAG GTAACCTATT TCCCAGATGA GGAAGATAAG
3951 GCCCAAGGAG GTGAAATGCC TTTCCAGAG TTACACAGAG TGCTGGAGCT
4001 GGAATACTG ACCCAGGCAG TCTAGCTCTT AACAGCTCAC TCCACTGTTT
4051 CCTTGGAGGT GATGCACAGA TGCTACTGGG AAACCCAAAG GAGAGGGGGT
4101 TGGCTGTGTG TGTGTGTGTT GGGCAGGCAG GTAAGGGGAG TAAGACCAGG
4151 ACAAGTGTTC CTGGCAAAGT TCCGGTGACA GCATTAAACA TTCAGATGGT
4201 GAGGGAGTTA ATATGGTTGG AGAACAACAA CTTTAGAGAG AGCAGAGGGG
4251 TCAGTTTACA ACCATCTGCT CAGGAGGGTC AAGATGGGTG GTCCTTTATG
4301 TGAAGTCTG TGATTAGAGG AGCTGGTTGC TAAATTTTGA GGAGTACCTT
4351 TTGCTCTGTG CTGGACATCT AAATATGCAT GTTAACTGTG TTCTTTAACA
4401 TCGCTGTGAG ACTATAAACA TGTTTGAAAG GAACATTGTT GACATGGTAG
4451 GACTGTTTAT CGAAATGTG CAAAGCCTAT ATCCTTCTG TGATGACCTT
4501 CCCCATGGGG AGGTGCTACA GAGCCCTGCG GCTTGTCCCG GCCTCTGGAC
4551 AAAAGAAATG TCCACAGGCT CTGAGGAGGT TTCCCGACCC TCAGAACAAT
4601 GATGGCCTGG TTAGAGCTGT GGTTTGGATG CCCAGAGGGA CAACATCCAA
4651 ACTGTTTGCA GTAGGCTCCC AGCATGATTG TTCTCATATG AGTGATGTTT
4701 ACTAGGAAAT GTGTTGCAAG GTGTTGCAAG CAAGCACACT CTGGGGTTGA
4751 GGCAACCCCT ACCTGGAAGA CACTATAAGG AGTACATCAG GTGAAATGTT
4801 AGGGTGAGGA GCCAACATCG GAGCATGGCC AACCTTCTT CCACCCGAAC
4851 TCAGGGCACT CCACATGGGG CAAACTGCTG TGCTCCAGCT AGCAGCAGCC
4901 CTGTGGTCTT GCCCTCCTGG GGCTCACAGT CCCTCAGGGA GACAAGTTGT
4951 AGAGGCAACA AGTGGTGCCA AATGCACAGG GTGAGAAGCA GTTAACCCAG
5001 AGGCCAGGAG CTTCCATGCA GGAGGGAGAG AAGAGTTGTA TGGCAGGGGC
5051 CGAGGGTCCG TCCGAGGTGT GGGGAGGGGG CAGGGAGTCG AGGAAGGCCC
5101 AGGGTTCGGA GCTTGTGAGT GGACGGTGCT GCCAGCCAGA ATTTCCGAGC
5151 TCGCCTTGGG CCCTTAAAGT CTGTCTCCCG CCGTCTGAGA GCATCAGGGA
5201 CGCGCCGGGC CTGCTCCTCC CGGGCCTTTG CTAACTCGG GGCTGCACGA
5251 TGGCTCAGTG CCGGGACCTG GAGAATCACC ACCACGAGAA GCTCCTGGAG
5301 ATCTCTATCA GCACCTTGA GAAGATTGTC GAGGGCGACC TGGACGAGGA
5351 CTGCTTAAC GACCTGCGCG CGCTTTTGT CGATAAAGAT ACGATTGTTA
5401 ATGCTGTGCG GGCATCGCAC GACATCCACC TCCTGAAGAT TGACAATCGA
5451 GAAGATGAGC TGGTGACCG AATCAACTCT TGGTGTACAC GTTTAATAGA
5501 CAGGATTAC AAGGATGAGA TCATGAGGAA CCGCAAGCGC GTGAAGGAGA
5551 TCAATCAGTA CATCGACCAC ATGCAGAGCG AACTGGACAA CCTGGAATGT
5601 GGCACATCCC TAGACTAGAT GAATGTCAGC CACAGGAGCT TCTTCAAAAC
5651 ATAGCACCAG CCCAGCCAG GAGAAGGAAG TGCACACGCC TCACCCGCAC
5701 CTCTAGAGAG TTGCTGGGCA TCTCTCAACC GCGATCCCCA ACACCATCT
5751 TCCCCACCC CTGGAAAAAC TTCCAAAAGT AGAGAAAATA AAGGACTCAT
5801 TTCACAAAAA AAAAAAAAAA AA
```

BLAST Results

Entry HS1292248 from database EMBL:
human STS SHGC-53917.
Score = 874, P = 3.3e-33, identities = 180/185

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 202 bp to 876 bp; peptide length: 225
Category: similarity to known protein

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1 MNQPCNSMEP RVMDDDMLKL AVGDQGPQEE AGQLAKQEGI LFKDVLSLQL
51 DFRNLRIDN LWQFENLRKL QLDNNIEKI EGLENLAHLV WLDLSFNNIE
101 TIEGLDTLVN LEDLSLFNNR ISKIDSLDAL VKLQVLSLGN NRIDNMMNII
151 YLRRFKCLRT LSLSRNPIS AEDYKMFICA YLPDLMYLDY RRIDDHTASV
201 SLSVSQPCET DSSSPQVSWK RGIEE

```

BLASTP hits

Entry S68209 from database PIR:
sds22 protein homolog - human >TREMBL:HSSDS22MR_1 gene: "sds22";
product: "yeast sds22 homolog"; H.sapiens sds22-like mRNA
Score = 234, P = 1.2e-19, identities = 61/143, positives = 93/143

Entry A38439 from database PIR:
suppressor protein sds22(+) - fission yeast (Schizosaccharomyces pombe)
>SWISSPROT:SD22_SCHPO PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT
>TREMBL:SPSDS22_1 gene: "sds22+"; S.pombe sds22+ gene, complete cds.
Score = 208, P = 5.6e-17, identities = 52/127, positives = 71/127

Entry S43988 from database PIR:
protein suppressor sds22 - fission yeast (Schizosaccharomyces pombe)
>SWISSPROT:SD22_SCHPO PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT
SDS22. >TREMBL:SPAC4A8_12 gene: "sds22"; product: "phosphatases pp1
regulatory subunit"; S.pombe chromosome I cosmid c4A8.
Score = 208, P = 8.5e-17, identities = 52/127, positives = 71/127

Entry CEK10D2_5 from database TREMBL:
gene: "K10D2.1"; Caenorhabditis elegans cosmid K10D2.
Score = 214, P = 3.6e-16, identities = 50/125, positives = 75/125

Alert BLASTP hits for DKFZphut1_20ml1, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphut1_20ml1, frame 1

Report for DKFZphut1_20ml1.1

```

[LENGTH]      225
[MW]           25955.87
[pI]           4.63
[HOMOL]        PIR:S68209 sds22 protein homolog - human 1e-18
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YKL193c] 2e-11
[FUNCAT]       30.10 nuclear organization [S. cerevisiae, YKL193c] 2e-11
[FUNCAT]       06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YKL193c] 2e-11
[FUNCAT]       30.05 organization of centrosome [S. cerevisiae, YOR373w] 2e-06
[FUNCAT]       01.03.10 metabolism of cyclic and unusual nucleotides [S. cerevisiae,
YJL005w] 3e-05
[FUNCAT]       03.10 sporulation and germination [S. cerevisiae, YJL005w] 3e-05
[FUNCAT]       30.02 organization of plasma membrane [S. cerevisiae, YJL005w] 3e-05
[FUNCAT]       10.04.03 second messenger formation [S. cerevisiae, YJL005w] 3e-05
[FUNCAT]       04.07 rna transport [S. cerevisiae, YPL169c] 9e-04
[FUNCAT]       04.05.01.04 transcriptional control [S. cerevisiae, YCR065w] 9e-04
[EC]           4.6.1.1 Adenylate cyclase 2e-06
[PIRKW]        nucleus 5e-16
[PIRKW]        duplication 2e-06
[PIRKW]        tandem repeat 2e-06
[PIRKW]        cAMP biosynthesis 2e-06
[PIRKW]        glycoprotein 2e-06
[PIRKW]        phosphorus-oxygen lyase 2e-06
[SUPFAM]       leucine-rich alpha-2-glycoprotein repeat homology 5e-16
[SUPFAM]       fibromodulin 3e-07
[SUPFAM]       yeast adenylate cyclase catalytic domain homology 2e-06
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[PROSITE]      CK2_PHOSPHO_SITE 2
[PROSITE]      PKC_PHOSPHO_SITE 1

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[KW]

All_Alpha

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PRD  cccccccccccccccccchhhhhhhccccccccchhhhhhhhhhhchhhhhhhhhccccccccccccc

SEQ  LWQFENLRKLQLDNNIIEKIEGLENLAHLVWLDLSFNNIETIEGLDTLVNLEDLSLFNNR
PRD  hhhhhhhhhhhccccccccccccchhhhhhhhhccccccccccccchhhhhhhhhcccccc

SEQ  ISKIDSLDALVKLQVLSLGNNRIDNMMNIIYLRREFKCLRTLSSLRNPISEAEDYKMFICA
PRD  cccchhhhhhhhhhhccccccccccccccccchhhhhhhhhccccccccccccchhhhhhhhh

SEQ  YLPDLMYLDYRRIDDHTASVSLSVSQPCETDSSSPQVSWKRGIEE
PRD  hhccccccccccccchhhhhhhhhcccccccccccccccccccccc
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Prosites for DKFZphut1_20m11.1

PS00005	218->221	PKC_PHOSPHO_SITE	PDOC00005
PS00006	122->126	CK2_PHOSPHO_SITE	PDOC00006
PS00006	169->173	CK2_PHOSPHO_SITE	PDOC00006

(No Pfam data available for DKFZphut1_20m11.1)

DKFZphutel_20m24

group: metabolism

DKFZphutel_20m24 encodes a novel 611 amino acid protein with similarity to a hypothetical *C.elegans* protein and to yeast Alg9 protein.

This protein is a putative mannosyl transferase that is involved in the assembly of the core oligosaccharide Glc3Man9GlcNAc2.

The new protein can find application in modulation of glycosylation of proteins and as a new enzyme for biotechnologic production processes.

strong similarity to *S.cerevisiae* Alg9p

complete cDNA, complete cds, potential start at Bp 23, few EST hits
Alg9 is involved in the assembly of the core oligosaccharide
Glc3Man9GlcNAc2

HSAC381 corresponding genomic DNA (2 exons)

HSB8954 corresponding genomic DNA (1 exon)

Sequenced by AGOWA

Locus: /map="11"

Insert length: 1986 bp

Poly A stretch at pos. 1966, polyadenylation signal at pos. 1949

```
1 TTCTTTTTC CCCAGGCTTG CCATGGCTAG TCGAGGGGCT CGGCAGCGCC
51 TGAAGGGCAG CGGGGCCAGC AGTGGGGATA CGGCCCGGCG TCGCGACAAG
101 CTGCGGGAGC TGCTGGGCAG CCGAGAGGCG GCGGCGCGCG AGCACCGGAC
151 CGAGTTATCT GGGAACAAAG CAGGACAAGT CTGGGCACCT GAAGGATCTA
201 CTGCTTCAA GTGTCTGCTT TCAGCAAGGT TATGTGCTGC TCTCCTGAGC
251 AACATCTCTG ACTGTGATGA AACATTCAAC TACTGGGAGC CAACACACTA
301 CCTCATCTAT GGGGAAGGGT TTCAGACTTG GGAATATTCC CCAGCATATG
351 CCATTCCGCTC CTATGCTTAC CTGTTGCTTC ATGCCTGGCC AGCTGCATTT
401 CATGCAAGAA TTCTACAAAC TAATAAGATT CTTGTGTTT ACTTTTTCG
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801 TACTATTTCT GGTGCCTGTG GTGGTCATTG ACAGCTACTA TTATGGGAAG
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1051 AGGCCACCCG TATTGGCTTA CCTTGGCTCC AATGTATATT TGGTTTATAA
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1201 TTACCACTTT GTGTTTCAAC GATATCGCCT GGAGCACTAT ACTGTGACAT
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1801 CTACACCATC CTCAAACCCC GGAAAGCAAA GCAAAATCAGG AAGAAAAGTG
1851 GAGGTTAGCA ACACACCTGT GGCCCCAAG GACAACCATC TTGTTAACTA
1901 TTGATTCCAG TGACCTGACT CCCTGCAAGT CATCGCCTGT AACATTTGTA
1951 ATAAAGGTCT TCTGACATGA AAAAAAAAAA AAAAAA
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BLAST Results

Entry HSAC381 from database EMBL:
Homo sapiens chromosome 11 pac pDJ159o1, complete sequence.
Length = 42,771

Entry HSB8954 from database EMBL:

cSRL-50A3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-50A3.
Length = 601

Medline entries

96293493:

Stepwise assembly of the lipid-linked oligosaccharide in the endoplasmic reticulum of *Saccharomyces cerevisiae*: identification of the ALG9 gene encoding a putative mannosyl transferase.

Peptide information for frame 2

ORF from 23 bp to 1855 bp; peptide length: 611
Category: strong similarity to known protein

```

1 MASRGARQRL KGSGASSGDT APAADKLREL LGSREAGGAE HRTLSGNKA
51 GOVWAPEGST AFKCLLSARL CAALLSNISD CDETFNYWEP THYLIYGEGF
101 QTWEYSPAYA IRSYAYLLH AWPAAFHARI LQTNKILVfy FLRCLLAFVS
151 CICELYFYKA VCKKFGLHVS RMMLAFLVLS TGMFCSSSAF LPSSFCMYTT
201 LIAMTGWYMD KTSIAVLGVA AGAILGWPFs AALGLPIAFD LLVMKHRWKS
251 FFHWSLMALI LFLVPVVVID SYYYGKLVIA PLNIVLYNVF TPHGPDLYGT
301 EPWYFYLING FLNFNVAFAL ALLVLPLTSL MEYLLQRFHV QNLGHPYWLT
351 LAPMYIWFII FFIQPHKEER FLFPVYPLIC LCGAVALSAL QKCYHFVFQR
401 YRLEHYTVTS NWLALGTVEL FGLLSFSRSV ALFRGYHGPL DLYPEFYRIA
451 TDPTIHTVPE GRPVNVCVGK EWYREFSSFL LPDNWQLQFI PSEFRGQLPK
501 PFAEGPLATR IVPTDMNDQN LEEPSRYIDI SKCHYLVLDL TMRETPREP
551 YSSNKEEWIS LAYRPFLDAS RSSKLLRAFY VPFLSDQYTV YVNYTILKPR
601 KAKQIRKKSG G

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_20m24, frame 2

SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II., N = 1, Score = 957, P = 2.7e-96

PIR:S63177 mannosyl transferase (EC 2.4.1.-) - yeast (*Saccharomyces cerevisiae*), N = 1, Score = 533, P = 2.3e-51

SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II., N = 1, Score = 957, P = 2.7e-96

PIR:S63177 mannosyl transferase (EC 2.4.1.-) - yeast (*Saccharomyces cerevisiae*), N = 1, Score = 533, P = 2.3e-51

>SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II.

Length = 653

HSPs:

Score = 957 (143.6 bits), Expect = 2.7e-96, P = 2.7e-96
Identities = 206/514 (40%), Positives = 296/514 (57%)

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      N   W   + FK LLS R+  A+  I+DCDE +NYWEP H  +YGEFGQTWEYSP
Sbjct: 43 NNPNDNDWPFsFGSVFKMLLSIRISGAIWGIINDCDEVYNYWEPLHLFLYGEFGQTWEYSP 102

Query: 108 AYAIRSYAYLLHAWPAAFHARILQTNKILVfyFLRCLLAFVSCICELYFYKAVCKKFGL 167
      YAIRSY Y+ LH PA+  A+  KI+VF +R  +  + E Y + A+CKK +
Sbjct: 103 VYAIRSYFYIYLHYIPASLFANLFGDTKIVVFTLIRLTIGLFCLLGEYYAFDAICKKINI 162

Query: 168 HVS RMMLAFLVLSTCMFCSSSAFLPSSFCMYTTLIAMTGWYMDKTSIAVLGVAAGAILCW 227
      R  + F + S+GMF +S+AF+PSSFCM T  +  +  +  +  + VA  ++GW
Sbjct: 163 ATGRFFILFSIFSSGMFLASTAFVPSFCAITFYILGAYLNENWTAGIFCVAFSTMVGW 222

Query: 228 PFSAALGLPIAFDILLVMKHRWKSFFHWSLMALILFLVPVVVIDSYYYGKLVIAPLNIVLY 287

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Sbjct: 223 PFSA LGLPI D+L++K F SL+ + V+ DS+Y+GK V+APLNI LY
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 NV + GP LYG EP FY+ N F N+N+ A PL+ + Y + + Q+
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 + AP+ + W +IF Q HKEERFLFP+YP I A+AL A + ++
 Sbjct: 341 YQRFAPILLAVTTAAWLLIFGSAHKEERFLFPYPIAFFAALALDATNR---LCLKK 397
 Query: 401 YRLEHYTVTSNWLALGTVFLFGLLSFSRSVALFRGYHGPLDLYPEFYRIATDPTIHTVPE 460
 ++ N L++ + F +LS SR+ ++ Y +++Y T+ T +
 Sbjct: 398 LGMD-----NILSILFILCFAILASRTYSIHNNYGSHEVIYRSLNAELTNRT-NFKNF 450
 Query: 461 GRPVNVCGKWEYRFPSSFLPDNW-----QLQFIPSEFRGQLPKPFAEGPL---ATRI 511
 P+ VCVGKEW+RFPSSF +P +++FI SEFRG LPKPF + TR
 Sbjct: 451 HDPIRVCVGKEWHRFPSSFFIPQTVSDGKKVEMRFIQSEFRGLLPKPFLKSDKLVEVTRH 510
 Query: 512 VPTDMNDQNLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEW 558
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 Sbjct: 511 IPTEMNNLNQEEISRYVDLSDCDYVVDVD-MPQSDREPDFRKMQRNY 556

Pedant information for DKFZphutel_20m24, frame 2

Report for DKFZphutel_20m24.2

{LENGTH} 611
 {MW} 69863.78
 {pI} 8.91
 {HOMOL} SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II. 2e-93
 {FUNCAT} 09.01 biogenesis of cell wall [S. cerevisiae, YNL219c] 4e-69
 {FUNCAT} 01.06.01 lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YNL219c] 4e-69
 {FUNCAT} 01.05.01 carbohydrate utilization [S. cerevisiae, YNL219c] 4e-69
 {PIRKW} glycosyltransferase 9e-68
 {PIRKW} transmembrane protein 9e-63
 {PIRKW} hexosyltransferase 9e-68
 {PROSITE} MYRISTYL 9
 {PROSITE} CAMP_PHOSPHO_SITE 1
 {PROSITE} CK2_PHOSPHO_SITE 7
 {PROSITE} PKC_PHOSPHO_SITE 6
 {PROSITE} ASN_GLYCOSYLATION 2
 {KW} TRANSMEMBRANE 7
 {KW} LOW_COMPLEXITY 6.71 %

SEQ MASRGARQRLKSGSGSDTAPADKRLRELGSRAGGAERHTELSGNKAGQVWAPEGST
 SEG
 PRD ccchhhhhhhccccccccccccchhhhhhhhhccccccccceccccccccccccch
 MEMMMMMMM

SEQ AFKCLLSARLCAALLSNISDCDETENYWEPTHYLIYGEFGQTWEYSPAYAIRSYAYLLH
 SEG
 PRD hhhhhhhhhhhhhhhhhhhccccceccccceccccceccccchhhhhhhhhhhc
 MEM MMMMMMMMMMMMMMMMM.....M

SEQ AWPAAFHARILQTNKILVFYFLRCLLAFVSCICELYFYKAVCKKFGHLVSRMMLAFLVLS
 SEG
 PRD cchhhhhhhhhcchhhcc
 MEM MMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ TGMFCSSSAFLPSSFCMYTTLIAMTGWYMDKTSIAVLGVAAGAILGWPFSAALGLPIAFD
 SEG
 PRD cceeeccccccccchhhhhhhhhhhccccccccceeeehhhhhhhccccceeeecchhh
 MEMMMMMMMMMMMMMMM

SEQ LLVMKHRWKSFFHWSLMALILFLVPVVVIDSYGYGLVIAPLNIVLYNVFTPHGPDLYGT
 SEG
 PRD hhhhhhhhhhhhhhhhhhhhhheeeeeccccccccccccceeeeecccccccccc
 MEM MMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ EPWYFYLINGFLNFNVAALALLVPLTSLMEYLLQRFHVQNLGHPYWLTLAPMYIWFII
 SEG
 PRD cceeeccccccccchhh
 MEMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

Prosite for DKFZphutel 20m24.2

(No Pfam data available for DKFZphute1 20m24.2)

DKFZphutel_21d15

group: uterus derived

DKFZphutel_21d15 encodes a novel 191 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

Sequenced by MediGenomix

Locus: /chromosome="3"

Insert length: 5292 bp

Poly A stretch at pos. 5273, polyadenylation signal at pos. 5252

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1 CTCCCACTAG TGTATGCCTT AATGGTGCCG CTCTTGTCGG CGTCTACGCT
51 TGGGACCTTG GCTTCTGACT TGGAGAGTGT ACAGCTCTGC CCGACGGCAA
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151 AAGGCGGAGC CCGGCGCGGA CGCAGGCGGC TCCGGGCGGG CTCAGCACCC
201 CCAGGCACCG TCTCCTAGTG ACCGCGGCGC TCGCGGGCCT GGCGGCCGTT
251 GTCCGGGCGA CTGCGCAGCG CGGGCACCCC CGCGGCCCTT CCCCTGGGCG
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651 TCACCCGGCT GGAGGGCATC AAGGTGAGGA CCTCCCTGCC CCGCCGCGCT
701 CCAGGCCCTG CACGGCTGAG CCCGAGAGGA CCGGCGCTCA GCCCGGGTCC
751 CCACGCTGCC CCGGCGCGTG CTCTGCGTCC GTCCCGCGCG CTCCTACTCA
801 CTCGCTGCTG GTCGCTCTCC GGGCCGGGGC GACTTGCCCC TTTTGGGCA
851 GCGCGGTCTG GCGCCCCAGC TGCCCGCTGT GCGCCTTTTC CTTAGGTGGG
901 GCACGAGCGT ACGGCTCCAG TGGTCACCGA CAGGGATCAC TTCATCCGAA
951 CCCTCAGCCT CAAGCCGCTG CTCTTCGAAA TCCCCGGCTT CTTGACTGAT
1001 GAAGAGTGTC GGCTCATCAT CCATCTGGCG CAGATGAAGG GGTACAGCG
1051 CAGCCATGAT CTGCCCTACT AAGAGTATGA AGAGGCAATG AGCACTATGC
1101 AGGTGAGCCA GCTGACCTCT TTCCGGCTGC TGGACCAGAA CCGTGATGGG
1151 CACCTTCAGT TCCGTGAGGT TCTGGCCAG ACTCGCCTGG GAAATGGATG
1201 GTGGATGACT CCAGAGAGCA TTCAGGAGAT GTACGCGCGG ATCAAGGCTG
1251 ACCCTGATGG TGACGGTGAG CTCACACCTC TGCACAGTCC TATCCCGGTG
1301 AGCCTCTGTC CCACTCCAG GTGCACAATT TTGAAAACCT GGGCCCTTCC
1351 CCCACAGCCA GGCAGCCTCT CTGCACCCCT TTATAGTGGC CAGAGATGGG
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1451 CAGGCCCCCC GTTCCCTTGG GTGATGGTCT CGAGGGCAGT TCTTGGAGAC
1501 CCTTTTGATA ACATCAGGCA GAGTTGAGAG CCTGGGGACA GGAAGTAGGG
1551 CTGCTAGTTG GCAGAGAACA GAGTGGGTGG AGCAGGAGCA AGGCGACAGT
1601 GAGGCGAGCT AGAGCTTGGC TGTTTACCCT GCTCCATCCA TCTCTCCAGC
1651 CAGACACGAG GTCCACCCCA GCAGACAGCT TCCCTGGTCT AAGTGAGGTC
1701 TCCCTTGCTT TCCTCTGTGC CACCTGGAGT CATGCCGAAG CGCCTAAAAT
1751 GGTAGTGCTG CTACCTGTGC TAACTGCTGG GGAGGGGTGG GCAGGGAAGC
1801 TGTCATGCAA GTGGTGCCCC CTCTGGTAAT AACTCTCAGG AGGTTTCTGA
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2151 CCTGCTTAAT GGTTTGAGCA GGGACAGTGG AGAATGTICT CATGAGAGGG
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2801 TCCACAAGTA CATGAGGAGC CACAAGGCAG AGTCCAGTGA GCTGGTGCGG
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3001 AGGACAGAAT GGATTAACCC ATTTGGGATT AAGTCCATT TGTTAGACCA
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3251 GGACCTCAGG ACTCCCGGCC CCCTTTATTT AGTGGAAATG TCAACATTTT
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5101 GCCAGTTGCC CAAGATCAGG GGTCCGGCTG TCCTTCTGTC CTGCTGCAGA
5151 CTAAGGCTCT GGCCAATGTC TTGCCCCACC CCGCCAGCCG CGATACGGCG
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```

BLAST Results

Entry HSU64252 from database EMBL:
 Human STS sequence NOTI-225.
 Score = 959, P = 1.2e-36, identities = 195/199

Medline entries

No Medline entry

Peptide information for frame 1

ORF from the beginning to 351 bp; peptide length: 118
 Category: questionable ORF
 Classification: no clue

```

1 LPLVYALMVP LLSASTLGL ASDLESVQLC PTATQLGKRS PSVGWGSRRR
51 KAEPGADAGG SGRAQHPQAP SPSDRGARGP GGRCPGDCAA RAPPRPLPWA
101 RARPGCHGGS GDRPAA

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_21d15, frame 1

No Alert BLASTP hits found

Peptide information for frame 2

ORF from 320 bp to 892 bp; peptide length: 191
Category: putative protein
Classification: no clue

```

1 MAAAAVTGQR PETAAEEAS RPQWAPPDHC QAQAAAGLGD GEDAPVRPLC
51 KPRGICSRAY FLVLMVFVHL YLGNVLALLL FVHYSNGDES SDPGPOHRAQ
101 GPGPEPTLGP LTRLEGIVR TSLPRRAPGP ARLSPRGPAL SPGPHAAPGA
151 ALRRSRALPL TRLLSLSGPG RLGPFWAARS GAPAARCAFF P

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_21d15, frame 2

PIR:EDBE75 immediate-early protein IE175 - human herpesvirus 1, N = 2,
Score = 106, P = 0.0067

>PIR:EDBE75 immediate-early protein IE175 - human herpesvirus 1
Length = 1,298

HSPs:

Score = 106 (15.9 bits), Expect = 6.7e-03, Sum P(2) = 6.7e-03
Identities = 36/103 (34%), Positives = 44/103 (42%)

```

Query:      87 GDESSDPGPQHRAQGGPEPTLGPLTRLEGIVRTSLPRRA-PGPARLS-PRGPALSPGP 144
             G +  PCP      G GP P  P T+  G      S  R  P PA  S P GP  +P
Sbjct:     726 GRKRKSPGPAPRPPGGGGPRP---PKTKKSGADAPGSDARAPLPAPAPPSTPPGPPEPAPAQ 782

```

```

Query:     145 HAAPGAALRRSRALPLT-RLLSLSGPGRLGPFWAARS GAPAARCAP 189
             AAP AA ++R  P+              GP LG W +  P+  AP
Sbjct:     783 PAAPRAAAQARPRPVAVSRRAEGPDPLGG-WRRQPPGPSHTAAP 827

```

Score = 40 (6.0 bits), Expect = 6.7e-03, Sum P(2) = 6.7e-03
Identities = 8/21 (38%), Positives = 9/21 (42%)

```

Query:      28 DHCQAQAAAGLGDGEDAPVRP 48
             DH +  A G G  AP  P
Sbjct:     212 DHAREARAVGRGPSSAAPAAP 232

```

Pedant information for DKFZphut1_21d15, frame 1

Report for DKFZphut1_21d15.1

```

[LENGTH]      117
[MW]           11797.32
[pI]           10.68
[KW]           Irregular
[KW]           SIGNAL_PEPTIDE 22
[KW]           LOW_COMPLEXITY 38.46 %

```

```

SEQ  LPLVYALMVPLLSASTLGTSLASDLESVQLCPTATQLGKRSPSVGWGSRRRKAEPGADAGG
SEG  .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD  cccccccccccccccccccccchhhhhhhhhccccccccccccccccccccccccccccccccc

SEQ  SGRAQHPQAPSPSDRGARGPGGRC PGDC AARAPRPLPWARARPGCHGGSGGDRPAA
SEG  .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

(No Prosite data available for DKFZphut1_21d15.1)

(No Pfam data available for DKFZphute1_21d15.1)

Pedant information for DKFZphute1_21d15, frame 2

Report for DKFZphute1_21d15.2

[LENGTH] 191
[MW] 19916.88
[pI] 10.43
[KW] TRANSMEMBRANE 1
[KW] LOW_COMPLEXITY 29.84 %

SEQ MAAAAVTGQRPETAAEEASRPQWAPPDHCQAQAAAGLGDGEDAPVRPLCKPRGICSRAY
SEG
PRD cccceeeccccchhhhhhhhhccccccchhhhhhhccccccccccccccccccccchhh
MEM
SEQ FLVLMVFVHLYLGNVLALLLFVHYSNGDESSDPGPQHRAGPGPEPTLGPLTRLEGIKVR
SEGxxxxxxxxxxxxxxxx.....
PRD hhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccccccccccccccceeeee
MEMMMMMMMMMMMMMMMMM.....
SEQ TSLPRRAPGPARLSPRGPALSPGPHAAPGAALRRSRALPLTRLLSLSPGRLGPFWAARS
SEGxx.....xxxx
PRD eccccccccccccccccccccccccccccchhhhhhhccccceeeccccccccchhhhhc
MEM
SEQ GAPAARCAPFP
SEG xxxxxxxxxxxx..
PRD ccccccccccc
MEM

(No Prosite data available for DKFZphute1_21d15.2)

(No Pfam data available for DKFZphute1_21d15.2)

DKF2phutel_22d2

group: signal transduction

DKF2phutel_22d2 encodes a novel 580 amino acid putative GTP-binding protein related to the ras protein. Additionally, the putative protein contains an EF-hand for calcium-binding.

G-proteins are involved in various signal transduction pathways, transferring the signal of a cellular receptor to an intracellular signal cascade.

The new protein can find clinical application in modulating/blocking the response to a cellular receptor.

similarity to GTP-binding proteins

complete cDNA, complete cds, potential start at Bp 64, EST hits
complete cds according to K08F11.5 and YAL048c

Sequenced by BMFZ

Locus: /map="17"

Insert length: 3247 bp

Poly A stretch at pos. 3230, no polyadenylation signal found

```

1 CTCTGGTGA GAGGAGTCCA CTCCGTGCGT GCGGGCGGAG GCCGGCCCCC
51 GAGAGCCGCC GACATGAAGA AAGACGTGCG GATCCTGCTG GTGGGAGAAC
101 CTAGAGTTGG GAAGACATCA CTGATTATGT CTCTGGTCAG TGAAGAATTT
151 CCAGAAGAGG TTCCTCCCCG GGCAGAAGAA ATCACCATTG CAGCTGATGT
201 CACCCAGAG AGAGTTCCAA CACACATTGT AGATTACTCA GAAGCAGAAC
251 AGAGTGATGA ACAACTTCAT CAAGAAATAT CTCAGGCTAA TGTCATCTGT
301 ATAGTGATG CCGTTAACAA CAAGCATTCT ATTGATAAGG TAACAAGTCG
351 ATGGATTCCCT CTCATAAATG AAAGAACAGA CAAAGACAGC AGGCTGCCTT
401 TAATATTGGT TGGGAACAAA TCTGATCTGG TGGAAATATG TAGTATGGAG
451 ACCATCCTTC CTATTATGAA CCAGTATACA GAAATAGAAA CCTGTGTGGA
501 GTGTTTCAGCG AAAAACCTGA AGAACATATC AGAGCTCTTT TATTACGCAC
551 AGAAAGCTGT TCTTCATCCT ACAGGGCCCC TGTACTGCCC AGAGGAGAAG
601 GAGATGAAAC CAGCTTGTAT AAAAGCCCTT ACTCGTATAT TTAAATATC
651 TGATCAAGAT AATGATGGTA CTCTCAATGA TGCTGAAGTC AACTTCTTTC
701 AGAGGATTGG TTTCAACACT CCATTAGCTC CTCAAGCTCT GGAGGATGTC
751 AAGAATGTAG TCAGAAAACA TATAAGTGAT GGTGTGGCTG ACAGTGGGTT
801 GACCCTGAAA GGTTTTCTCT TTTTACACAC ACTTTTATC CAGAGAGGGA
851 GACACGAAAC TACTTGGACT GTGCTCGAC GATTTGGTTA TGATGATGAC
901 CTGGATTGGA CACCTGAATA TTTGTTCCCC CTGCTGAAAA TACCTCCTGA
951 TTGCACTACT GAATTAATC ATCATGCATA TTTATTCTC CAAAGCACCT
1001 TTGACAAGCA TGATTGGAT AGAGACTGTG CTTTGTCAAC TGATGAGCTT
1051 AAAGATTAT TTAAGTTTT CCCTTACATA CCTTGGGGGC CAGATGTGAA
1101 TAACACAGTT TGTACCAATG AAAGAGGCTG GATAACCTAC CAGGGATTCC
1151 TTTCCAGTG GACGCTCACG ACTTATTTAG ATGTACAGCG GTGCCTGGAA
1201 TATTTGGGCT ATCTAGGCTA TTCAATATTG ACTGAGCAAG AGTCTCAAGC
1251 TTCAGCTGTT ACAGTGACAA GAGATAAAAA GATAGACCTG CAGAAAAAAC
1301 AACTCAAAG AAATGTGTTT AGATGTAATG TAATTGGAGT GAAAAACTGT
1351 GGGAAAAGTG GAGTCTTCA GGCTCTTCTT GGAAGAAACT TAATGAGGCA
1401 GAAGAAAATT CGTGAAGATC ATAAATCCTA CTATGCGATT AACACTGTTT
1451 ATGTATATGG ACAAGAGAAA TACTTGTGTG TGCATGATAT CTCAGAATCG
1501 GAATTTCTAA CTGAAGCTGA AATCATTGTG GATGTTGTAT GCCTGGTATA
1551 TGATGTCAGC AATCCCAAAT CCTTTGAATA CTGTGCCAGG ATTTTAAAGC
1601 AACACTTTAT GGACAGCAGA ATACCTTGCT TAATCGTAGC TGCAAAGTCA
1651 GACCTGCATG AAGTTAAACA AGAATACAGT ATTTACCTA CTGATTCTG
1701 CAGGAAACAC AAAATGCCTC CACCACAAGC CTTCACTTGC AATACTGCTG
1751 ATGCCCCCAG TAAGGATATC TTTGTTAAAT TGACAACAAT GGCCATGTAT
1801 CCGTAAGTAC TTGCTGTCTT CATTTCATG TTGCATGGTT CATAACATTG
1851 CATGCCATTA TTAGCCATGA AGGGAATATC TTTGTCACAT AGGAATTGTT
1901 CAGCAACAGA AAGATACTTT GTAATGAGAA GGTACAAATT TGAGTAAATG
1951 CAAGTTTGGT TTGAATGCCA TAATAAAATG ATATAACAG TGCTTCTGAC
2001 AATATCTGTA TATTTTGTAG CAGGCTGTAA CTATCTTAAT AGAATAGTAC
2051 AATAAAACAC AACCCCCCAC CCAGCATTAA AAAATAGTTT TACTGGAATA
2101 AAATGGGTTT GGCATCATGT TGTTTTATGC TTATAAGCA TTTTCATATG
2151 AACAGAAAAGT TTATATTTTT CTGTTTTTGA CCTTAGGTAT ATGAAGTTTT
2201 CTAAAATATT TTATTAATTT ATGTTGAAAT TGTGGGTATG CTTCAAGTAG
2251 GATATGTCTT TTTTAAGTGC TGTAAGAGT AGTTGTAATT GGAATTTCTA
2301 CTGTATAAAT GTTTTACATT AAGTGTACG AGCCACAAAT TTCATGTACA
2351 TTTATTATAT ATCTATACAT GCATATGCAC AAGCACATAA CTGTGGTCAT
2401 CTCGTAGTAT TACTAACTGC CTTAAATTTG CATGGTCTT AATGGCATTC
2451 GCCTCAAGTA GTGTGTTTGT ATAAATCTCG TTTTGTAAAC AAATAGTTTT
2501 TCAGGCAGTG CGTTTCTCAG GACTTTATAG CTTATTCTAC TTATTCTTAT
2551 GTTAGTCTCT AAATTATTTT TCTTCTTATG AAAACTACAG TGTAACACAG

```

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2601 AGTAATAATC AACATTGCT ATAAACCAAG AATGACATTT TTCAAAAAGG
2651 TGTTGATTTG TACAGATTTT TAAAGTCAGT TAACTTTACT GCTATTTTAT
2701 TACCTAATAC TTTTTTTAGA TGCAACAAAC CCTTGAATTT CTATTTGTAT
2751 TCGAAGACAA GTCATTCTTA TTATTATAGA ATAACCAAAA CCTTATTTAT
2801 GTTTTACCTT TGCTTTAAAA CTCTCATGTA TGTTATCTAC AGAGAGGATC
2851 ATTACAGAGA CAGACTCTCC CGAGACATGG GCCACACTGA TAGAATAGAG
2901 AATTTGAGAA AAATCTGGGT CTTTCTAAAA ACTGCTTTGT AAGTTACTTT
2951 TTCTTTATGA CTTCTGTGGG ATTTTGTGTA TATTTTCTTA GAGAATGACC
3001 AAATCTCCTT TCTTGCCATA ATTAACATTT AGTAATTATG TAGAAACGCA
3051 CTGCTTGGTC AGGCTTCCTG CCTAGCTATA TATTACGTTG TCTTCCTTAC
3101 TACATAAATG TACTTCTTTA ATCTTGTGAT TACAGTAACT GCAAGTGTGT
3151 TTTTACATCT GCATTTTAA AACATTTTAC TGTAATTCTG TTGTGTGTGT
3201 GTGTGTTATA TGATAAATGT ACATACATGG AAAAAAAAAA AAAAAA

```

BLAST Results

Entry AC004527 from database EMBL:
 *** SEQUENCING IN PROGRESS *** Nfl-related locus, Direct Submission;
 HTGS phase 1, 10 unordered pieces.
 Score = 1899, P = 1.1e-78, identities = 387/396

Entry HS148355 from database EMBL:
 human STS SHGC-31220.
 Score = 1826, P = 7.5e-78, identities = 388/406

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 64 bp to 1803 bp; peptide length: 580
 Category: similarity to known protein

```

1 MKKDVRIILLV GEPRVGKTSI IMSLVSEEFV EEVPPRAEEI TIPADVTPER
51 VPTHIVDYSE AEQSDEQLHQ EISQANVICI VYAVNNKHSI DKVTSRWIPL
101 INERTDKDSR LPLILVGNKS DLVEYSSMET ILPIMNQYTE IETCVECSAK
151 NLKNISELFY YAKKAVLHPT GPLYCPEEKE MKPACIKALT RIFKISDQDN
201 DGTLNDAELN FFQRICFNTP LAPQALDVK NVVRKHISDG VADSGTLTKG
251 FLFLHLLFIQ RGRHETTWTV LRRFGYDDDL DLTPEYLFPL LKIPPDCTTE
301 LNHAYLFLQ STFDKHDLDL DCALSPDELK DLFKVFPYIP WGPDPVNTVC
351 TNERGWITYQ GFLSQWTLTT YLDVQRCLEY LGYLGYSILT EQESQASAVT
401 VTRDKKIDLO KKQTORNVFR CNVIGVKNGC KSGVLQALLG RNLMRQKKIR
451 EDHKSYYAIN TVVYVGOEY LLLHDISESE FLTEAEIICD VVCLVYDVSN
501 PKSFYECARI FKQHFMDSRI PCLIVAAKSD LHEVKQEYSI SPTDFCRKHK
551 MPPPQAFTCN TADAPSKDIF VKLTTMAMYP

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutell_22d2, frame 1

TREMBL:CEUK08F11_3 gene: "K08F11.5"; Caenorhabditis elegans cosmid
 K08F11., N = 1, Score = 1357, P = 1.1e-138

TREMBL:SPCC320_4 gene: "SPCC320.04c"; product: "hypothetical protein";
 S.pombe chromosome III cosmid c320., N = 1, Score = 839, P = 4.4e-89

TREMBL:CEUC47C12_3 gene: "C47C12.4"; Caenorhabditis elegans cosmid
 C47C12., N = 2, Score = 408, P = 5.6e-74

PIR:S51971 probable membrane protein YAL048c - yeast (Saccharomyces
 cerevisiae), N = 1, Score = 677, P = 1.3e-66

>TREMBL:CEUK08F11_3 gene: "K08F11.5"; Caenorhabditis elegans cosmid
 K08F11.

Length = 625

HSPs:

Score = 1357 (203.6 bits), Expect = 1.1e-138, P = 1.1e-138
Identities = 263/582 (45%), Positives = 380/582 (65%)

Query: 4 DVRILLVGEPRVGKTSLSIMSLVSEEFPEEVPPRAEEITIPADVTPERVPHIVDYSEAEQ 63
DVRI+L+G+ GKTSL+MSL+ +E+ + VP R + + IPADVTPE V T IVD S E+
Sbjct: 9 DVRIVLIGDEGCGKTSLSVMSLLEDEWVDAVPRRLDRVLIPADVTPEVNTTSIVDLSIKEE 68

Query: 64 SDEQLHQEISQANVICIVYAVNNKHSIDKVTSRWIPLINERTDKDSRLPLILVGNKSDLV 123
+ + EI QANVIC+VY+V ++ ++D + ++W+PLI + + P+ILVGNKSD
Sbjct: 69 DENWIVSEIRQANVICVVYSVTDESTVDGIQTKWLPRIQSFGYHETPVILVGNKSDGT 128

Query: 124 EYSSMETILPIMNQYTEIETCVECSAKNKNISELFYYAQKAVLHPTGLYCPEEKEMKP 183
++ + ILPIM TE+ETCVECSA+ +KN+SE+FYAQKAV++PT PLY + K++
Sbjct: 129 A-NNTDKILPIMEANTEVETCVECSARTMKNVSEIFYAQKAVIYPTREPLYDADTKQLTD 187

Query: 184 ACIKALTRIFKISDQDNDGTLNDAELNFFQRICFNTPLAPQALEDVKNVVRKHISDGVAD 243
KAL R+FKI D+DNDG L+D ELN FQ++CF PL ALEDVK V DGVA+
Sbjct: 188 RARKALIRVFKICDRDNDGYLSDTELNDQKLCFGIPLTSTALEDVKRAVSDGCPDGVAN 247

Query: 244 SGLTLKGFLLHFLHTLFIQGRHETTWTVLRRFYDQDDDLTPEYLFPLKIPPDCTTELNH 303
L L GFL+LH LFI+RGRHETT WVR+FGY+ L L+ +YL+P + IP C+TEL+
Sbjct: 248 DSLMLAGFLYLHLLFIERGRHETT WAVLRKFGYETSLKLSIEDYLYPRITIPVGCSTELSP 307

Query: 304 HAYLFLQSTFDKHDLDROCALSPDELKDLFKVFPYIPWGPVNNVTCTNERGWITYQGFL 363
F+ + F+K+D D+D LSP EL++LF V P D + TN+RGW+TY G++
Sbjct: 308 EGVQFVSALFEKYDEKDGCLSPSELQNLFSVCPVPVITKDNILAETNQRGWLTNGYM 367

Query: 364 SQWTLTTYLDVQRCLEYLGYLSILTEQESQAS----AVTVTRDKKIDLQKKQTORNVF 419
+ W +TT +++ + E L YLG+ + +A ++ VTR++K DL+ T R VF
Sbjct: 368 AYWNMTTLINLTQTFFQLAYLGFVGRSGPGRAGNTLDSIRVTRERKKDLENHGTDKRVF 427

Query: 420 RCNVIGVKNCGSGVLQALLGRNLMRQKKIREDHKSYYAINTVYVYGQEKYLLLDHI--- 476
+C V+G K+ GK+ +Q+L GR + +I H S + IN V V + KYLLL ++
Sbjct: 428 QCLVVGAKDAGKTVFMQSLAGRGMDVAQIGRRH-SPFVINRVRVKEESKYLLREVDVL 486

Query: 477 SESEFLTEAEIICDVCVCLYVDVSNPKSFEYCARIFKQHFMDSRIPCLIVAAKSDLHEVKQ 536
S + L E DVV +YD+SNP SF +CA +++++F ++ PC+++A K + EV Q
Sbjct: 487 SPQDALGSGETSADVVAFLYDISNPDSFAFCATVYQKYFYRTKTPCVMIA TKVEREEVDQ 546

Query: 537 EYSISPTDFCRKHKMPPPPQAFTCNTADAPSKDIFVKLTMMAMYP 580
+ + P +FCR+ ++P P F+ S IF +L MA+YP
Sbjct: 547 RWEVPPEEFCRQFELPKPIKFSTGNIGQSSSPIFEQLAMMAVYP 590

Pedant information for DKF2phutel_22d2, frame 1

Report for DKF2phutel_22d2.1

[LENGTH] 580
[MW] 66541.61
[pI] 5.56
[HOMOL] TREMBL:CEUK08F11_3 gene: "K08F11.5"; Caenorhabditis elegans cosmid K08F11. 1e-149
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YAL048c] 5e-81
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YKR055w] 3e-11
[FUNCAT] 03.99 other cell growth, cell division and dna synthesis activities [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 10.04.07 g-proteins [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 11.01 stress response [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 01.03.13 regulation of nucleotide metabolism [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR101w] 4e-08
[FUNCAT] 11.10 cell death [S. cerevisiae, YOR101w] 4e-08
[FUNCAT] 10.02.07 g-proteins [S. cerevisiae, YPR165w] 7e-08
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YPR165w] 7e-08
[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YPR165w] 7e-08
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YFL005w] 9e-08
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YFL005w] 9e-08
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YFL005w] 9e-08
[FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YNL093w] 1e-07

[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YNL093w] 1e-07
 [FUNCAT] 08.19 cellular import [S. cerevisiae, YNL093w] 1e-07
 [FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YLR229c] 8e-07
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR229c] 8e-07
 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YCR027c] 3e-06
 [FUNCAT] 09.09 biogenesis of intracellular transport vesicles [S. cerevisiae, YGL210w] 9e-04
 [BLOCKS] BL00410A Dynamin family proteins
 [SCOP] dlplk_ 3.25.1.3.1 CH-p21 Ras protein [human (Homo sapiens)] 2e-42
 [SCOP] dlguaa_ 3.25.1.3.10 Rap1A [Human (Homo sapiens)] 5e-59
 [PIRKW] transmembrane protein 1e-79
 [PIRKW] membrane trafficking 2e-06
 [PIRKW] acetylated amino end 3e-09
 [PIRKW] prenylated cysteine 3e-09
 [PIRKW] signal transduction 1e-07
 [PIRKW] transforming protein 3e-09
 [PIRKW] immediate-early protein 8e-06
 [PIRKW] alternative splicing 4e-08
 [PIRKW] P-loop 1e-10
 [PIRKW] lipoprotein 7e-10
 [PIRKW] proto-oncogene 3e-09
 [PIRKW] methylated carboxyl end 3e-09
 [PIRKW] membrane protein 3e-09
 [PIRKW] GTP binding 1e-10
 [PIRKW] thiolester bond 7e-10
 [SUPFAM] ras transforming protein 1e-10
 [PROSITE] ATP_GTP_A 2
 [PROSITE] MYRISTYL 3
 [PROSITE] EF_HAND 1
 [PROSITE] CAMP_PHOSPHO_SITE 1
 [PROSITE] CK2_PHOSPHO_SITE 14
 [PROSITE] TYR_PHOSPHO_SITE 4
 [PROSITE] PKC_PHOSPHO_SITE 5
 [PROSITE] ASN_GLYCOSYLATION 3
 [PFAM] Ras family (contains ATP/GTP binding P-loop)
 [KW] Irregular
 [KW] 3D

SEQ MKKDVRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEETIPADVTPERVPTHIVDYSE
 1jai- ...EEEEEEETTTTCHHHHHHHHHHCCCCCCCCCEEEEEETTEEEEEEECC
 SEQ AEQSDQLHQEISQANVICIVYAVNNKHSIDKVTSRWIPLINERTDKDSRLPLILVGNKS
 1jai- CGGGHHHHHHHHHTTEEEEEETTTTHHHHHHH-HHHHHHHHHHCTTT-TCEEEEEET
 SEQ DLVEYSSMETILPIMNQYTEIETCVECSAKNLKNISELFYYAQKAVLHPTGPLYCPREEKE
 1jai- TTTTTTTTHHHHHHHHHHCCCE-EECTTTTTTHHHHHH.....
 SEQ MKPACIKALTRIFKISDQNDGTLNDAELNFFQRICFNTPLAPQALEDVKNVVRKHISDG
 1jai-
 SEQ VADSGTLKGLFLHTLFIQRGRHETTWTVLRRFGYDDDLDTPEYLFPLLKIPPDCTTE
 1jai-
 SEQ LNHHAYLFLOSTFDKHDLDRLDCALSPDELKDLFKVFPYIPWGPVNNVTCTNERGWITYQ
 1jai-
 SEQ GFLSQWTLTTYLDVQRCLEYLGYLGYSILTEQESQASAVTVTRDKKIDLQKKQTRNVFR
 1jai-
 SEQ CNVIGVKNCCKSGVLQALLGRNLMRQKKIREDHKSYYAINTVYVYGQEKYLLLDISESE
 1jai-
 SEQ FLTEAEIICDVCLVYDVSNPKSFEYCARIKQHFMDSRIPCLIVAAKSDLHEVKQEYSI
 1jai-
 SEQ SPTDFCRKHKMPPPPQAFTCNTADAPSKDIFVKLTMTMAMP
 1jai-

Prosites for DKFzphut1_22d2.1

PS00001	118->122	ASN_GLYCOSYLATION	PDOC00001
PS00001	154->158	ASN_GLYCOSYLATION	PDOC00001
PS00001	346->350	ASN_GLYCOSYLATION	PDOC00001
PS00004	411->415	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	94->97	PKC_PHOSPHO_SITE	PDOC00005
PS00005	105->108	PKC_PHOSPHO_SITE	PDOC00005

PS00005	148->151	PKC_PHOSPHO_SITE	PDOC00005
PS00005	247->250	PKC_PHOSPHO_SITE	PDOC00005
PS00005	414->417	PKC_PHOSPHO_SITE	PDOC00005
PS00006	59->63	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	126->130	CK2_PHOSPHO_SITE	PDOC00006
PS00006	139->143	CK2_PHOSPHO_SITE	PDOC00006
PS00006	143->147	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00006	203->207	CK2_PHOSPHO_SITE	PDOC00006
PS00006	311->315	CK2_PHOSPHO_SITE	PDOC00006
PS00006	325->329	CK2_PHOSPHO_SITE	PDOC00006
PS00006	370->374	CK2_PHOSPHO_SITE	PDOC00006
PS00006	390->394	CK2_PHOSPHO_SITE	PDOC00006
PS00006	477->481	CK2_PHOSPHO_SITE	PDOC00006
PS00006	483->487	CK2_PHOSPHO_SITE	PDOC00006
PS00006	541->545	CK2_PHOSPHO_SITE	PDOC00006
PS00007	153->161	TYR_PHOSPHO_SITE	PDOC00007
PS00007	376->384	TYR_PHOSPHO_SITE	PDOC00007
PS00007	153->162	TYR_PHOSPHO_SITE	PDOC00007
PS00007	448->457	TYR_PHOSPHO_SITE	PDOC00007
PS00008	240->246	MYRISTYL	PDOC00008
PS00008	425->431	MYRISTYL	PDOC00008
PS00008	433->439	MYRISTYL	PDOC00008
PS00017	11->19	ATP_GTP_A	PDOC00017
PS00017	425->433	ATP_GTP_A	PDOC00017
PS00018	197->210	EF_HAND	PDOC00018

Pfam for DKF2phutel_22d2.1

HMM_NAME	Ras family (contains ATP/GTP binding P-loop)		
HMM	*KLVLIGDSGVGKSCLLIRFTQNeFnEeYIPTIGvDFYtKTIIEIDGKtIK		
Query	6	RILLVGEP RVGKTS LIMSLVSEEFPEE-VPPR-AEEITIPADVTPERV	52
HMM	LQIWDTAGQERYRsMRPMYYRGAMGFMLVYDITNRqSFENIr.NWweEIr		
Query	53	THIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDKVTSRWIPLIN	102
HMM	RHCDrDENVPIMLVGNKCDLEDQRQVStEEGQeFAREWGAIPFMETS AKT		
Query	103	ERTDKDSRLPLILVGNKSDLVEYSSMETILPIMNQYTEI-ETCVCESAKN	151
HMM	NiNVEEAFMEIvReIlqrMqeqNqteNinidQpsrnrkrCCCIM*		
Query	152	LKNISELFYYAQKAVLHPT-----GLPYCPEEKEMK-PACI--	186

DKFZphut1_22e12

group: signal transduction

DKFZphut1_22e12 encodes a novel 92 amino acid protein, with similarity to yeast, C.elegans, Drosophila and mammalian proteins.

The Drosophila cni and mammalian cornicon proteins are part of a signal transduction pathway involving the EGF-receptor.

The new protein can find application in modulating the cornicon modulated signal transduction way and also the EGF receptor signaling processes.

strong similarity to S.cerevisiae YGL054c and cornicon

complete cDNA, complete cds, EST hits
cornicon is required for signal transduction in the EGF-receptor
signal processing

Sequenced by BMFZ

Locus: unknown

Insert length: 519 bp

Poly A stretch at pos. 499, no polyadenylation signal found

```
1  GTCGGGGCAT CCGAGCGGGT TTGACGGAAG GAGCGGCGGC GACGGAGGAG
51  GAGGATGGAG GCGGTGGTGT TCGTCTTCTC TCTCCTCGAT TGTTCGCGGC
101 TCATCTTCCT CTCGGTCTAC TTCATAATTA CATTGTCTGA TTTAGAATGT
151 GATTACATTA ATGCTAGATC ATGTTGCTCA AAATTAAACA AGTCGGTAAT
201 TCCAGAATTG ATTGGCCATA CCATTGTCAC TGTATTACTG CTCATGTCAT
251 TGCACGGGTT CATCTTCCTT CTCAACTTAC CTGTTGCCAC TTGGAATATA
301 TATCGTATGA TCTTAGCTTT GATAAATGAC TGAAGCTGGA GAAGCCGTGG
351 TTGAAGTCAG CCTACACTAC AGTGCACAGT TGAGGAGCCA GAGACTTCTT
401 AAATCATCCT TAGAACCGTG ACCATAGCAG TATATATTTT CCTCTTGGAA
451 CAAAAAATA TTTTGTGTGT ATTTTACCA TATAAAGTAT TTAATAAACA
501 TGAATAAATA AAAAAAATA
```

BLAST Results

No BLAST result

Medline entries

95300228:

cornicon and the EGF receptor signaling process are necessary for both
anterior-posterior
and dorsal-ventral pattern formation in Drosophila.

Peptide information for frame 1

ORF from 55 bp to 330 bp; peptide length: 92
Category: strong similarity to known protein

```
1  MEAVVFVFSL LDCCALIFLS VYFIITLSDL ECDYINARSC CSKLNKQVIP
51  ELIGHTIVTV LLLMSLHWFI FLLNLPVATW NIYRMILALI ND
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_22e12, frame 1

PIR:S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae), N = 2, Score = 185, P = 5.7e-17

TREMBL:SPAC2C4_5 gene: "SPAC2C4.05"; product: "cornicon homolog";

S.pombe chromosome I cosmid c2C4., N = 1, Score = 163, P = 3.7e-12

PIR:S46084 probable membrane protein YBR210w - yeast (Saccharomyces cerevisiae), N = 1, Score = 162, P = 4.8e-12

TREMBL:AF104398.1 product: "cornichon"; Homo sapiens cornichon mRNA, complete cds., N = 1, Score = 141, P = 8e-10

SWISSPROT:CNI_DROVI CORNICHON PROTEIN., N = 1, Score = 139, P = 1.3e-09

>PIR:S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae)
Length = 138

HSPs:

Score = 185 (27.8 bits), Expect = 5.7e-17, Sum P(2) = 5.7e-17
Identities = 35/85 (41%), Positives = 56/85 (65%)

Query: 1 MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWWIPELIGHTIVTV 60
M A +F+ +++ C +F V+F I +DLE DYIN CSK+NK + PE H +++
Sbjct: 1 MGAWLFILAVVVCINLFGQVHFTILYADLEADYINPIELCSKVNKLITPEAALHGALS 60

Query: 61 LLLMSLHWFIFLLNLPVATWNIYRM 85
L L++ +WF+FLLNLPV +N+ ++
Sbjct: 61 LFLNGYWFVFLNLPVLAYNLNKI 85

Score = 37 (5.6 bits), Expect = 5.7e-17, Sum P(2) = 5.7e-17
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 82 IYRMILALI 90
+YRMI+ALI
Sbjct: 123 LYRMIMALI 131

Pedant information for DKFZphutel_22e12, frame 1

Report for DKFZphutel_22e12.1

[LENGTH] 92
[MW] 10614.98
[pI] 5.04
[HOMOL] PIR:S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae)
5e-14
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YGL054c]
2e-15
[PIRKW] transmembrane protein 2e-11
[PROSITE] CK2_PHOSPHO_SITE 3
[KW] SIGNAL PEPTIDE 33
[KW] TRANSMEMBRANE 2

SEQ MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWWIPELIGHTIVTV
PRD ccchhhhhhhhhhhhhhhhhhhheeeccccccccccccccccceehhhhhhhhhhhhh
MEMMMMMMMMMMM

SEQ LLLMSLHWFIFLLNLPVATWNIYRMILALIND
PRD hhhhhhhheeeccccchhhhhhhhhhhhhccccc
MEM MMMMMMMMMMMMMMMMMMMMM..MMMMMM....

Prosite for DKFZphutel_22e12.1

PS00006 9->13 CK2_PHOSPHO_SITE PDOC00006
PS00006 26->30 CK2_PHOSPHO_SITE PDOC00006
PS00006 28->32 CK2_PHOSPHO_SITE PDOC00006

(No Pfam data available for DKFZphutel_22e12.1)

DKF2phutel_22n2

group: uterus derived

DKF2phutel_22n2 encodes a novel 304 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by BMF2

Locus: /map="553.3 cR from top of Chr11 linkage group"

Insert length: 1556 bp

Poly A stretch at pos. 1534, no polyadenylation signal found

```
1 ACAACAGGCT GGTGCTTGG CGTGAATCC TAAAGTGCC TGGCTTTGAG
51 ACTGGAGTGA GACCCAGCC CTAGGCTGGG GTTCTTTCCA TTATAGAGGA
101 GACGGATTCA GAAGGGCTAC AGACCAAGGT TGTTCAAAAC CAGACATATG
151 ATGAGCGTCT AGAGATTAAC GACTCCGAAG AGGTTGCAAG TATTTATACT
201 CCAACCCCAA GACACCAAGG ACTTCCTCGT TCTGCCCATC TTCCTAACAA
251 GGTATGGCT GATAACAGCA GTGATGAGTG TGAAGAGGAA AATAACAAGG
301 AGAAGAAGAA GACCTCACAG TTGACACCTC AACGGGGCTT TAGTGAAAAT
351 GAGGATGACG ATGATGATGA TGATGATTCA TCTGAACTG ATTCTGATTG
401 TGATGATGAT GATGAAGAGC ATGGAGCCCC TCTGGAAGGG GCCTATGACC
451 CTGCAGACTA TGAGCATTTG CCAGTTTCTG CTGAAATTAA GGAACCTTTC
501 CAGTACATCA GTAGGTACAC ACCTCAGTTG ATTACCTGG ACCACAAACT
551 GAAGCCTTTC ATTCCTGATT TTATCCCAGC TGTCGGGGAT ATTGATGCAT
601 TCTTAAAGGT CCCACGTCCT GATGGAAAGC CTGACAACTT TGGCCTATTG
651 GTATTGGATG AACCTTCTAC AAAGCAGTCA GACCCACGG TGCTCTCACT
701 CTGTTAAACA GAGAATTCTA AGCAGCACAA CATCACACAA CATATGAAAG
751 TAAAAAGCCT AGAAGATGCA GAAAAGAATC CCAAAGCCAT TGACACGTGG
801 ATTGAGAGCA TCTCTGAATT ACACCGTTCT AAGCCCCCTG CGACTGTGCA
851 CTACACCAGG CCCATGCCCG ACATTGACAC GCTGATGCAG GAATGGTCCC
901 CGGAGTTTGA AGAGCTTTTG GGCAAGGTAA GCCTGCCCAC GGCAGAGATT
951 GATTGCAGCC TGGCAGAGTA CATTGACATG ATCTGTGCCA TTCTAGACAT
1001 CCCTGTCTAC AAGAGTCGGA TCCAGTCCCT CCATCTGCTC TTTTCCCTCT
1051 ACTCAGAATT CAAGAACTCA CAGCATTTTA AAGCTCTCGC TGAAGGCAAG
1101 AAAGCATTCA CTCCTTCATC CAATTCCACC TCCCAAGCTG GAGACATGGA
1151 GACATTAACC TTCAGCTGAG ACACTTCCCA AGCTGCTGTT TCAAGGCTGA
1201 GCTGGCCCCCT CTGCCCCAGC TGAGATGGAC AGATCGTTGT CAGCTACTTG
1251 ATGTCCTTGC CCATGCCACA GCTTGGCTCA GGGGCAGTGC ATGTCCTGCT
1301 GCCCTCTCTG CCAGAGGGCA CAGAACATGT TTGTTAATG AACCTGCCTG
1351 CCTCAGATTG CTGTCCCCGG GGAGTTAATG CATCTACACC ACTGTGGGGA
1401 TTTGAGTTAT AAGAATTGGA ATTTCTGAGA TCCCATGGAG GTTAGATTGG
1451 GAGGAAAGCT TAAAGATGT CTTTTTGTG AGAGGGATGG AATTGTTTTT
1501 TTTCAATTCG AAAGTTAGTG AGTAAAGATT TTATAATCA AAAAAAAAAA
1551 AAAAAA
```

BLAST Results

Entry HS188252 from database EMBL:

human STS WI-12265.

Score = 2554, P = 4.1e-109, identities = 556/587

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 255 bp to 1166 bp: peptide length: 304
Category: putative protein

```

1  MADNSSDECE EENNKEKKKT SOLTPQRGFS ENEDDDDDDD DSSETDSDS
51  DDDEEHGAPL EGAYDPADYE HLPVSAEIKE LFQYISRYTP QLIDLHKLK
101 PFIPDFIPAV GDIDAFKVP RPDGKPDNLG LLVLDEPSTK QSDPTVLSLW
151 LTENSKQHNI TQHMVKVSL EAEKNPKAID TWIESISELH RSKPPATVHY
201 TRMPDIDTL MQEWSPEFEE LLGKVSLEPTA EIDCSLAEYI DMICAILDIP
251 VYKSRIQSLH LLFSLYSEFK NSQHFALAE GKKAFTPSSN STSQAGDMET
301 LTFS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_22n2, frame 3

PIR:S38149 SIS2 protein - yeast (*Saccharomyces cerevisiae*), N = 1,
Score = 132, P = 1e-05

>PIR:S38149 SIS2 protein - yeast (*Saccharomyces cerevisiae*)
Length = 562

HSPs:

Score = 132 (19.8 bits), Expect = 1.0e-05, P = 1.0e-05
Identities = 24/63 (38%), Positives = 35/63 (55%)

```

Query:      3  DNSSDECEEENNKEKKKTSQLTPQRGFSENEEDDDDDDDSSSETDSDSDDDEEHGAPLEG 62
              +   DE EEE++ E++ T               +++DDDDDDDD + D D DDD++E A  G
Sbjct:    497 EEDDDDEEEDDDDEEDTEDKNNNNDDDDDDDDDDDDDDDDDDDEDEDEAETPG 556

```

```

Query:      63 AYD 65
              D
Sbjct:    557 IID 559

```

Score = 122 (18.3 bits), Expect = 1.4e-04, P = 1.4e-04
Identities = 20/52 (38%), Positives = 33/52 (63%)

```

Query:      4  NSSDECEEENNKEKKKTSQLTPQRGFSENEEDDDDDDDSSSETDSDSDDDEE 55
              N1 +E ++E+ +E      + T + + N+DDDDDDDD + D D DDD++
Sbjct:    494 NNEEEDDEEEDDEEEDTEDKNNNNDDDDDDDDDDDDDDDDDDDDDD 545

```

Pedant information for DKFZphut1_22n2, frame 3

Report for DKFZphut1_22n2.3

```

[LENGTH]      304
[MW]           34285.85
[pI]           4.37
[PROSITE]      AMIDATION      1
[PROSITE]      CAMP_PHOSPHO_SITE  2
[PROSITE]      CK2_PHOSPHO_SITE  10
[PROSITE]      PKC_PHOSPHO_SITE   1
[PROSITE]      ASN_GLYCOSYLATION  3
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY    11.84 %

```

```

SEQ  MADNSSDECEEENNKEKKKTSQLTPQRGFSENEEDDDDDDDSSSETDSDSDDDEEHGAPL
SEG  .....XXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXXXXXXXXXX.....
PRD  cccccchhhhhhhchhhhhhhcccccccccccccccccccccccccccccccccccccc

```

```

SEQ  EGAYDPADYEHLPVSAEIKELFQYISRYTPQLIDLHKLKPFIPDFIPAVGDIDAFKVP
SEG  .....
PRD  cccccccccccccchhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccecc

```

```

SEQ  RPDGKPDNLGLLVLEPSTKQSDPTVLSLWLTENSKQHNIHQHMVKVSLAEKNPKAID
SEG  .....
PRD  cccccccccceeeccccccccccccchhhhhhhccccccccccccccccccccccccchhhhhhhccccch

```

```

SEQ  TWIESISELHRSKPPATVHYTRMPDIDTLMQEWSPEFEELLGKVSLEPTAEIDCSLAEYI
SEG  .....
PRD  hhhhhhhhhhhccccceeeccccccccchhhhhhhccccchhhhhccccccccccccchhhhhhh

```

```

SEQ  DMICAILDIPVYKSRIQSLHLLFSLYSEFKNSQHFALAEKGKAFTPSSNSTSQAGDMET
SEG  .....

```

Prosites for DKFZphutel1_22n2.3

(No Pfam data available for DKFZphut1_22n2.3)

DKFZphutel_22o2

group: uterus derived

DKFZphutel_22o2 encodes a novel 537 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

similarity to S.pombe SPBC3E7.03c

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: map="11p15.5"

Insert length: 2714 bp

Poly A stretch at pos. 2695, polyadenylation signal at pos. 2677

```
1 GCAGGGGCACG GTGGGGGCTG AGATCGTTTC CTGTTGGAAC TTCTGGCCCA
51 AGAAGCGCGG GTCACAAGGA GAGGGGTCTG TTCGGTTCAG AGCGACTCAG
101 CCCCTCGACT CGGGTCTTAA AACCTCCGAG CCGCCAGTTC TGCCTCAGGC
151 CGCGCCCCCT TAAAGCGCCA CCAGACGCTG CGCCCCGTTA AAGCGCCACC
201 AGACGCCCGG CCCCGTCCCG GCCTCCCCCG CGCGCTGGCG CGGGGCTTTC
251 TGGGCCAGGG CGGGGCCGGC GAACTGCGGC CCGGAACGGC TGAGGAAGGG
301 CCCGTCCCGC CTCCCCGGC GCGCCATGGA GCCCCGGGCG GTTGCAGAAG
351 CCGTGGAGAC GGGTGAAGAG GATGTGATTA TGGAAGCTCT GCGGTCTATC
401 AACCAAGGAG ACTCCCAGAG CTTACGTTT GATGATGCC AACAGGAGGA
451 CCGGAAGAGA CTGGCGGAGC TGCTGGTCTC CGTCTGGAA CAGGGCTTGC
501 CACCTCCCA CCGTGTCTATC TGGCTGCAGA GTGTCCGAAT CCTGTCCCGG
551 GACCGCAACT GCCTGGACCC GTTCAACAGC CGCCAGAGCC TGCAGGCACT
601 AGCCTGCTAT GCTGACATCT CTGTCTCTGA GGGTCCGTC CCAGAGTCCG
651 CAGACATGGA TGTGTACTG GAGTCCCTCA AGTGCCTGTG CAACCTCGTG
701 CTCAGCAGCC CTGTGGCACA GATGCTGGCA GCAGAGGCC GCCTAGTGGT
751 GAAGCTCACA GAGCGTGTGG GGCTGTACCG TGAGAGGAGC TTCCCCCAGC
801 ATGTCCAGTT CTTTGACTTG CGGCTCCTCT TCCTGCTAAC GGCCTCCCGC
851 ACCGATGTGC CCGCAGAGCT GTTTCAGGAG CTGAAAGGAG TGCGCTTGCT
901 AACTGACACA CTGGAGCTGA CGCTGGGGGT GACTCCTGAA GGAACCCCCC
951 CACCCACGCT CCTTCCTTCC CAAGAGACTG AGCGGGCCAT GGAGATCCTC
1001 AAAGTGTCTT TCAACATCAC CCTGGACTCC ATCAAGGGGG AGGTGGACGA
1051 GGAAGACGCT GCCTTTTACC GACACCTGGG GACCTTCTC CGGCACTGTG
1101 TGATGATCGC TACTGCTGGA GACCGCACAG AGGAGTTCCA CGGCCACGCA
1151 GTGAACCTCC TGGGGAACCTT GCCCTCAAG TGTCTGGATG TTCTCCTCAC
1201 CTTGGAGCCA CATGGAGACT CCACGGAGTT CATGGGAGTG AATATGGATG
1251 TGATTCTGAG CCTCTCATC TTCTAGAGA AGCGTTTGCA CAAGACACAC
1301 AGGCTGAAAG AGAGTGTAGC TCCCGTGTCT AGCGTGTCTG CTGAATGTGC
1351 CCGGATGACG CGCCACGCA GGAAGTTCTT GAAGGCCAGG GGATGGCCAC
1401 CTCCCCAGGT GCTGCCCCCT CTGCGGGATG TGAGGACAGC GCCTGAGGTT
1451 GGGGAGATGC TGCGGAACAA GCTTGTCCGC CTCATGACAC ACCTGGACAC
1501 AGATGTGAAG AGGTGGGTG CCGAGTTCTT GTTGTCTCTG TGCTCTGAGA
1551 GTGTGCCCGG ATTCATCAAG TACACAGGCT ATGGGAATGC TGCTGGCCTT
1601 CTGGCTGCCA GGGGCTCAT GGCAGGAGGC CGGCCGAGG GCCAGTACTC
1651 AGAGGATGAG GACACAGACA CAGATGAGTA CAAGGAAGCC AAAGCCAGCA
1701 TAAACCTGTG GACCGGGAGG GTGGAGGAGA AGCCGCTTAA CCCTATGGAG
1751 GGCATGACAG AGGAGCAGAA GGAGCACGAG GCCATGAAGC TGGTGACCAT
1801 GTTTGACAAG CTCTCCAGGA ACAGAGTCAT CCAGCCAATG GGGATGAGTC
1851 CCGGGGTGTA TCTTACGTCC CTGCAGGATG CCATGTGCGA GACTATGGAG
1901 CAGCAGCTCT CCTCGGACCC TGA CTGCTGAGC CCTGACTGAG GATGGCAGCT
1951 CTTCTGTCTC CCCATCAGGA CTGGTGTCTG TTCCAGAGAC TTCTTGGGG
2001 TTGCAACCTG GGAAGCCAC ATCCCACTGG ATCCACACCC GCCCCACTT
2051 CTCCATCTTA GAAACCCCTT CTCTTGAATC CCGTTCTGTT CATGATTTGC
2101 CTCTGGTCCA GTTTCTCATC TCTGGACTGC AACGGTCTTC TTGTGCTAGA
2151 ACTCAGGCTC AGCCTCGAAT TCCACAGACG AAGTACTTTC TTTTGTCTGC
2201 GCCAAGAGGA ATGTGTTTCA AAGCTGCTGC CTGAGGGCAG GGCCTACCTG
2251 GGCACACAGA AGAGCATATG GGAAGGCAGG GGTGTTGGTG TGGGTGCACA
2301 CAAAGCAAGC ACCATCTGGG ATTGGCACAC TGGCAGAGCC AGTGTGTTGG
2351 GGTATGTGCT GCACTTCCCA GGGAGAAAAC CTGTCAGAAC TTTCCATACG
2401 AGTATATCAG AACACACCTT TCCAAGGTAT GTATGCTCTG TTGTTCTGTG
2451 CTTGTCTTCA CTGAGCGCAG GGCTGGAGGC CTCTTAGACA TTCTCCTTGG
2501 TCCTCGTTCA GCTGCCCACT GTAGTATCCA CAGTGCCCGA GTTCTCGCTG
2551 GTTTTGGCAA TTAACCTTCC TTCTACTTGG TTTAGACTAC ACTTACAACA
2601 AGGAAAATGC CCTCTGTGTG ACCATAGATT GAGATTTATA CCACATACCA
2651 CACATAGCCA CAGAAACATC ATCTTGAAAT AAAGAAGAGT TTTGGACAAA
2701 AAAAAAAAAA AAAA
```


BLAST Results

Entry AF015416 from database EMBL:
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
Score = 3356, P = 2.0e-144, identities = 672/673

Entry HS263253 from database EMBL:
human STS SHGC-15914.
Score = 1143, P = 9.0e-46, identities = 245/255

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 326 bp to 1936 bp; peptide length: 537
Category: similarity to unknown protein

```

1 MEPRVAEAV ETGEEDVIME ALRSYNQEH SFTFDDAQQ EDRKRLAELL
51 VSVLEQGLPP SHRVIWLQSV RILSRDRNCL DPFTSRQSLQ ALACYADISV
101 SEGSPESAD MDVVLES LKLCN LVSSPV AQMLAAEARL VVKLTERVGL
151 YRERSFP HDV QFFDLRLFL LTALRTDVRQ QLFQELKGVR LLTDTLELTL
201 GVTPEGNPPP TLLPSQETER AMEILKVLFN ITLDSIKGEV DEEDAALYRH
251 LGTLLRHCV M IATAGDRTEE FHGHAVNLLG NLPLKCLDVL LTLEPHGDST
301 EFMGVNMDVI RALLIFLEKR LHKTHRLKES VAPVLSVLTE CARMHRPARK
351 FLKAQGWPPP QVLPPLRDVR TRPEVGEMLR NKLVLMLTHL DTDVKRVAEE
401 FLFVLCSESV PRFIKYTYG NAAGLLAARG LMAGGRPEGO YSEDEDTDT
451 EYKEAKASIN PVTGRVEEKP PNPMEG MTEE QKEHEAMKLV TMFDKLSRNR
501 VIQPMGMSPR GHLTSLQDAM CETMEQQLSS DPDSDDP

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_22o2, frame 2

TREMBL:SPBC3E7_3 gene: "SPBC3E7.03c"; product: "hypothetical protein";
S.pombe chromosome II cosmid c3E7., N = 1, Score = 112, P = 0.0023

>TREMBL:SPBC3E7_3 gene: "SPBC3E7.03c"; product: "hypothetical protein";
S.pombe chromosome II cosmid c3E7.
Length = 362

HSPs:

Score = 112 (16.8 bits), Expect = 2.3e-03, P = 2.3e-03
Identities = 71/289 (24%), Positives = 124/289 (42%)

```

Query: 215 SQETERAM-EILKVLFNITLDSIKGEVDEEDAALYRHLGTLRLHCVMIATAGDRTEEFHG 273
      SQ+ E + EIL++LF I+ S E DE+ L L+ + +
Sbjct: 12 SQDNEMVLTEILRLFLPISKRSY LKEEDEQKILL-----LVIEIWASSLNNPNNSPLRW 65

Query: 274 HAVN-LLG-NLPLKCLDVLTLLEPHGDSTEFMGVNMDVIRALLIFLEKRLHKTH----RL 327
      HA N LL NL L LD + + - T - + + I - + + LEK L+ +
Sbjct: 66 HATNALLSFNLQLLSLDQAIYVSEIACQT----LQSILISREVEYLEKGLNLCFDIAAKY 121

Query: 328 KESVAPVLSVLTECARMHRPARKFLKAQGWPPQVLPPLRDVRTRP-EVGEMLRNKLVLRL 386
      + ++ P+L++L + +L P DR + + G+ R L+RL
Sbjct: 122 QNTLPPIAILLSLLSFFNIKQNL-----SMLLPNTDDRKQSLQKGKSFRCLLLRL 173

Query: 387 MT-HLDTDVKRVAEEFLFVLCSESVPRFIKYTYGNAAGLLAARGLMAGGRPEGQYS--- 442
      +T + + A L LC + + G G A G+ M P + +
Sbjct: 174 LTIPIVEPIGTYASLLNELCDGDSQQIARIFGAGYAMGISQHSSETMPFFSPLSKAASPV 233

Query: 443 -EDEDTDDEYKEAKASINPVTGRV--EEKPPNPMEG MTEEQKEHEAMKLV TMFDKLSRN 499
      + + +E +I+P+TG + +E +++E+KE EA +L +F +L +N
Sbjct: 234 FQKNSRGQENTENNLAIDPITGSMCTNRNKSQRLE-LSQEEKEREAEERLFYLFQRLEKN 292

```

Pedant information for DKFZphutel_22o2, frame 2

[illegible]

PS000001	230->234	ASN_GLYCOSYLATION	PDOC000001
PS000005	61->64	PKC_PHOSPHO_SITE	PDOC000005
PS000005	69->72	PKC_PHOSPHO_SITE	PDOC000005
PS000005	84->87	PKC_PHOSPHO_SITE	PDOC000005
PS000005	117->120	PKC_PHOSPHO_SITE	PDOC000005
PS000005	145->148	PKC_PHOSPHO_SITE	PDOC000005
PS000005	218->221	PKC_PHOSPHO_SITE	PDOC000005
PS000005	235->238	PKC_PHOSPHO_SITE	PDOC000005
PS000005	324->327	PKC_PHOSPHO_SITE	PDOC000005
PS000005	463->466	PKC_PHOSPHO_SITE	PDOC000005
PS000005	508->511	PKC_PHOSPHO_SITE	PDOC000005
PS000006	12->16	CK2_PHOSPHO_SITE	PDOC000006
PS000006	34->38	CK2_PHOSPHO_SITE	PDOC000006
PS000006	52->56	CK2_PHOSPHO_SITE	PDOC000006
PS000006	99->103	CK2_PHOSPHO_SITE	PDOC000006
PS000006	104->108	CK2_PHOSPHO_SITE	PDOC000006
PS000006	263->267	CK2_PHOSPHO_SITE	PDOC000006
PS000006	371->375	CK2_PHOSPHO_SITE	PDOC000006

PS00006	388->392	CK2_PHOSPHO_SITE	PDOC00006
PS00006	442->446	CK2_PHOSPHO_SITE	PDOC00006
PS00006	447->451	CK2_PHOSPHO_SITE	PDOC00006
PS00006	491->495	CK2_PHOSPHO_SITE	PDOC00006
PS00006	515->519	CK2_PHOSPHO_SITE	PDOC00006
PS00006	530->534	CK2_PHOSPHO_SITE	PDOC00006
PS00008	57->63	MYRISTYL	PDOC00008
PS00008	420->426	MYRISTYL	PDOC00008
PS00008	424->430	MYRISTYL	PDOC00008
PS00008	430->436	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphut1_22o2.2)

DKFZphut1_23e13

group: metabolism

DKFZphtes3_15j18 encodes a novel 148 amino acid protein with similarity to 27K heat shock proteins.

The novel protein contains a serine protease of the subtilase family with an aspartic acid-containing active site. Subtilases are an extensive family of serine proteases whose catalytic activity is provided by a charge relay system similar to that of the trypsin family of serine proteases but which evolved by independent convergent evolution. The sequence around the residues involved in the catalytic triad (aspartic acid, serine and histidine) are completely different from that of the analogous residues in the trypsin serine proteases. Thus the novel protein is a new member of this family.

The new protein can find application in modulation of proteinase activity in cells and as a new enzyme for proteomics and biotechnologic production processes.

heat shock protein HSP27

strong similarity to heat shock 27K proteins

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: /map="578.9 cR from top of Chr12 linkage group"

Insert length: 1854 bp

Poly A stretch at pos. 1831, polyadenylation signal at pos. 1810

```

1  GGGTTATTAA  GCTCCTGGCT  CCGCTCTAGA  CCTCAGCGGT  TCTGGCTGCC
51 AGCCTGGGCA  GCCTGGGAAG  CCTGGGAGGA  CGGTGGCTTG  CCGGTCTGTC
101 GTGAGGCAGT  GCGGACGGGG  ACCCTCTGGG  ATTCTGCTGG  ATCTGCCCGG
151 GGGGTTACCT  TTGGGGGCTG  GGACCCCACT  CGAGGGGACA  CAACCGTCCC
201 TGGCAGTGGT  TGGTTCTGCT  TCTCCCTGCA  GAAAAGCAGC  ATTTTCGGAA
251 GCTGAAGAAT  AAGCTAGCCC  AGCCACACCA  CCTTGTTGTG  TGACCTTGGG
301 CAGGTGGTTC  TGTCTCTCTG  AGCCTCTGTT  TCTCTCTGAG  CTGAGCAGCC
351 ACCATGGCTG  ACGGTGAGAT  GCCCTTCTCC  TGCCACTACC  CAAGCCGCCT
401 GCGCCGAGAC  CCCTTCGGGG  ACTCTCCCT  CTCCTCTCGC  CTGCTGGATG
451 ATGGCTTTGG  CATGGACCCC  TTCCAGACAG  ACTTGACAGC  CTCTTGGCCC
501 GACTGGGCTC  TGCCTCGTCT  CTCCTCCGCC  TGGCCAGGCA  CCCTAAGGTC
551 GGGCATGGTG  CCCCAGGGCC  CCACTGCCAC  CGCCAGGTTT  GGGGTGCCTG
601 CCGAGGGCAG  GACCCCCCA  CCCTTCCTG  GGGAGCCCTG  GAAAGTGTGT
651 GTGAATGTGC  ACAGCTTCAA  GCCAGAGGAG  TTGATGGTGA  AGACCAAAGA
701 TGGATACGTG  GAGGTGTCTG  GCAAACATGA  AGAGAAACAG  CAAGAAGGTG
751 GCATTGTTC  TAAGAACTTC  ACAAAGAAAA  TCCAGCTTCC  TGCAGAGGTG
801 GATCCTGTGA  CAGTATTTC  CTCCTTCTCC  CCAGAGGGTC  TGCTGATCAT
851 CGAAGCTCCC  CAGGTCCCTC  CTTACTCAAC  ATTTGGAGAG  AGCAGTTTCA
901 ACAACGAGCT  TCCCCAGGAC  AGCCAGGAAG  TCACCTGTAC  CTGAGATGCC
951 ACTACTGGCC  CATCTTGT  TTGTCCCAA  CCTAGGGCT  TCTCTGATTC
1001 CAGGATACAT  TACTTTAGCT  GAACTCAGAT  TTAGTGCAAG  TAAATGTTA
1051 GAGGGTGCGG  GGGTGAGGAC  TGACCACAGA  TTCCCTGGAT  AGTGTAGTGG
1101 TAGATTCTC  CACAGGATAG  CGCAATTGGC  AAATCATGCT  TGGTTGTGTT
1151 AGGCCAAAAT  ACTAGTTTTG  CTTTCTTAC  CTTTCTATC  TTGATGAAAA
1201 TGTTGCACAT  TCTATAGTTG  CAAAACACAT  AAAAGGGGAC  TTAACATTTC
1251 ACGTTGTATC  TTAATTGCAG  TGAATGCAAG  GGTACTTTT  CTCTGGGGAC
1301 CTCCCCATC  ACCCAGGTTT  CTACTCTGGG  CTCCCGATTC  CCATGGCTCC
1351 CAAACCATGC  CGCATGTTT  GGTTAATGAA  ACCCAGTAGC  TAACCCCACT
1401 GTGCTTCCAC  ATGCCTGGCC  TAAAATGGGT  GATATACAGG  TCTTATATCC
1451 CCATATGAA  TTTATCCATC  AACCACATAA  AAACAAACAG  TGCCTTCTGC
1501 CCTCTGCCCA  GATGTGTCCA  GCACGTCTC  AAAGTTTCCA  CATTAGCACT
1551 CCTAAGGAC  GTGGGAGCC  TGTCAGTTA  TGATCTGACC  TAGGTCCCCC
1601 CTTTCTCTG  TCCCCTGTGT  TTAAGTCGGG  ATTTTACAG  AGGGAGCTGT
1651 CTCCAGACAG  TCCATCAGG  AACCAAGCAA  AGGCCAGATA  GCCTGACAGA
1701 TAGGCTAGTG  GTATTGTGTA  TATGGGCGGG  ACGTGTGTGT  CATTATTATT
1751 TGAGTTATGC  TGTGTTTAG  GGGTAAATAA  CAGTAAATAA  TTAATAATAA
1801 TAATAATAAT  AATAAAGGAG  CTGACGTTCT  TAAAAAGAA  AAAAAAATAA
1851 AAAA

```

BLAST Results

Entry HS286348 from database EMBL:
human STS TIGR-A002J47.
Score = 510, P = 1.2e-16, identities = 102/102

Medline entries

95394379:
Cloning and sequencing of a cDNA encoding the canine HSP27 protein.

94110260:
Physiological and pathological changes in levels of the two small stress proteins, HSP27 and alpha B crystallin, in rat hindlimb muscles

Peptide information for frame 3

ORF from 354 bp to 941 bp; peptide length: 196
Category: strong similarity to known protein
Prosites motifs: SUBTILASE_ASP (28-39)

1 MADGQMPFSC HYPSRLRRDP FRDSPPLSSRL LDDGFGMDPF PDDLTASWPD
51 WALPRLSSAW PGTLRSGMVP RGPTATAREFG VPAEGRTPPP FPGEPPWKVCV
101 NVHSFKPEEL MVKTKDGYVE VSGKHEEKQQ EGGIVSKNFT KKIQLPAEVD
151 PVTVFASLSP EGLLIIEAPQ VPPYSTFGES SFNNELPQDS QEVTCT

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_23e13, frame 3

PIR:JC4244 heat-shock 27K protein - dog, N = 1, Score = 304, P = 4.3e-27

PIR:JN0924 heat shock 27 protein - rat, N = 1, Score = 301, P = 8.9e-27

TREMBL:MM03561.1 product: "heat shock protein HSP27"; Mus musculus heat shock protein HSP27 internal deletion variant b mRNA, complete cds., N = 1, Score = 301, P = 8.9e-27

>PIR:JC4244 heat-shock 27K protein - dog
Length = 209

HSPs:

Score = 304 (45.6 bits), Expect = 4.3e-27, P = 4.3e-27
Identities = 80/182 (43%), Positives = 102/182 (56%)

Query: 1 MADGQMPFSC-HYPSRLRRDPFRD-SPLSSRLDDGFGMDPFDDLTASWPDWALPRLSS 58
M + ++PFS PS DPFRD P SRL D EG+ P++ W W S
Sbjct: 1 MTERRVPFSLRSPSW---DPFRDWYPAHSRLFDQAFGLPRLPEE---WAQWFG---HS 50

Query: 59 AWPGLRSGMVP---RGPTATAREFGVPAEGR--TPPPFG-----EPWKVCVNVHSF 105
WPG +R +P GP A A PA R + G + W+V ++V+ F
Sbjct: 51 GWPGYVRP--IPPAVEGPAAAAAAPAYSRLSRQLSSGVSEIRQTADRWRVSLDVNHF 108

Query: 106 KPEELMVKTKDGYVEVSGKHEEKQQEGGIVSKNFTKKIQLPAEVD PVTVFASLSPEGLLI 165
PEEL VKTKDG VE++GKHEE+Q E G +S+ T K LP VDP V +SLSPEG L
Sbjct: 109 APEELTVKTKDGVVEITGKHEERQDEHGYSRRLTPKYTLPPGVDPTLVSSSLSPGTLT 168

Query: 166 IEAPQVPPYSTFGE 179
+EAP P + E
Sbjct: 169 VEAPMPKPATQSAE 182

Pedant information for DKFZphut1_23e13, frame 3

Report for DKFZphut1_23e13.3

[LENGTH] 196
[MW] 21604.37

```

[pI]                5.00
[HOMOL]             PIR:JC4244 heat-shock 27K protein - dog 3e-22
[BLOCKS]            BL01031C
[PIRKW]             blocked amino end 1e-13
[PIRKW]             acetylated amino end 4e-13
[PIRKW]             phosphoprotein 7e-21
[PIRKW]             glycoprotein 2e-11
[PIRKW]             heat shock 7e-21
[PIRKW]             molecular chaperone 4e-13
[PIRKW]             alternative splicing 1e-19
[PIRKW]             eye lens 6e-14
[PIRKW]             stress-induced protein 7e-21
[SUPFAM]            alpha-crystallin 7e-21
[PROSITE]           SUBTILASE_ASP 1
[PROSITE]           MYRISTYL 2
[PROSITE]           CK2_PHOSPHO_SITE 2
[PROSITE]           PKC_PHOSPHO_SITE 6
[PROSITE]           ASN_GLYCOSYLATION 1
[PFAM]             Heat shock hsp20 proteins
[KW]               All_Beta
[KW]               LOW_COMPLEXITY 7.14 %

SEQ      MADGQMPFSCHYPSRLRRDPFRDSPLSSRLDDGFGMDFFPDDLTASWPDWALPRLSSAW
SEG      .....XXXXXXXXXXXXXXXXX.....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      PGTLRSGMVRPGPTATARFGVPAEGRTPPPFPGEPPWKVCNVVHSFKPEELMVKTGDGYVE
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      VSGKHEEKQQEGGIVSKNFTKKIQLPAEVDVPTVFASLSPEGLLIIIEAPQVPPYSTFGES
SEG      .....
PRD      cccchhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      SFNNELPQDSQEVCT
SEG      .....
PRD      cccccccccccccccccc

```

Prosites for DKFZphut1_23e13.3

PS00001	138->142	ASN_GLYCOSYLATION	PDOC00001
PS00005	27->30	PKC_PHOSPHO_SITE	PDOC00005
PS00005	63->66	PKC_PHOSPHO_SITE	PDOC00005
PS00005	76->79	PKC_PHOSPHO_SITE	PDOC00005
PS00005	104->107	PKC_PHOSPHO_SITE	PDOC00005
PS00005	122->125	PKC_PHOSPHO_SITE	PDOC00005
PS00005	140->143	PKC_PHOSPHO_SITE	PDOC00005
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	176->180	CK2_PHOSPHO_SITE	PDOC00006
PS00008	62->68	MYRISTYL	PDOC00008
PS00008	132->138	MYRISTYL	PDOC00008
PS00136	28->39	SUBTILASE_ASP	PDOC00125

Pfam for DKFZphut1_23e13.3

```

HMM_NAME      Heat shock hsp20 proteins
HMM            *AMMrpPWDWRE.....DpDHFeVrMDMPGFKPEEIKVkvEDNNVLvIeG
               A   P++ R   + ++V++++ FKPEE+ VK+ D+ +++++G
Query         77 ARFGVPAEGR-TPPPFPGEPPWKVCNVVHSFKPEELMVKTGDG-YVEVSG 123

HMM            EHEREEEREDDKWWHERIYRHFMRFRrLPENVDPdQikAsMSdNGVLTII
               +HE E++   + + ++ F +++LP +VDP + AS+S++G+L I
Query         124 KHE---EKQQ---EGGIVSKNFTKKIQLPAEVDVPTVFASLSPEGLLII 166

HMM            TVPKpEP*
               ++P ++P
Query         167 EAPQVPP 173

```

DKFZphutel_23g11

group: uterus derived

DKFZphutel_23g11 encodes a novel 256 amino acid protein with similarity to S.pombe SPAC31G5.12c and S. cerevisiae Maf1p.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

similarity to SPAC31G5.12c and Maf1p

complete cDNA, complete cds, EST hits

Sequenced by EM3L

Locus: unknown

Insert length: 1674 bp

Poly A stretch at pos. 1664, polyadenylation signal at pos. 1644

```
1 GGGGGAGGCG GAGGTCGCTC GCTCGCTCGC TCGGCTCGCT GACTCGCCGG
51 AGCGCTCTGT GCGGTCGCGC GGCAGGTCGG TCGCGAGAGC GGGCTCTGTG
101 GAAGGGGGCG AGGCTATGTC GCGGTGGCAG CCCGGATGGG CCGGCAGGGC
151 CGGGAGTAAC GGGACGTCGC CGCGGASCTT CTTCCCCCGG ATACAGTGCG
201 GCGCGAGCGG AGGCCGCGGC GCGGCCCTCC GATCTTGAAG AGCCCGCGCT
251 GCGCGAGGCC CGCCCCCGCC TGCGCACCGG CACCGACGCG GAGCGACCAAG
301 CCCAGCCAGA CCCGCCCGCG GCGGCCCTGA TCTAACCCAG CCAGGCAGGC
351 AATACTAGCC CCTCTGGAGC ACGGAGCTCC TTCCCCAAG ACATGAAGCT
401 ATTTGAGAAC TCGAGCTTTG AAGCCATCAA CTCACAGCTG ACTGTGGAGA
451 CCGGAGATGC CCACATCATT GGCAGGATTG AGAGCTACTC ATGTAAGATG
501 GCAGGAGACG ACAAACACAT GTTCAAGCAG TTCTGCCAGG AGGGCCAGCC
551 CCACGTGCTG GAGGCACTTT CTCCACCCCA GACTTCAGGA CTGAGCCCCA
601 GCAGACTCAG CAAAAGCCAA GGCGGTGAGG AGGAGGGGCC CCTCAGTGAC
651 AAGTGCAGCC GCAAGACCCCT CTTCTACCTG ATTGCCACGC TCAATGAGTC
701 CTTCAGGCCT GACTATGACT TCAGCACAGC CCGCAGCCAT GAGTTCAGCC
751 GGGAGCCCCAG CCTTAGCTGG GTGGTGAATG CAGTCAACTG CAGTCTGTTC
801 TCAGCTGTGC GGGAGGACTT CAAGGATCTG AAACCACAGC TGTGGAACGC
851 GGTGGACGAG GAGATCTGCC TGGCTGAATG TGACATCTAC AGCTATAACC
901 CAGACTTGGA CTCAGATCCC TTCGGGGAGG ATGGTAGCCT CTGGTCCTTC
951 AACTACTTCT TCTACAACAA GCGGCTCAAG CGAATCGTCT TCTTTAGCTG
1001 CCGTTCCATC AGTGGCTCCA CCTACACACC CTCAGAGGCA GGCAACGAGC
1051 TCGACATGGA GCTGGGGGAG GAGGAGGTGG AGGAAGAAAG CAGAAGCAGG
1101 GGCAGTGGGG CCGAGGAGAC CAGCACCATG GAGGAGGACA GGGTCCCAGT
1151 GATCTGTATT TGATGAGGAG GAGCCGAGGC CCCAGCTTCA TCCAGCTTCA
1201 ACCAATGCCT GGACCTGTCC ACCTGAGAGG CCCCTGGGGC CTCCTCAGCT
1251 GCTGGCCAGA CCCTGGCGCT GCCACAGTCC TGGCACTGCC CAAGGCCATA
1301 CCTGCCTAGC CTTTGGCTC CATCTGTGG ATGCCCACTC ACCCTCAGA
1351 CTCCTGCTGC CCATGCTGTG GCCGGACTTG TCAGCAGGGG GCCTGGTGGG
1401 AGGAGCGACT GCCCTGCCCA AATGAAGTGC CACAGCAGGG ACAGCTGGAC
1451 CGCAGAGTTT ATTTTGTAT TTCTACTGGG CCTGCACACT CCAGCCCCAA
1501 GGGTCTGTGG CCGGAGGCCC CACGAGCAGG CCCCAGCAGT CACCGGCTCT
1551 GGTCTTGGGC CGGCCCGGCT GCCACCTGT ACCCCACCT CGCCCATTTG
1601 GCCGCGTGCA CTGAGTGCA CTTTGCTGCA GTCGTTTCT TTCCAATAAA
1651 AGTTTCTGTG ACTTAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 393 bp to 1160 bp; peptide length: 256
Category: similarity to known protein

```

1 MKLENSSEFE AINSQLTVET GDAHIIGRIE SYSCKMAGDD KHMFKQFCQE
51 GQPHVLEALS PPQTSGLSPLS RLSKSQGGEE EGPLSDKCSR KTLFYLIATL
101 NESFRPDYDF STARSHEFSR EPSLSWVVNA VNCSLFSAVR EDFKDLKPQL
151 WNAVDEEICL AECDIYSYNP DLSDPFGED GSLWSFNFF YNKRLKRIVF
201 FSCRSISGST YTPSEAGNEL DMELGEEVE EESRSRSGA EETSTMEEDR
251 VPVICI

```

BLASTP hits

Entry SPAC31G5_12 from database TREMBL:

gene: "SPAC31G5.12c"; product: "hypothetical protein"; S.pombe chromosome I cosmid c31G5.

Score = 272, P = 9.3e-24, identities = 51/127, positives = 80/127

Entry SPD656_1 from database TREMBL:

product: "ORF N150"; Yeast DNA for bfr2+ protein/pad1+ protein/sks1+ protein, ORF N313, ORF N150, complete cds, and for ORF N118, partial cds.

Score = 263, P = 8.4e-23, identities = 50/127, positives = 79/127

Entry S50986 from database PIR:

MAF1 protein - yeast (Saccharomyces cerevisiae) >SWISSPROT:MAF1_YEAST

MAF1 PROTEIN. >TREMBL:SC19492_1 gene: "MAF1"; product: "Maf1p";

Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds.

>TREMBL:SC8119_11 gene: "MAF1p"; product: "Maf1p"; S.cerevisiae chromosome IV cosmid 8119.

Score = 180, P = 2.3e-17, identities = 43/133, positives = 75/133

Entry AF098499_2 from database TREMBL:

gene: "C43H8.2"; Caenorhabditis elegans cosmid C43H8.

Score = 263, P = 9.2e-23, identities = 78/252, positives = 118/252

Alert BLASTP hits for DKFZphut1_23g11, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphut1_23g11, frame 3

Report for DKFZphut1_23g11.3

```

[LENGTH]      256
[MW]           28869.95
[pI]           4.51
[HOMOL]        TREMBL:SPAC31G5_12 gene: "SPAC31G5.12c"; product: "hypothetical protein";
S.pombe chromosome I cosmid c31G5. 4e-23
[FUNCAT]       06.04 protein targeting, sorting and translocation [S. cerevisiae, YDR005c]
6e-13
[PROSITE]      MYRISTYL          3
[PROSITE]      CK2_PHOSPHO_SITE      5
[PROSITE]      PKC_PHOSPHO_SITE      6
[PROSITE]      ASN_GLYCOSYLATION     3
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY        7.81 %

```

```

SEQ  MKLENSSEFE AINSQLTVETGDAHIIGRIE SYSCKMAGDDKHMFKQFCQEGQPHVLEALS
SEG  .....
PRD  cccccchhhhhhhhhhhhhccccceeeecchhhhhccchhhhhhhhhccccceeeeccc

```

```

SEQ  PPQTSGLSPLSRLSKSQGGEEEGPLSDKCSRKTLFYLIATL NESFRPDYDFSTARSHEFSR
SEG  .....
PRD  cccccccccccccccccccccccccchhhhhhhhhhhhhcccccccccccccccccccc

```

```

SEQ  EPSLSWVVNAVNC SLFS AVREDFKDLKPQLWNAVDEEICLAECDIYSYNPDLDSDPFGED
SEG  .....
PRD  cccccchhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhccccceeeeccccccccccc

```

```

SEQ  GSLWSFNFFYFNKRLKRIVFFSCRSISGSTYTPSEAGNELDMELGEEVEEESRSRSGA
SEG  .....
PRD  cceeeceeechhhhhhhhhhhccccccccccccccccchhhhhhhhhhhhhhhcccccc

```

```

SEQ  EETSTMEEDRVPVICI
SEG  xx.....
PRD  cccccccccceeeccc

```


Prosites for DKFZphut1_23g11.3

PS00001	6->10	ASN_GLYCOSYLATION	PDOC00001
PS00001	101->105	ASN_GLYCOSYLATION	PDOC00001
PS00001	132->136	ASN_GLYCOSYLATION	PDOC00001
PS00005	33->36	PKC_PHOSPHO_SITE	PDOC00005
PS00005	85->88	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	103->105	PKC_PHOSPHO_SITE	PDOC00005
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	202->205	PKC_PHOSPHO_SITE	PDOC00005
PS00006	7->11	CK2_PHOSPHO_SITE	PDOC00006
PS00006	99->103	CK2_PHOSPHO_SITE	PDOC00006
PS00006	212->216	CK2_PHOSPHO_SITE	PDOC00006
PS00006	238->242	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	181->187	MYRISTYL	PDOC00008
PS00008	239->245	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphut1_23g11.3)

DKFZphut1_24c19

group: transmembrane protein

DKFZphut1_24c19 encodes a novel 195 amino acid protein without similarity to known proteins.

The novel protein contains 1 transmembrane region.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of uterus-specific genes and as a new marker for uterine cells.

unknown

membrane regions: 1

Summary DKFZphut1_24c19 encodes a novel 195 amino acid protein, with no similarity to known proteins.

unknown

complete cDNA, complete cds, EST hits

TRANSMEMBRANE 1

Sequenced by Qiagen

Locus: unknown

Insert length: 769 bp

Poly A stretch at pos. 746, polyadenylation signal at pos. 735

```

1 ACGAGTCAGC CAAAGATGGC TGCGCCAGG TAATTGAGC AAAGGCCACA
51 GTGAAGTCCG GCGTGGCTGA GGAAGACCGG AGGAGGCACC CACAGGCTGC
101 TGGGAGGAGA GCATAAGGCT CAAAATGGAA AATCATAAAT CCAATAATAA
151 GGAAACATA ACAATTGTTG ATATATCCAG AAAAATTAAC CAGCTTCCAG
201 AAGCAGAAAG GAATCTACTT GAAAATGGAT CGGTTTATGT TGGATTAAAT
251 GCTGCTCTTT GTGGCCTCAT AGCAAACAGT CTTTTCGAC GCATCTTGAA
301 TGTGACAAAG GCTCGCATAG CTGCTGGCTT ACCAATGGCA GGGATACCTT
351 TTCTTACAAC AGACTTAACT TACAGATGTT TTGTAAGTTT TCCTTTGAAT
401 ACAGGTGATT TGGATTGTGA AACCTGTACC ATAACACGGA GTGGACTGAC
451 TGGTCTTGTT ATTGGTGGTC TATACCCTGT TTTCTTGGCT ATACCTGTAA
501 ATGGTGGTCT AGCAGCCAGG TATCAATCAG CTCTGTTACC ACACAAAGGG
551 AACATCTTAA GTTACTGGAT TAGAACTTCT AAGCCTGTCT TTAGAAAGAT
601 GTTATTTTCT ATTTTGCTCC AGACTATGTT TTCAGCATAC CTTGGGTCTG
651 AACAAATATA ACTACTTATA AAGGCCCTTC AGTTATCTGA ACCTGGCAAA
701 GAAATTCACG GATTTTAAAC AAATATGTAA ACAAAAATAA AATGGTAAAA
751 ACAAAAAAAA AAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 125 bp to 709 bp; peptide length: 195
 Category: putative protein

```

1 MENHKSNNKE NITIVDISRK INQLPEAERN LLENGSVYVG LNAALCGLIA
51 NSLFERRILNV TKARIAAGLP MAGIPFLTLD LTYRCFVSFP LNTGDLDCET
101 CTITRSGLTG LVIGGLYPVF LAIPVNGGLA ARYQSALLPH KGNILSYWIR
151 TSKPVFRKML FPILLQTMFS AYLGSEQYKL LIKALQLSEP GKEIH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_24c19, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphut1_24c19, frame 2

Report for DKFZphut1_24c19.2

[LENGTH] 195
 [MW] 21527.45
 [pI] 9.36
 [PROSITE] MYRISTYL 6
 [PROSITE] CK2_PHOSPHO_SITE 1
 [PROSITE] PKC_PHOSPHO_SITE 3
 [PROSITE] ASN_GLYCOSYLATION 3
 [KW] TRANSMEMBRANE 1

SEQ MENHKSNNKENITIVDISRKINQLPEAERNLLENGSVYVGLNAALCGLIANSLFRRILNV
 PRD cccccccccceeeehhhhhccchhhhhccccceeeecchhhhhhhhhhhhhhhhh
 MEM

SEQ TKARIAAGLPAGIPFLTDLTYRCFVSFPLNTGDLDCETCTITRSGLTGLVIGGLYPVF
 PRD hhhhhhccccccccceeeccccccccccccccccccccccccccccceeeccceee
 MEMMMMMMMMMMMMMMM

SEQ LAIPVNGGLAARYQSALLPHKGNILSYWIRTSKPVFRKMLFPILLQTMFSAYLGSEQYKL
 PRD eeccccccchhhhhccccccccceeeccccchhhhhchhhhhhhhhhhhhcchhhh
 MEM MMM.....

SEQ LIKALQLSEPGKEIH
 PRD hhhhhhcccccccc
 MEM

Prosites for DKFZphut1_24c19.2

PS00001	11->15	ASN_GLYCOSYLATION	PDOC00001
PS00001	34->38	ASN_GLYCOSYLATION	PDOC00001
PS00001	59->63	ASN_GLYCOSYLATION	PDOC00001
PS00005	18->21	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	151->154	PKC_PHOSPHO_SITE	PDOC00005
PS00006	13->17	CK2_PHOSPHO_SITE	PDOC00006
PS00008	40->46	MYRISTYL	PDOC00008
PS00008	47->53	MYRISTYL	PDOC00008
PS00008	68->74	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	127->133	MYRISTYL	PDOC00008
PS00008	142->148	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphut1_24c19.2)

DKFZphutel_24e11

group: intracellular transport and trafficking

DKFZphutel_24e11 encodes a novel 226 amino acid protein, with similarity to human/mouse golgi 4-transmembrane spanning transporter MTP. MTP may function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment. Thus, the novel protein also seems to be involved in nucleotide sugar transport.

The new protein can find application in modulating the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartments.

similarity to 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP

complete cDNA, complete cds, EST hits

potential start at 184,

TRANSMEMBRANE 4

function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment?

Sequenced by Qiagen

Locus: /map="8"

Insert length: 2005 bp

Poly A stretch at pos. 1988, polyadenylation signal at pos. 1963

```

1  ACGCGTCCGG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCCC
51  GCGGGCGCAC GGGCGAGCGG GCCGGGAGCC GGAGCGGCGG AGGAGCCGGC
101 AGCAGCGGCG CGGCGGGCTC CAGGCGAGGC GGTTCGACGCT CCTGAAAAC
151 TGCGCGCGCG CTCGCGCCAC TCGCGCCGGA GCGATGAAGA TGGTCGCGCC
201 CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC CATGTCCGCA
251 CCGGCACCAT CCTGCTCGGC GTCTGGTATC TGATCATCAA TGCTGTGGTA
301 CTGTTGATTT TATTGAGTGC CCTGGCTGAT CCGGATCAGT ATAACCTTTC
351 AAGTTCTGAA CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT
401 GCATTGCCAT TGCGATTCTT CTTCTCATGA TCCTGATATG TGCTATGGCT
451 ACTTACGGAG CGTACAAGCA ACGCGCAGCC TGGATCATCC CATTCTTCTG
501 TTACCAGATC TTTGACTTTG CCCTGAACAT GTTGTTGCA ATCACTGTGC
551 TTATTTATCC AAACCTCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT
601 ACTTCCCTACA GAGATGATGT CATGTCAAGT AATCCTACCT GTTTGGTCCT
651 TATTATTCTT CTGTTTATTA GCATTATCTT GACTTTTAA GGTACTTGA
701 TTAGCTGTGT TTGGAAGTGC TACCGATACA TCAATGGTAG GAACTCCTCT
751 GATGTCCCTGG TTTATGTTAC CAGCAATGAC ACTACGGTGC TGCTACCCCC
801 GTATGATGAT GCCACTGTGA ATGGTGCTGC CAAGGAGCCA CCGCCACCTT
851 ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGGC AGCAGCTTGA
901 CTTTGAGAGC ATCTGAGCAA TAGTTCTGTT ATTTCACTTT TGCCATGAGC
951 CTCTCTGAGC TTGTTTGTTG CTGAAATGCT ACTTTTAAAT ATTTAGATGT
1001 TAGATTGAAA ACTGTAGTTT TCAACATATG CTTTGCTAGA ACACTGTGAT
1051 AGATTAACTG TAGAATTCTT CCTGTACGAT TGGGGATATA ACGGGCTTCA
1101 CTAACCTTCC CTAGGCATTG AAACCTCCCC CAAATCTGAT GGACCTAGAA
1151 GTCTGCTTTT GTACCTGCTG GGCCCCAAAG TTGGGCATTT TTCTCTCTGT
1201 TCCCTCTCTT TTCAAAATCT AAAATAAAAC CAAAAATAGA CAACTTTTTC
1251 TTCAGCCATT CCAGCATAGA GAACAAAACC TTATGGAAAC AGGAATGTCA
1301 ATTGTGTAAT CATTGTTCTA ATTAGGTAAG TAGAAGTCCT TATGTATGTG
1351 TTACAAGAAT TTCCCCCACA ACATCCTTTA TGAAGTGAAG TCAATGACAG
1401 TTTGTGTTTG GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT TAAGACCATT
1451 AGAAAGCACC AGGCCGTGGG AGCAGTGACC ATCTACTGAC TGTTCTGTG
1501 GATCTGTGTG CCAGGGACAT GGGGTGACAT GCCTCGTATG TGTTAGAGGG
1551 TGGAATGGAT GTGTTTGGCG CTGCATGGGA TCTGGTGCCC CTCTTCTCCT
1601 GGATTACACAT CCCCACCCAG GGCCCGCTTT TACTAAGTGT TCTGCCCTAG
1651 ATTGGTTCAA GGAGTGCATC CAACTGACTT TATCAAGTGG AATTGGGATA
1701 TATTTGATAT ACTTCTGCCT AACAACATGG AAAAGGGTTT TCTTTTCCCT
1751 GCAAGCTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTCACCTTT
1801 TAAAATGTAA ACATTTTCAG AAAAATGAGG ATTGCCTTCC TTGTATGCGC
1851 TTTTACCTT GACTACCTGA ATTGAAGGG ATTTTATAT ATTCATATGT
1901 TACAAAGTCA GCAACTCTCC TGTTGGTTCA TTATTGAATG TGCTGTAAT
1951 TAAGTCGTTT GCAATTAAAA CAAGGTTTGC CCACATCCAA AAAAAA
2001 AAAAA

```

BLAST Results

Entry HS012351 from database EMBL:

human STS SHGC-31823.

Score = 1629, P = 3.1e-67, identities = 343/354

Medline entries

96199248:

Identification of a novel membrane transporter associated with intracellular membranes by phenotypic complementation in the yeast *Saccharomyces cerevisiae*.

Peptide information for frame 1

ORF from 184 bp to 861 bp; peptide length: 226
Category: strong similarity to known protein

```

1 MKMVAPWTRF YSNSCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP
51 DQYNFSSSEL GGDFFEMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW
101 IIPFFCYQIF DFALNMLVAI TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN
151 PTCLVLIILL FISIILTFKG YLISCVWNCY RYINGRNSD VLVYVTSNDT
201 TVLLPPYDDA TVNGAAKEPP PPYVSA

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_24e11, frame 1

SWISSPROT:MTRP_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108)., N = 1, Score = 551, P = 2.9e-53

SWISSPROT:MTRP_MOUSE GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP., N = 1, Score = 539, P = 5.3e-52

TREMBL:HS304981_1 product: "E3 protein"; Human retinoic acid-inducible E3 protein mRNA, complete cds., N = 1, Score = 127, P = 3.4e-06

>SWISSPROT:MTRP_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108).

Length = 233

HSPs:

Score = 551 (82.7 bits), Expect = 2.9e-53, P = 2.9e-53
Identities = 102/221 (46%), Positives = 148/221 (66%)

```

Query:      9 RFYSNSCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQY---NFSSSELGGDF- 64
             RFYS CC CCHVRTGTI+LG WY+++N ++ ++L  + P+  N  +G  +
Sbjct:     13 RFYSTRCCGCCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQYEVIGNYYS 72

Query:     65 -EFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVL 123
             E M D N C+ A+S+LM +I +M . YGA  + W+IPFFCY++FDF L+ LVAI+ L
Sbjct:     73 SERMAD-NACVLFAVSVLMFISSMLVYGAISYQVGWLIPFFCYRLFDVLSCLVAISSL 131

Query:    124 IYPNSIQEYIRQLPPNFYRDDVMSVNPCLVLIILLFISIILTFKGYLISCVWNCYRYI 183
             Y  I+EY+ QLP +FPY+DD+++++ +CL+ I+L+E ++ + FK YLI+CVWNCY+YI
Sbjct:    132 TYLPRIKEYLDQLP-DFPYKDDLALDSSCLLFIVLVFFALFIIFKAYLINCWNCYKYI 190

Query:    184 NGRNSSDVLVYVTSN-DTTVLLPPYDDATVNGAAKEPPPPYVSA 226
             N RN  ++ VY  +LP Y+ A V  KEPPPPY+ A
Sbjct:    191 NNRNVPEIAVYPAFEAPPQYVLPTYEMA-VKMPEKEPPPPYLPA 233

```

Pendant information for DKFZphutel_24e11, frame 1

Report for DKFZphutel_24e11.1

[LENGTH] 226
[MW] 25419.11

[pI] 4.65
 [HOMOL] SWISSPROT:MTRP_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108).
 5e-40
 [PROSITE] CK2_PHOSPHO_SITE 3
 [PROSITE] TYR_PHOSPHO_SITE 1
 [PROSITE] PKC_PHOSPHO_SITE 1
 [PROSITE] ASN_GLYCOSYLATION 3
 [KW] SIGNAL_PEPTIDE 49
 [KW] TRANSMEMBRANE 2
 [KW] LOW_COMPLEXITY 20.80 %

SEQ MKMVAPWTRFYNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQYNFSSEL
 SEGXXXXXXXXXXXXXXXXXXXXX.....
 PRD ccc
 MEM
 SEQ GGDFFFPMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI
 SEGXXXXXXXXXXXXXXXXXXXXX.....
 PRD ccc
 MEMMM
 SEQ TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILFISIILTFKGYLISCVWNCY
 SEGXXXXXXXXXXXXXXXXXXXXX.....
 PRD hhhcc
 MEM MMMMM.....MM
 SEQ RYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA
 SEG
 PRD ecc
 MEM
 MEM

Prosite for DKFZphut1_24e11.1

PS00001	54->58	ASN_GLYCOSYLATION	PDOC00001
PS00001	187->191	ASN_GLYCOSYLATION	PDOC00001
PS00001	198->202	ASN_GLYCOSYLATION	PDOC00001
PS00005	167->170	PKC_PHOSPHO_SITE	PDOC00005
PS00006	56->60	CK2_PHOSPHO_SITE	PDOC00006
PS00006	128->132	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00007	186->195	TYR_PHOSPHO_SITE	PDOC00007

(No Pfam data available for DKFZphut1_24e11.1)

DKFZphutel_24j6

group: cell structure and motility

DKFZphutes1_24j6 encodes a novel 571 amino acid protein with strong similarity to rat cell adhesion regulator (CAR1).

The novel protein is very similar to Carl and thus seems to be involved in regulation cell-cell adhesion. It contains a RGD cell attachment site.

The new protein can find application in modulation of cell-cell-adhesion.

strong similarity to rat CAR1 A.thaliana T19C21.5

complete cDNA, complete cds, EST hits
potential frame shift at Bp 1241 according to CAR1
but frame shift might be in CAR1 sequence!
ESTs T73366 AA362984 confirm this sequence

Sequenced by Qiagen

Locus: /map="939.9 cR from top of Chr2 linkage group"

Insert length: 3333 bp

Poly A stretch at pos. 3316, no polyadenylation signal found

```
1  ACGCGTCCGA GCTGGCTCAG GCGCTCCGCT AGGCTCGGAC GACCTGCTGA
51  GCCTCCCAAA CCGCTTCCAT AAGGCTTTGC CTTTCCAACT TCAGCTACAG
101 TGTTAGCTAA GTTTGGAAAAG AAGGAAAAAA GAAAATCCCT GGGCCCCCTT
151 TCTTTTGTTC TTGCCCAAAG TCGTCGTTGT AGTCTTTTGG CCCAAGGCTG
201 TTGTGTTTTT AGAGGTGCTA TCTCCAGTTC CTGCACTCC TGTTAAACAAG
251 CACCTCAGCG AGAGCAGCAG CAGCGATAGC AGCCGCAGAA GAGCCAGCGG
301 GGTCGCCCTAG TGTCATGACC AGGGCGGGAG ATCACAACCG CCAGAGAGGA
351 TGCTGTGGAT CCTTGGCCGA CTACCTGACC TCTGCAAAAT TCCTTCTCTA
401 CCTTGGTCAT TCTCTCTCTA CTTGGGGAGA TCGGATGTGG CACTTTGCCG
451 TGTCTGTGTT TCTGGTAGAG CTCTATGGAA ACAGCCTCCT TTTGACAGCA
501 GTCTACGGGC TGGTGGTGGC AGGGTCTGTT CTGGTCTGG GAGCCATCAT
551 CGGTGACTGG GTGGACAAGA ATGCTAGACT TAAAGTGGCC CAGACCTCGC
601 TGGTGGTACA GAATGTTTCA GTCATCCTGT GTGGAATCAT CCTGATGATG
651 GTTTTCTTAC ATAAACATGA GCTTCTGACC ATGTACCATG GATGGGTCTT
701 CACTTCTGTC TATATCCTGA TCATCACTAT TGCAAAATATT GCAAATTGG
751 CCAGTACTGC TACTGCAATC ACAATCCAAA GGGATTGGAT TGTTGTGTGT
801 GCAGGAGAAG ACAGAAGCAA ACTAGCAAAT ATGAATGCCA CAATACGAAG
851 GATTGACCAG TTAACCAACA TCTTAGCCCC CATGGCTGTT GGCCAGATTA
901 TGACATTGGG CTCGCCAGTC ATCGGCTGTG GCTTTATTTT GGGATGGAAC
951 TTGGTATCCA TGTGCGTGGA GTACGTCTCT CTCTGGAAGG TTTACCAGAA
1001 AACCCAGCT CTAGCTGTGA AAGCTGGTCT TAAAGAAGAG GAAACTGAAT
1051 TGAAACAGCT GAATTTACAC AAAGATACTG AGCCAAAACC CCTGGAGGGA
1101 ACTCATCTAA TGGGTGTGAA AGACTCTAAC ATCCATGAGC TTGAACATGA
1151 GCAAGAGCCT ACTTGTGCCT CCCAGATGGC TGAGCCCTTC CGTACCTTCC
1201 GAGATGGATG GGTCTCCTAC TACAACCAGC CTGTGTTTCT GGCTGGCATG
1251 GGTCTTGCTT TCCTTTATAT GACTGTCTCT GGCTTTGACT GCATCACCAC
1301 AGGGTACGCC TACACTCAGG GACTGAGTGG TTCCATCCTC AGTATTTTGA
1351 TGGGAGCATC AGCTATAACT GGAATAATGG GAACTGTAGC TTTTACTTGG
1401 CTACGTCGAA AATGTGGTTT GGTTCGGACA GGTCTGATCT CAGGATTGGC
1451 ACAGCTTTCC TGTTTGATCT TGTGTGTGAT CTCTGTATTC ATGCCTGGAA
1501 GCCCCCTGGA CTGTCTCGTT TCTCCTTTTG AAGATATCCG ATCAAGGTTC
1551 ATTCAGGAG AGTCAATTAC ACCTACCAAG ATACCTGAAA TTCAACTGA
1601 AATATACATG TCTAATGGGT CTAATTCTGC TAATATTGTC CCGGAGACAA
1651 GTCCTGAATC TGTGCCATA ATCTCTGTCA GTCTGTGTGT TGCAGGCGTC
1701 ATTGCTGCTA GAATCGGTCT TTGGTCCCTT GATTTAACTG TGACACAGTT
1751 GCTGCAAGAA AATGTAATTG AATCTGAAAG AGGCATTATA AATGGTGTAC
1801 AGAACTCCAT GAACTATCTT CTTGATCTTC TGCAATTCAT CATGGTCATC
1851 CTGGCTCCAA ATCCTGAAGC TTTTGGCTTG CTCGTATTGA TTTCACTCTC
1901 CTTTGTGGCA ATGGGCCACA TTATGTATTT CCGATTGTGC CAAAATATCTC
1951 TGGGAAACAA GCTCTTTGCT TGCGGTCTCT ATGCAAAAGA AGTTAGGAAG
2001 GAAATCAAG CAAATACATC TGTTGTTTGA GACAGTTTAA CTGTTGCTAT
2051 CCTGTACTAG AGCATATGAG AGCAGATGTT CTTATTTTGT ACTGCGAAT
2101 TCCAATAAAT GGCTGGGTGT TTTGCTCTGT TTTTACCACA GCTGTGCTT
2151 GAGAACTAAA AGCTGTTTAG GAAACCTAAG TCAGCAGAAA TTAAGTATT
2201 AATTTCCCTT ATGTTGAGGC ATGGAAAAAA AATTGGAAAA GAAAAACTCA
2251 GTTTAAATAC GGAGACTATA ATGATAACAC TGAATTCCTT TATTTCTCAT
2301 GAGTAGATAC AATCTTACGT AAAAGAGTGG TTAGTCACGT GAATTCAGTT
2351 ATCATTGAC AGATTCTTAT CTGTACTAGA ATTCAGATAT GTCAGTTTTC
2401 TGCAAACTC ACTCTTGTTC AAGACTAGCT AATTTATTTT TTTGCATCTT
2451 AGTTATTTTT AAAACAAAT TCTTCAAGTA TGAAGACTAA ATTTTGATAA
2501 CTAATATTAT CCTATTGATC CTTAAGTATT TACATGTATG
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2551 TGGAAAAACA AAACACTTAA CTAGAATTCT CTAATAAGGT TTATGGTTTA
2601 GCTTAAAGAG CACCTTTGTA TTTTATTAT CAGATGGGGC AACATATTGT
2651 ATGAAGCATA TGAGCACTT CACAGCATGG TTATCATGTA AGCTGCAGGT
2701 AGAAGCAAAG CTGTAAAGTA GATTATCAC ACAATGACTG CATACAGACT
2751 TCAAATATGT CAATAGTTTG GTCATAGAAC CTAGAAGCCA AAAGCCACAC
2801 AGAAGGGCAA GAATCCCAAT TTAACATGTT TATCATCAT TAGTGATCTG
2851 TGTGTAGAAA CATGAGGGTG TAAGCCTTCA GCCTGGCAAG TTACATGTAG
2901 AAAGCCACCA CTTGTGAAGG TTTTGTTTTA CAAATCACTT GATTAAACAC
2951 ACTCAGGTAG AATATTTTAA TTTTACTGT TTTATACCCA GAAGTTATTT
3001 CTACATTGTT CTACAGCAAG AATATTCATA AAAGTATCCC TTTCAAATGC
3051 CTTTGAGAAG AATAGAAGAA AAAAAGTTTG TATATATTTT AAAAAATTGT
3101 TTTAAAAAGT AGTTTGCAAC ATGTCTGTAC CAAGATGGTA CTTTGCCTTA
3151 ACCGTTTATA TGCACCTTCA TGGAGACTGC AATACGTTGC TATGAGCACT
3201 TTCTTTATCC TTGGAGTTTA ATCCTTTGCT TCATCTTTCT ACAGTATGAC
3251 ATAATGATT GCTATGTTT AAAATCTTTG TAAAAAATT CTATATAAAA
3301 ATATTTTGAA AATCTTAAAA AAAAAAAAAA AAA

```

BLAST Results

Entry HS389210 from database EMBL:
human STS SHGC-10164.
Score = 1592, P = 1.5e-64, identities = 346/364

Entry HS933343 from database EMBL:
human STS WI-16551.
Score = 1193, P = 5.7e-46, identities = 241/244

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 315 bp to 2027 bp; peptide length: 571
Category: strong similarity to known protein

```

1 MTRAGDHNHQ RGCCGSLADY LTSAKFLLYL GHSLSTWGDR MWHFAVSVFL
51 VELYGNLLEL TAVYGLVVAG SVLVLGAIIG DWVDKNARLK VAQTSLLVQN
101 VSVILCGIIL MMVFLHKHEL LTMVHGWLVT SCYILIITIA NIANLASTAT
151 AITIQRDWIV VVAGEDRSKL ANMNATIRRI DQLTNILAPM AVGQIMTFGS
201 PVIGCGFISG WNLVSMCWEY VLLWKVYQKT PALAVKAGLK EEETELKQLN
251 LHKDTEPKPL EGTHLMGVKD SNIHELEHEQ EPTCASQMAE PFRTFRDQWV
301 SYYNQPVFLA GMGLAFLYMT VLGFDCTITG YAYTQGLSGS ILSILMGASA
351 ITGMGTAVAF TWLRRKCGLV RTGLISGLAQ LSCLILCVIS VFMPGSPDL
401 SVSPFEDIRS RFIQGESITP TKIPEITTEI YMSNGSNSAN IVPETSPESV
451 PIISVSLLEF GVIAARIGLW SFDLTVTQLL QENVIESERG IINGVQNSMN
501 YLLDLLHFIM VILAPNPEAF GLLVLISVSF VAMGHIMYFR FAQNTLGKNI
551 FACGPDKEV RKENQANTSV V

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_24j6, frame 3

TREMBLNEW:U76714_1 gene: "CAR1"; product: "cell adhesion regulator";
Rattus norvegicus cell adhesion regulator (CAR1) mRNA, complete cds., N
= 1, Score = 1472, P = 7.2e-151

TREMBL:AC004683_5 gene: "T19C21.5"; Arabidopsis thaliana chromosome II
BAC T19C21 genomic sequence, complete sequence., N = 2, Score = 437, P
= 2.8e-60

TREMBL:AF039046_2 gene: "R09B5.4"; Caenorhabditis elegans cosmid
R09B5., N = 2, Score = 323, P = 1.5e-43

>TREMBLNEW:U76714_1 gene: "CAR1"; product: "cell adhesion regulator";
Rattus norvegicus cell adhesion regulator (CAR1) mRNA, complete cds.
Length = 405

Score = 1472 (220.9 bits), Expect = 7.2e-151, P = 7.2e-151
Identities = 288/319 (90%), Positives = 297/319 (93%)

Query:	1	MTRAGDHNRRQGCCGLADYLTSAKFLLYLGHSLSTWGD RMWHFAVS VFLVELYGN SLLL	60
		MT++ D Q GCCGSLA+YLTSAKFLLYLGHSLSTWGD RMWHFAVS VFLVELYGN SLLL	
Sbjct:	1	MTKSRDQTHQEGCCGLANYLTSAKFLLYLGHSLSTWGD RMWHFAVS VFLVELYGN SLLL	60
Query:	61	TAVYGLVVAGSVLVLGAIIGDWVDKNARLKV AQTSLVVQNVSVILCGIILMMVFLHKHEL	120
		TAVYGLVVAGSVLVLGAIIGDWVDKNARLKV AQTSLVVQNVSVILCGIILMMVFLHK+EL	
Sbjct:	61	TAVYGLVVAGSVLVLGAIIGDWVDKNARLKV AQTSLVVQNVSVILCGIILMMVFLHKHEL	120
Query:	121	LTMYHGVLVLTSCYILIITIANIANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRI	180
		L MYHGWLVT CYILIITIANIANLASTATAITIQRDWIVVVAGE+RS+LA+MNATIRRI	
Sbjct:	121	LNMYHGWLTVCYILIITIANIANLASTATAITIQRDWIVVVAGENRSRLADMNATIRRI	180
Query:	181	DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMC VEYVLLWKVYQKTPALAVKAGLK	240
		DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMC VEY LLWKVYQKTPALAVKA LK	
Sbjct:	181	DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMC VEYFLLWKVYQKTPALAVKAALK	240
Query:	241	EEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRFDGWV	300
		EE+ELKQL K DTEPKPLEGTHLMG KDSNI ELE EQEPTCASQ+AE PFRTRFDGWV	
Sbjct:	241	VEESELKQLTSPK DTEPKPLEGTHLMGEKDSNIRELECEQEPTCASQIAEPFRTRFDGWV	300
Query:	301	SYYNQPVFLAGMGLAF-LY	318
		SYYNQPVFL G F LY	
Sbjct:	301	SYYNQPVFLGWHGPGFPLY	319

Pedant information for DKFZphutel 24j6, frame 3

Report for DKFZphutel 24j6.3

```

[LENGTH]          571
[MW]               62542.72
[pI]               6.08
[HOMOL]            TREMBL:U76714_1 gene: "CAR1"; product: "cell adhesion regulator"; Rattus
norvegicus cell adhesion regulator (CAR1) mRNA, complete cds. 1e-141
[BLOCKS]           BL00341D
[PROSITE]          MYRISTYL             15
[PROSITE]          MITOCH_CARRIER 1
[PROSITE]          CK2_PHOSPHO_SITE      6
[PROSITE]          PROKAR_LIPOPROTEIN    1
[PROSITE]          PKC_PHOSPHO_SITE      4
[PROSITE]          ASN_GLYCOSYLATION     4
[PFAM]             Laminin B (Domain IV)
[KW]               TRANSMEMBRANE 4
[KW]               LOW COMPLEXITY        8.76 %

```

```

SEQ      MTRAGDHNRRQRCGCCSLADYLTSAKFLLYLGHSLSTWGD RMW HFAVS VFLVELYGN SLL
SEG
PRD      cccccccccccccccccchhhhhhhheeeecceeeccchhhhhhhhhheeeeccccce
MEM      .....MMMMMMMMMMMMMM

SEQ      TAVYGLVVGAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL
SEG      .xxxxxxxxxxxxxxxxx.....
PRD      ehhhhhhhccceeeecccccchhhhhhhhhhhhhheeeccchhhhhhhhhhhhhhhhhhhhh
MEM      MMMMMMMMMMMMMMMMM.....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ      LTMYHGWLVTSCYILITIANIANLASTATAITIORDWIVVAGEDRSKLANMNATIRRI
SEG      .xxxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      hhccccchhhhhhhhhhhhhhhhhhhhhheeeecceeeeeecccccchhhhhhhhhhhhh
MEM      MMMMMMMM.....

SEQ      DQLTNI LAPMAVGQIMTFGSPVIGCGFISGWNLVSMC VEYVLLWKVYQKTPALAVKAGLK
SEG
PRD      hhhhhhccceeeceeeeeeceeeeeeecchhhhhhhhhhhhhhhhhhhccchhhhhhhhh
MEM      .....

SEQ      EEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRFDGWV
SEG
PRD      hhhhhhhhhhhccccccccccceeeeeeccccccccccccccccccccccccccccccce
MEM      .....

SEQ      SYYNQPVFLAGMGLAFLYMTVLGFDCITTGAYAYTOGLSGSILSILMGASAITGIMGTVAF
SEG
PRD      eeecceeeeccccchhhhhhhccccceeeeeeecceeeceeeeeeccccceeeehhhhhh

```

```

MEM .....
SEQ  TWLRRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPFEDIRSRFIQGESITP
SEG  .....xxx
PRD  hhhhhccccccccchhhhhhhhhhhhhhhhhccccccccchhhhhcccccccc
MEM  .....

SEQ  TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL
SEG  xxxxxxxxxxxx.....
PRD  cccccceeeeeccccccccccccccccceeeeeehhhhhhhhhccccchhhhhhhhh
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ  QENVIESERGIINGVQNSMNYLLDLLHFIMVILAPNPEAFGLLVLSVSFVAMGHIMYFR
SEG  .....
PRD  hhhhhccccceeeeeccccchhhhhhhhhhhheeeeeccccccccceeeeeccccccccce
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ  FAQNTLGKGLFACGPDACEVRKENQANTSVV
SEG  .....
PRD  eccccccccceeeeeccccchhhhhhhhhcccccc
MEM  .....

```

Prosites for DKFZphut1_24j6.3

PS00001	100->104	ASN_GLYCOSYLATION	PDOC00001
PS00001	174->178	ASN_GLYCOSYLATION	PDOC00001
PS00001	434->438	ASN_GLYCOSYLATION	PDOC00001
PS00001	567->571	ASN_GLYCOSYLATION	PDOC00001
PS00005	23->26	PKC_PHOSPHO_SITE	PDOC00005
PS00005	176->179	PKC_PHOSPHO_SITE	PDOC00005
PS00005	294->297	PKC_PHOSPHO_SITE	PDOC00005
PS00005	487->490	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	36->40	CK2_PHOSPHO_SITE	PDOC00006
PS00006	294->298	CK2_PHOSPHO_SITE	PDOC00006
PS00006	396->400	CK2_PHOSPHO_SITE	PDOC00006
PS00006	403->407	CK2_PHOSPHO_SITE	PDOC00006
PS00006	445->449	CK2_PHOSPHO_SITE	PDOC00006
PS00008	12->18	MYRISTYL	PDOC00008
PS00008	65->71	MYRISTYL	PDOC00008
PS00008	76->82	MYRISTYL	PDOC00008
PS00008	193->199	MYRISTYL	PDOC00008
PS00008	267->273	MYRISTYL	PDOC00008
PS00008	311->317	MYRISTYL	PDOC00008
PS00008	336->342	MYRISTYL	PDOC00008
PS00008	339->345	MYRISTYL	PDOC00008
PS00008	353->359	MYRISTYL	PDOC00008
PS00008	368->374	MYRISTYL	PDOC00008
PS00008	373->379	MYRISTYL	PDOC00008
PS00008	435->441	MYRISTYL	PDOC00008
PS00008	461->467	MYRISTYL	PDOC00008
PS00008	490->496	MYRISTYL	PDOC00008
PS00008	494->500	MYRISTYL	PDOC00008
PS00013	122->133	PROKAR_LIPOPROTEIN	PDOC00013
PS00215	404->414	MITOCH_CARRIER	PDOC00189

Pfam for DKFZphut1_24j6.3

```

HMM_NAME      Laminin B (Domain IV)
HMM            *YWR1PERFLGDQvTsYGGkLe*
               Y+R + LG+++ + G + +
Query         538 YRFAQNTLGKGLFACGPDAK 558

```

DKFZphutel_2h3

group: differentiation/development

DKFZphutel_2h3 encodes a novel 267 amino acid protein, with similarity to ITM2 (integral membrane protein 2) of chicken and mouse.

The novel protein contains a prenyl group binding site (CAAX box) and seems to be post-translationally modified by the attachment of either a farnesyl or a geranyl-geranyl group. The similar gallus G. protein E25 a marker for chondro-osteogenic differentiation.

The new protein can find application as a useful marker for chondro-osteogenic cell differentiation and for the modulation of chondro-osteogenic cell differentiation.

strong similarity to mouse E25 and gallus E3-16

complete cDNA, EST hits

complete cds according to E25 start at Bp 56
putative transmembrane protein (1 TM)

Sequenced by AGOWA

Locus: unknown

Insert length: 2033 bp

Poly A stretch at pos. 2007, polyadenylation signal at pos. 1986

```
1 GGACCGAGGC TGCACCGGCA GAGGCTGCGG GCGCGACGCG CGGGCCGGCG
51 CAGCCATGGT GAAGATTAGC TTCCAGCCCG CCGTGGCTGG CATCAAGGGC
101 GACAAGGCTG ACAAGGCGTC GCGCTCGGCC CCTGCGCCCG CCTCGGCCAC
151 CGAGATCCTG CTGACGCCCG CTAGGGAGGA GCAGCCCCCA CAACATCGAT
201 CCAAGAGGGG GAGCTCAGTG GCGGCGGTGT GCTACCTGTC GATGGGCATG
251 GTCGTGCTGC TCATGGGCCT CGTGTTCCGC TCTGTCTACA TCTACAGATA
301 CTTCTTTCTT GCACAGCTGG CCGGAGATAA CTTCTTCCGC TGTGGTGTGC
351 TGTATGAGGA CTCCTGTGCC TCCAGGTCC GGACTCAGAT GGAGCTGGAA
401 GAGGATGTGA AAATCTACCT CGACGAGAAC TACGAGCGCA TCAACGTGCC
451 TGTGCCCCAG TTTGGCGGCG GTGACCCTGC AGACATCATC CATGACTTCC
501 AGCGGGGTCT GACTGCGTAC CATGATATCT CCCTGGACAA GTGCTATGTC
551 ATCGAACTCA ACACCACCAT TGTGCTGCCC CCTCGCAACT TCTGGGAGCT
601 CCTCATGAAC GTGAAGAGGG GGACCTACCT GCCGCAGACG TACATCATCC
651 AGGAGGAGGT GTGGTCCACG GAGCATGTCA GTGACAAGGA GGCCTTGGGG
701 TCCTTCATCT ACCACCTGTG CAACGGGAAA GACACCTACC GGCTCCGGCG
751 CCGGGCAACG CGGAGGCGGA TCAACAAGCG TGGGGCCAAG AACTGCAATG
801 CCATCCGGCA CTTGAGAAC ACCTTCGTGG TGGAGACGCT CATCTGCGGG
851 GTGGTGTGAG GCCTCTCTCC CCCAGAACCC CCTGCCGTGT TCCTCTTTTC
901 TTCTTTCCAG CTGCTCTCTG GCCCTCTCTC TTCCCTCTGC TTAGCTTGTA
951 CTTTGGACGC GTTTCTATAG AGGTGACATG TCTCTCCATT CCTCTCCAAC
1001 CCTGCCCCACC TCCTGTATCC AGAGCTGTGA TCTCTCGGTG GGGGGCCCAT
1051 CTTGCTGAC CTGGGTGTGG CGGAGGGAGA GCGATGCTG CAAAGTGTTT
1101 TCTGTGTCCC ACTGTCTTGA AGCTGGGCCT GCCAAAGCCT GGGCCCACAG
1151 CTGACCCGGC AGCCCAAGGG GAAGGACCGG TTGGGGGAGC CGGGCATGTG
1201 AGGCCCTGGG CAAGGGGATG GGGCTGTGGG GCGGGGCGG CATGGGCTTC
1251 AGAAGTATCT GCACAATTAG AAAAGTCTCT AGAAGCTTTT TCTTGGAGGG
1301 TACACTTTCT TCACTGTCCC TATTCCTAGA CCTGGGGCTT GAGCTGAGCA
1351 TGGGACGATG TGCCGAGGGA GGGACCCACC AGAGCACAAG AGAAGGTGGC
1401 TACCTGGGGG TGTCCAGGG ACTCTGTGAG TGCCTTCAGC CCACCAGCAG
1451 GAGCTTGGAG TTTGGGGAGT GGGGATGAGT CCGTCAAGCA CAACTGTTCT
1501 CTGAGTGGAA CCAAAGAAGC AAGGAGCTAG GACCCCCAGT CCTGCCCCCC
1551 AGGAGCACAA GCAGGGTCCC CTCAGTCAAG GCAGTGGGAT GGGCGGCTGA
1601 GGAACGGGGC AGGCAAGGTC ACTGCTCAGT CACGTCCACG GGGGACGAGC
1651 CGTGGGTCTT GCTGAGTAGG TGGAGCTCAT TGCTTTCTCC AAGCTTGGAA
1701 CTGTTTTGAA AGATAACACA GAGGAAAGG GAGAGCCACC TGGTACTTGT
1751 CCACCTGCCC TCCTCTGTTC TGAAATTCCA TCCCCTCAGC CTTAGGGGAA
1801 TGCACCTTTT TCCTTTTCTT TCTCACTTTT GCATGTTTTT ACTGATCATT
1851 CGATATGCTA ACCGTTCTCA GCCCTGAGCC TTGGAGAGGA GGGCTGTAAC
1901 GCCTTCAGTC AGTCTCTGGG GATGAACTC TTAATGCTT TGTATATTTT
1951 CTCAATTAGA TCTTTTCA GAAGTGTCTA TAGAACAATA AAAATCTTTT
2001 ACTTCTGAAA AAAAAAAAAA AAAAGGGCGG CCG
```

BLAST Results

Entry B64417 from database EMBL:

CIT-HSP-2023A7.TR CIT-HSP Homo sapiens genomic clone 2023A7.

Length = 715

Plus Strand HSPs:

Score = 1546 (232.0 bits), Expect = 7.8e-64, P = 7.8e-64
Identities = 310/311 (99%)

Medline entries

96325063:
Isolation of markers for chondro-osteogenic differentiation using cDNA library subtraction.
Molecular cloning and characterization of a gene belonging to a novel multigene family of integral membrane proteins.

Peptide information for frame 2

ORF from 56 bp to 856 bp; peptide length: 267
Category: strong similarity to known protein

```

1 MVKISFQPAV AGIKGDKADK ASASAPAPAS ATEILLTPAR EEQPPQHRSK
51 RGSSVGGVCY LSMGMVVLLM GLVFASVYIY RYFFLAQLAR DNFFRCGVLY
101 EDSLSSQVRT QMELEEDVKI YLDENYERIN VVPVQFGGGD PADIHDFQR
151 GLTAYHDISL DKCYVIELNT TIVLPPRNFV ELLMNVKRGY YLPQTYIIQE
201 EMVTEHVSD KEALGSFIYH LCNGKDTYRL RRRATRRRIN KRGAKNCNAI
251 RHFENTFVVE TLICGVV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphut1_2h3, frame 2

SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) ., N = 1, Score = 573, P = 1.3e-55

SWISSNEW:ITMB_MOUSE INTEGRAL MEMBRANE PROTEIN 2B (E25B PROTEIN) ., N = 1, Score = 560, P = 3.2e-54

SWISSNEW:ITMA_HUMAN INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) ., N = 1, Score = 456, P = 3.3e-43

>SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) .
Length = 262

HSPs:

Score = 573 (86.0 bits), Expect = 1.3e-55, P = 1.3e-55
Identities = 117/264 (44%), Positives = 172/264 (65%)

```

Query:      1 MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY 60
             MVK+SF  A+A   + A+K  ++      ++L+ P  ++P      G
Sbjct:      1 MVKVSFNSALA--HKEAANKEEENS-----QVLILPPDAKEPEDVVVPAGHKRAWCWC 51

Query:     61 LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSLS-----SQVRTQM-- 112
             +  G+  +L G++  Y+Y+YF  Q      + CG+ Y ED LS      +Q+++
Sbjct:     52 MCFGLAFMLAGVILGGAYLYKYFAFQQ---GGVYFCGIKYIEDGLSLPESGAQLKSARYH 108

Query:     113 ELEEDVKIYLDENYERINVPVPQFGGGDPADIHDFQRGLTAYHDISLDKCYVIELNTTI 172
             +E+++++I  +E+ E I+VPVP+F  DPADI+HDF R LTAY D+SLDKCYVI LNT++
Sbjct:     109 TIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRLTAYLDLSLDKCYVIPLNTSV 168

Query:     173 VLPPRNFVWELLMNVKRGTYLPQTYIIQEEMVTEHVSDKEALGSFIYHLCNGKDTYRLRR 232
             V+PP+NF ELL+N+K GTYLPQ+Y+I E+M+VT+ + + + LG FIY LC GK+TY+L+R
Sbjct:     169 VMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVVDQLGFFIYRLCRGKETYLQR 228

Query:     233 RATRRRINKRGAKNCNAIRHFENTFVVETLIC 264
             +   + I KR A NC IRHFEN F +ETLIC
Sbjct:     229 KEAMKGIQKREAVNCRKIRHFENRFAMETLIC 260

```

Pedant information for DKFZphut1_2h3, frame 2

```

[LENGTH]      267
[MW]           30253.96
[pI]           8.16
[HOMOL]        SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16).
le-49
[PROSITE]      MYRISTYL      4
[PROSITE]      PRENYLATION   1
[PROSITE]      CAMP_PHOSPHO_SITE      3
[PROSITE]      CK2_PHOSPHO_SITE      3
[PROSITE]      TYR_PHOSPHO_SITE      1
[PROSITE]      PKC_PHOSPHO_SITE      4
[PROSITE]      ASN_GLYCOSYLATION      1
[KW]           TRANSMEMBRANE 1
[KW]           LOW COMPLEXITY 15.36 %

```

```
SEQ      MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGSSVVGVCY
SEG      ..xxxxxxxxxxxxxxxxxxxxx.....
PRD      cccccccccchhhhhhhhhhhhhhhhhcccccceeeccccccccccccccccccccchh
MEM      .....MMM

SEQ      LSMGMVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLIEDSLSSQVRTQMELEEDVKI
SEG      ..xxxxxxxxxxxxx.....
PRD      hhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhccceeeeeeccccccccchhhhhhhhhhhhh
MEM      MMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ      YLDENYERINVPVPQFGGDPADI IHDFQRGLTAYHDISLDKCYVIELNTTIVLPPRNF
SEG      .....
PRD      hhccccceeeccccccccccccccccchhhhhhhhhhhhhhhhhccceeeeeeccceeeccccchh
MEM      .....

SEQ      ELLMNVKRGTYLPQTYIIQEEMVUTEHVSDEKALGSFIYHLCNGKDTYRLRRRATRRRIN
SEG      .....xxxxxxxxxxxxx.....
PRD      hhhhhccccccccceeeehhhhhhhccccchhhhhheeeccccchhhhhhhhhhhhhhh
MEM      .....

SEQ      KRGAKNCNAIRHFENTFVETLICGV
SEG      xx.....
PRD      hhhhccceeeccccchhhhhheeeccc
MEM      .....
```

PS000001	169->173	ASN_GLYCOSYLATION	PDOC000001
PS000004	50->54	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	187->191	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	232->236	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	49->52	PKC_PHOSPHO_SITE	PDOC000005
PS000005	209->212	PKC_PHOSPHO_SITE	PDOC000005
PS000005	227->230	PKC_PHOSPHO_SITE	PDOC000005
PS000005	235->238	PKC_PHOSPHO_SITE	PDOC000005
PS000006	30->34	CK2_PHOSPHO_SITE	PDOC000006
PS000006	110->114	CK2_PHOSPHO_SITE	PDOC000006
PS000006	209->213	CK2_PHOSPHO_SITE	PDOC000006
PS000007	119->127	TYR_PHOSPHO_SITE	PDOC000007
PS000008	52->58	MYRISTYL	PDOC000008
PS000008	71->77	MYRISTYL	PDOC000008
PS000008	138->144	MYRISTYL	PDOC000008
PS000008	243->249	MYRISTYL	PDOC000008
PS00294	264->268	PRENYLATION	PDOC00266

542

DKFZphmcfl_1a11

group: transmembrane protein

DKFZphmcfl_1a11 encodes a novel 393 amino acid protein with weak similarity to S.pombe SPBC29A3_3 protein and S. cerevisiae putative membrane protein YDR255c.

The novel protein contains 1 transmembrane region.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of mammary carcinoma-specific genes and as a new marker for mammary carcinoma cells.

similarity to YDR255c and SPBC29A3.03c
membrane regions: 1

Summary DKFZphmcfl_1a11 encodes a novel 393 amino acid protein, with similarity to YDR255c and SPBC29A3.03c.

similarity to YDR255c and SPBC29A3.03c

complete cDNA, complete cds, EST hits
potential start at Bp 110 matches kozak consensus

Sequenced by DKFZ

Locus: /map="542.7 cR from top of Chr5 linkage group"

Insert length: 1819 bp

Poly A stretch at pos. 1808, no polyadenylation signal found

```

1  CCCGGCCCAG  CCCCCGAAGA  GCCGCCTCAG  CCGGGGGGAG  TTGCTCGGAC
51  TCAAACGTCC  AGTCCTCGTG  CGACCGCGCT  GGGTCGGAAG  TGAGCAGGCT
101  GAGGCCACCA  TGGAGCAGTG  TGCCTGCGTG  GAGAGAGAGC  TGGACAAGGT
151  CCTGCAGAAG  TTCCTGACCT  ACGGGCAGCA  CTGTGAGCGG  AGCCTGGAGG
201  AGCTGCTGCA  CTACGTGGGC  CAGCTGCGGG  CTGAGCTGGC  CAGCGCAGCC
251  CTCCAGGGGA  CCCCTCTCTC  AGCCACCCTC  TCTCTGGTGA  TGTCACAGTG
301  CTGCCGGAAG  ATCAAAGATA  CGGTGCAGAA  ACTGGCTTCG  GACCATAAGG
351  ACATTACAG  CAGTGTATCC  CGAGTGGGCA  AAGCCATTGA  CAGGAAC TTC
401  GACTCTGAGA  TCTGTGGTGT  TGTGTCAGAT  GCGGTGTGGG  ACGCGCGGGA
451  ACAGCAGCAG  CAGATCCTGC  AGATGGCCAT  CGTGGAACAC  CTGTATCAGC
501  AGGGCATGCT  CAGCGTGGCC  GAGGAGCTGT  GCCAGGAATC  AACGCTGAAT
551  CTGGACTTGG  ATTTCAACCA  GCCTTTCCTA  GAGTTGAATC  GAATCCTGGA
601  AGCCCTGCAC  GAACAAGACC  TGGGTCTGTC  GTTGGAATGG  GCCGCTCTCC
651  ACAGGCAGCG  CCTGTGGAA  CTCAACAGCT  CCCTGGAGTT  CAAGCTGCAC
701  CGACTGCACT  TCATCCGCCT  CTTGGCAGGA  GGCCCCGCGA  AGCAGCTGGA
751  GGCCCTCAGC  TATGCTCGGC  ACTTCCAGCC  CTTTGCTCGG  CTGCACCAGC
801  GGGAGATCCA  GGTGATGATG  GGCAGCCTGG  TGTACCTGCG  GCTGGGCTTG
851  GAGAAAGTCA  CCTACTGCCA  CCTGTGGGAC  AGCAGCCACT  GGGCAGAGAT
901  CTGTGAGACC  TTTACCCGGG  ACGCCTGTTC  CCTGTGGGGG  CTTTCTGTGG
951  AGTCCCCCTT  TAGCGTCAGC  TTTGCCTCTG  GCTGTGTGGC  GCTGCCTGTG
1001  TTGATGAACA  TCAAGGCTGT  GATTGAGCAG  CGGCAGTGCA  CTGGGGTCTG
1051  GAATCACAAG  GACGAGTTAC  CGATTGAGAT  TGAAGTAGGC  ATGAAGTGCT
1101  GGTACCACTC  CGTGTTCGCT  TGCCCCATCC  TCCGCCAGCA  GACGTCAGAT
1151  TCCAACCCCT  CCATCAAGCT  CATCTGTGGC  CATGTTATCT  CCCGAGATGC
1201  ACTCAATAAG  CTCATTAATG  GAGGAAAGCT  GAAGTGTCCC  TACTGTCCCA
1251  TGGAGCAGAA  CCCGGCAGAT  GGGAAACGCA  TCATATTCTG  ATTCTACCT
1301  GGAAGGAATT  TTGTGAAAG  GGGTTTTCAC  CTGTGAGCCT  TGGTCTGTCT
1351  CGGTAGGGTG  GTCAACTTCA  GTGGACTGTG  GTTGGTTTCA  GAGCGCCTGG
1401  CTGAGGAGTT  CCACTGAGGG  GAGCACTGGA  GCAGCCCTTT  GGCAGAGGCT
1451  GAGGAGGGAG  ATGGACCAGC  CCACGCCTGG  CACCTGGCTC  CATGGCATAA
1501  GGAAAGGGAG  ATGCTGGCCT  CTGTGCTCCT  GCTGTCTTTT  CCTGTTCTG
1551  TTTGCGTTTC  ACTTAGTAGC  AACCGACAGA  GTGGCAAGGG  ATTTGGTCTT
1601  CAGCAGTAGA  CATCCTTCCA  CCCCTGCCCT  CAGCCAAGTC  TCTTGCTGCC
1651  ATGCCAATGC  TATGTCCACC  CTTGCCCTTC  GGCCCAAGAG  TGTCCAGCGG
1701  TGGCCACCT  CTTCTCCCA  CTACAGCCTC  AACAGTATGT  ACCATCTCCC
1751  ACTGTAAATA  GTCCAGTTA  GAACGGAATG  CCGTTGTTTT  ATAACTTTGA
1801  ACAAATGTAA  AAAAAAAAAA

```

BLAST Results

Entry HS579359 from database EMBL:
human STS WI-6350.
Score = 1027, P = 9.9e-40, identities = 207/209

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 110 bp to 1288 bp; peptide length: 393
 Category: similarity to unknown protein

```

1 MEQCACVERE LDKVLQKFLT YGQHCCERSLE ELLHYVGQLR AELASAAALQG
51 TPLSATLSLV MSQCCRKIKD TVQKLASDHK DIHSSVSRVG KAIDRNFDSE
101 ICGVVSDAVW DAREQQQQIL QMAIVEHLYQ QGMLSVAEEL CQESTLNVDL
151 DFKQPFLELN RILEALHEQD LGPALEWAVS HRQRLLELNS SLEFKLHRLH
201 FIRLLAGGPA KQLEALSYAR HFQPFARLHQ REIQVMMGSL VYLRLGLEKS
251 PYCHLLDSSH WAEICETFTF DACSLGLSLV ESPLSVSFAS GCVALPVLMM
301 IKAVIEQRQC TGVWNHKKDEL PIEIELGMKC WYHSVFACPI LRQQTSDSNP
351 PIKLICGHVI SRDALNKLIN GGKLKCPYCP MEQNPADGKR IIF
  
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphmcf1_lall, frame 2

TREMBL:SPBC29A3_3 gene: "SPBC29A3.03c"; product: "hypothetical protein"; S.pombe chromosome II cosmid c29A3., N = 2, Score = 302, P = 3.4e-42

PIR:S67312 probable membrane protein YDR255c - yeast (Saccharomyces cerevisiae), N = 1, Score = 271, P = 5.3e-22

TREMBL:CET07D1_2 gene: "T07D1.2"; Caenorhabditis elegans cosmid T07D1., N = 1, Score = 193, P = 5.6e-13

>TREMBL:SPBC29A3_3 gene: "SPBC29A3.03c"; product: "hypothetical protein"; S.pombe chromosome II cosmid c29A3.
 Length = 398

HSPs:

Score = 302 (45.3 bits), Expect = 3.4e-42, Sum P(2) = 3.4e-42
 Identities = 55/142 (38%), Positives = 89/142 (62%)

```

Query: 252 YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVLMMNIKAVIEQRQCT 311
      Y +LD W + F R+ C+ LG+S+ESPL + +G +ALP+L+ ++++++
Sbjct: 258 YIDVLDLD-WKSLELLFVREFCAALGMSLESPLDIVNAGAIALPILLKMSSIMKKKHTE 316
  
```

```

Query: 312 GVVWNHKKDELPIEIELGMKCWYHSVFACPI LRQQTSDSNPPIKLICGHVISRDALNKLING 371
      W + ELP+EI L +HSVF CP+ ++Q ++ NPP+ + CGHVI +++L +L
Sbjct: 317 --WTSQGELPVEIFLPSSYHFHSVFTCPVSKEQATEENPPMMMSCGHVIVKESLRQLSRN 374
  
```

```

Query: 372 G--KLKCPYCPMEQNPADGKR IIF 393
      G + KCPYCP E AD R+ F
Sbjct: 375 GSQRFKCPYCPNENVAADAIRVYF 398
  
```

Score = 161 (24.2 bits), Expect = 3.4e-42, Sum P(2) = 3.4e-42
 Identities = 51/221 (23%), Positives = 102/221 (46%)

```

Query: 22 GQHCCERSLEELLHYVGQLRAELASAAALQGTPLSATLSLVMSQCCRKIKD TVQKLASDHKD 81
      G C L EL + + +L+ P++ LV C K + L K
Sbjct: 15 GNKCLAKLNEL---ESILKDAKKSCLKD-PTTSMKELVA--CSEKTQQVFDDLKRTEKK 67
  
```

```

Query: 82 IHSSVSRVGKAIDRNFDSEICGVVSDAVWDAREQQQQILQMAIVEHLYQQGMLSVAEELC 141
      H+S+R GK +++ F+ ++ + ++++++ + A+ H ++QG + +A C
Sbjct: 68 FHTSLNRFGKTLEKKFNFDLEDIKLHSSFSFESKKRE---IDTALSLHFFRQGDVELAHLFC 124
  
```

```

Query: 142 QESTLNVDLDFKQPFLELNRIEALHEQD LGPALEWAVSHRQRLLELNS SLEFKLHRLHF 201
      +E+ + + F L I++ ++DL +EWA R L SSLE+L +
Sbjct: 125 KEAGIEEPSLSLHVFTLLKSI VQGI RDKLKLPIEWASQRCGYLERKGS SLEYTLQKYRL 184
  
```

```

Query: 202 IRLLAGGPAKQL-EALSYAR-HFQPFARLHQREIQVMMGSLVY 242
      + K + A+ Y R + F + H +IQ M +L +
  
```

Pedant information for DKFZphmcf1 1a11, frame 2

Report for DKFZphmcf1 1a11.2

[illegible]

Prosites for DKF2phmcf1 la11.2

PS00001	189->193	ASN_GLYCOSYLATION	PDOC00001
PS00005	180->183	PKC_PHOSPHO_SITE	PDOC00005
PS00006	28->32	CK2_PHOSPHO_SITE	PDOC00006
PS00006	135->139	CK2_PHOSPHO_SITE	PDOC00006
PS00006	190->194	CK2_PHOSPHO_SITE	PDOC00006
PS00007	211->219	TYR_PHOSPHO_SITE	PDOC00007
PS00007	27->36	TYR_PHOSPHO_SITE	PDOC00007
PS00007	244->253	TYR_PHOSPHO_SITE	PDOC00007
PS00008	37->43	MYRISTYL	PDOC00008
PS00008	50->56	MYRISTYL	PDOC00008
PS00009	387->391	AMIDATION	PDOC00009
PS00013	282->293	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphmcfl 1a11.2)

DKFZphmcf1_1c23

group: mammary carcinoma derived

DKFZphmcf1_1c23.1 encodes a novel 311 amino acid proline rich protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of mamma carcinoma-specific genes.

unknown, proline rich protein

complete cDNA, complete cds? potential start at Bp 50, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 3077 bp

Poly A stretch at pos. 3067, polyadenylation signal at pos. 3048

```
1 AACTGGCCCC CTCCCCACC CCCTGCCCC CTGAGGAGCAGG ACCTGTCCAT
51 GGCTGACTTC CCCCCACCAG AGGAGGCTTT TTTCTCTGTG GCCAGCCCTG
101 AGCCTGCAGG CCCTTCAGGC TCCCCAGAGC TTGTCTAGCTC CCGGGCTGCT
151 TCGTCTCTCT CAGCTACTGC TTTGCAGATT CAGCCCCCGG GTAGCCCAGA
201 CCCTCCTCCA GCTCCGCCAG CCCCAGCTCC TGCTAGTTCC GCCCAGGGC
251 ATGTGGCCAA GCTCCCTCAG AAGGAACCGG TGGGCTGTAG CAAGGGTGGT
301 GGGCCTCCCA GGGAGGACGT AGGTGCGCCC CTGGTCACGC CCTCGCTCCT
351 GCAGATGGTG CGGCTGCGCT CCGTGGGTGC TCCAGGAGGG GCTCCACCCC
401 CAGCACTGGG GCCATCGGCC CCCCAGAAAC CACTGCGAAG GGCCCTGTCA
451 GGGCGGGCCA GCCCAGTGCC TGCCCCCTCC TCAGGGCTCC ATGCTGCGGT
501 CCGACTCAAG GCCTGCAGCC TGGCCGCCAG TGAAGGCCTC TCAAGTGCTC
551 AGCCCAACGG ACCGCTGAG GCAGAGCCAC GGCCCTCCCA GTCCCTGCC
601 TCAACGGCCA GTTTCATCTT CTCCAAGGGC TCTAGGAAGC TGCAGCTGGA
651 GCGGCCCGTG TCCCCTGAGA CCCAGGCTGA CCTCCAGCGG AATCTGGTGG
701 CAGAACTCCG GAGCATCTCA GAGCAGCGGC CACCCAGGGC CCAAAGAAG
751 TCACCTAAGG CTCCCCACC TGTGGCCCGC AAGCCGTCTG TGGGAGTCCC
801 CCCACCCGCC TCCCAGTT ACCCTCGAGC TGAGCCCTT ACTGCTCCTC
851 CCACCAATGG GCTCCCTCAC ACCCAGGACA GGACTAAGAG GGAGCTGGCC
901 GAGAATGGAG GTGTCTGCA GCTGGTGGG CCAGAGGAGA AGATGGGCCT
951 CCCGGGCTCA GACTCACAGA AAGAGCTGGC CTGACCACCA GGCACCTCAC
1001 TGGCACTGCT GACCCATCCC AGAAACACAA TCTCAGGGAC CCGAGCAGCT
1051 CCAAGGACAG GAGGATACAG CAGACACAAC CTAATAGAGA GGGCGCCTGC
1101 AGCCTTAACC TCCACGGCCT TCGATACTTA TGCAAGCCTG GTGTGTCTCC
1151 TGTCCTCAGA GTCATCTGC GCTCATGCCT TTTCCCGAAT GGGTTACCTT
1201 CTGGCAGTTG CGCCTTCAGT CTGGCCCTTA GCCTCATCTT GAAGTGGGTA
1251 GCTGGCGGGA GAGGGTGGCT GCGCCCCCTG CTGGCCCTGA GGTGTCAGAG
1301 TTGGGAGCAG GACACCTCAC CTGAGTTTCA TTTTTCCTCA TGTCCAAACC
1351 ATGCACATAC TATAGTCCAG AATCAAAGCA CTTTGAAAA GTGGCTGCAT
1401 GGCCATCTCT CAGGGCCCAG GAAGTTGCAT TCCAAGGGCC TGTTTACATG
1451 GCAGCAGAAAT CCATCCCCGG CAGTCAGCCC ATAGCTTGGG ACCAGTCTCT
1501 GCCCTCCTGT CCACTCCAGT TTACTCCTCT TGGTTCCTGA AGGTGGCCAA
1551 GTCATTGTGT TCCACAGGC TTCTCTAGGC TGGGGGCAGG TGTGGGGCTG
1601 TGAATTTCCA AAGCACAAAA GGTGCAGAGG GGATTGGCCT TCCTGTGCCT
1651 CACTCACCA ACCACCTCC TGCTTCCAG TTCTGCCAGG TGCTCCATGC
1701 TGGGGACAAG TAGGAGACTG CCAGGGCCCA AAGAAATGGG TGAGCAGTAG
1751 AGTCATCTCG GGGCACTTGG CAGTGTCAAG CACCTGCCCC TTGCCTCCTT
1801 GACCACTG TGCTGGGTGG GCCCCAGCA CTTCAGAGGC AGGAGCCTTT
1851 GGGCTGAGCA AGCACTGAGG AGGTGGATGG AAGGGAGCAT CTGGAGGGGG
1901 GGAGCTTCCCT TGAGCAGTGG GCCCAGGCCT GGCCCTCCAC ACTTCATTCT
1951 CTGACCTTTC TCTCTCCTCA TTTCCGGTGA TGTCTTTCT GCAGCTGCCT
2001 TTCAGCACAG GTGGTTCCAC TGGGGGCAGC TAACGCTGAG TGACAAGGAT
2051 GGGAGGCCAC AGGTGCATTT TACTCAAGTC TTCTCTAGTC AATGAGGGGC
2101 ACCCAGTGCT TCTAGGGCAG GCTGGGTGGT GGTCCCTTAG GTATCAGCCT
2151 CTCTTACTGT ACTCTCCGGG AATGTTAACC TTTCTATTTT CAGCCTGTGC
2201 CACCTGTCTA GGCAAGCTGG CTTCCTCATT GGCCCTGTG GGTCCACAGC
2251 AGCGTGGCTG CCCCCAGG CCACCGCTTC TTTCTGTATC CTCTTTCTT
2301 AACAGTGACT TGGGCTTGAG TCTGGCAAGG AACCTTGCTT TTAGCTTCAC
2351 CACCAAGGAG AGAGGTTGAC ATGACCTCCC CGCCCTCA CCAAGGCTGG
2401 GAACAGAGGG GATGTGGTGA GAGCCAGGTT CCTCTGGCCC TCTCCAGGGT
2451 GTTTTCCACT AGTCACTACT GTCTTCTCCT TGTAAGTAAT CAATCAATAT
2501 TCTTCCCTTG CCTGTGGGCA GTGGAGAGTG CTGCTGGGTG TACGCTGCAC
2551 CTGCCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTTCTGCTC
2601 AGAGCTCCTG ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT
2651 GCATGAAACC AGGCCCTGGC AGCAACCTGG GAATGGCTGG AGGTGGGAGA
2701 GAACCTGACT TCTCTTTCCC TCTCCTCCT CCAACATTAC TGAAGTCTA
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2751 TCCTGTTAGG ATCTTCTGAG CTTGTTTCCC TGCTGGGTGG GACAGAGGAC
2801 AAAGGAGAAG GGAGGGTCTA GAAGAGGCAG CCCTTCTTTG TCCTCTGGGG
2851 TAAATGAGCT TGACCTAGAG TAAATGGAGA GACCAAAAAGC CTCTGATTTT
2901 TAATTTCCAT AAAATGTTAG AACTATATAT ATACATATAT ATATTTCTTT
2951 AAATTTTGA GTCTTTGATA TGTCTAAAAA TCCATTCCCT CTGCCCTGAA
3001 GCCTGAGTGA GACACATGAA GAAAACTGTG TTTCATTAA AGATGTTAAT
3051 TAAATGATTG AACTTGAAA AAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 49 bp to 981 bp; peptide length: 311
 Category: putative protein
 Classification: unset

```

1 MADFPPPEEA FFSVASPEPA GPSGSPPELV SPAASSSSAT ALQIQPPGSP
51 DPPPAPPAPA PASSAPGHVA KLPQKEPVGC SKGGGPPRED VGAPLVTPSL
101 LQMVRLRSVG APGGAPTAL GPSAPQKPLR RALSGRASPV PAPSSGLHAA
151 VRLKACSLAA SEGLSSAQPN GPPEAEPRPP QSPASTASFI FSKGSRKLQL
201 ERPVSPETQA DLQNLVAEL RSISEQRPPQ APKKSPPKAP PVARKPSVGV
251 PPPASPSYPR AEPLTAPPTN GLPHTQDRTK RELAENGVL QLVGPEEKMG
301 LPGSDSQKEL A

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphmcf1_1c23, frame 1

PIR:S49915 extensin-like protein - maize, N = 1, Score = 215, P = 6.1e-15

PIR:A28996 proline-rich protein M14 precursor - mouse, N = 1, Score = 191, P = 3.8e-13

>PIR:S49915 extensin-like protein - maize
 Length = 1,188

HSPs:

Score = 215 (32.3 bits), Expect = 6.1e-15, P = 6.1e-15
 Identities = 81/269 (30%), Positives = 115/269 (42%)

```

Query:      5 PPPEEAFFS----VASPEPAGPSGSPPELVSSPAASSSSATALQIQPPGSP--DPPP---A 55
              PPP      S      V SP P P SP      PA +SS  ++ PP +P  PPP  +
Sbjct:    598 PPPPAPVASPPPVKSPPPPTPVASPP---PPAPVASSPPPMKSPPPPTPVSSPPPEKS 654

Query:     56 PPAPAPASSAPGHVAKLPQKEPVGC SKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGA 115
              PP P PA S P      + P P K PP + + P + PS      + P
Sbjct:    655 PPPPPAKSTPPP-EEYPT--PPTSVKSSPPEKSLPPPTLIPSPPPQEKPTPPSTPSKP 711

Query:    116 PTPALGPSAPQKPLRRA-LSGRASVPVAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPE 174
              P+      PS P++P+      + ++SP PAP S      +LA      S + + PP
Sbjct:    712 PSSPEKPSPPKEPVSSPQTTPKSSPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSPPPA 771

Query:    175 AEPRPPQSPASTASFIFSKGSRKLQLERPV-SPETQADLQNLVAELRSISEQRPPQAPK 233
              PP +P      +S      +Q+ P +P++ L V+      + + PP AP
Sbjct:    772 PLSSPPAPQVKSS-----PPPVQVSSPPAPKSSPPLAP--VSSPPQVEKTSPPAPL 823

Query:    234 KSPKAPPVARKPSVGV--PPPASPSYPRAEPLTAPPTNGLP 273
              SP P + P V V PPP S P P+++PP P
Sbjct:    824 SSPPLAPK-SSPPHVVSPPPVKSSPPAPVSSPPLTPKP 864

```

Score = 206 (30.9 bits), Expect = 9.1e-14, P = 9.1e-14

Identities = 82/261 (31%), Positives = 108/261 (41%)

Query: 17 PEPAG-PSGSPELVSSPAASS---SSATALQIQPPGSPDPPAP---PAPAPASSAPGHV 69
 P P G P SP + PAAS+ S T + P P+P P P P P P +P
 Sbjct: 410 PTPGGGPPSSP-VPGKPAASAPMPSHTPPDVSEPLPEPSPVPAPAPMPMPTPHSPPAD 468

Query: 70 AKLPQKEPV-GCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTALGPSAPQKP 128
 +P PV G S P V P + +V+L AP G+P P + ++P P
 Sbjct: 469 DYVPPTPPVPGKSPATSPSPQVQPPAASTPPPSLVKLSFPQAPVGSPPPPVKTTSPPAP 528

Query: 129 LRRALSGRASVPVAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSPASTAS 188
 + G SP P P S + +K+ A G + P PPE P PP AS
 Sbjct: 529 I-----GSPSP-PPPVSVVSPPPPVKSPPPAPVG---SPP--PPEKSPPPAPVASPPP 577

Query: 189 FIFSKGSRKLQLERPVSPETQADLQRLNVAELRSISEQRPPQAPKSPKAPPPVARKPS- 247
 + S L P P ++ VA + PP P SP P PVA P
 Sbjct: 578 PVKSPPPPPTLVASPP--PPVKSPPPPAPVASPPPPVKSPPPPPTVASPPPPAPVASSPPP 635

Query: 248 VGVPPP----ASPSYPRAEPLTAPPTNGLPHTQD 277
 + PPP +SP P P PP P ++
 Sbjct: 636 MKSPPPPPTPVSSPPPEKSPPPPPPAKSTPPPEE 669

Score = 202 (30.3 bits), Expect = 2.9e-13, P = 2.9e-13
 Identities = 81/254 (31%), Positives = 110/254 (43%)

Query: 16 SPEPAGPSGSPELV---SSP--AASSSSATALQIQPPGSP-DPPAPAPAPASSAPGHVA 70
 SP PA P SP L SSP SS ++ PP +P PP P PA S P HV+
 Sbjct: 817 SPPPA-PLSSPPLAPKSSPPHVVSPPPPVVKSSPPAPVSSPPLTPKPA---SPPAHVS 872

Query: 71 KLPQ---KEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTALGPSAPQ 126
 P+ P + PP E +P TP L ++S P +P + P +
 Sbjct: 873 SPPEVVKPSTPPAPTTVISPPSEPKSSPPPTPVSLPPPIVKSSPPPPAMVSSPPMTPKSSP 932

Query: 127 KPLRRAL---SGRASVPVAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSP 183
 P+ + ++SP PAP S A K+ A L P PPE + PP +P
 Sbjct: 933 PPVVVSPPPTVKSSPPAPVSSPPATP--KSSPPAPVNL----P--PPEVKSSPPPTP 984

Query: 184 ASTASFIFSKGSRKLQLERPVSPETQADLQRLNVAELRSISEQRPPQAPKSPKAPPPVA 243
 S+ + P PE ++ V+ + PP AP SP PPPV
 Sbjct: 985 VSSPPPAKSSPPPPAMSSPPPEVKSSPPPPAPVSSPPPVKSSPPPPAPVSSP--PPPVK 1042

Query: 244 RKPS---VGVPPPASPSYPRAEPLTAPP 268
 P V PPP S P P+++PP
 Sbjct: 1043 SPPPPAPVSSPPPPVKSPPPPAPISSP 1070

Score = 190 (28.5 bits), Expect = 7.9e-12, P = 7.9e-12
 Identities = 74/264 (28%), Positives = 111/264 (42%)

Query: 5 PPPEEAFFSVASPEPAGPSGSPELVSSPAAS-SSSATALQIQPPGSPDPPAPAPAPAS 63
 PPP S PE + P P + P + T+++ PP PP P+P
 Sbjct: 639 PPPPTPVSSPPPEKSPPPPPAKSTPPPEEYPTPTSVKSSPPPEKSLPPPTLIPSPPP 698

Query: 64 SAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTALGPS 123
 P K P K PP+E V +P TP V +P PTP P
 Sbjct: 699 QEKTPTPSTPSKPPSSPEKPS-PPKEPVSSPPQTPK--SSPPAPVSSP--PPTPVSSPP 753

Query: 124 APQKPLRRALSGRASVPVAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSP 183
 A P+ S ++SP PAP S A ++K+ + + P PP + PP +P
 Sbjct: 754 A-LAPVSSPPSVKSSPPPPAPLSSPPAPQVKS----SPPPVQVSSP--PPAPKSSPPLAP 806

Query: 184 ASTASFIFSKGSRKLQLERP-VSPETQADLQRLNVAELRSISEQRPPQAPKSPKAPPPV 242
 S+ + L P ++P++ +V+ + + PP AP SP P
 Sbjct: 807 VSSPPQVEKTSPPPPAPLSSPPLAPKSSPP--HVVVSSPPPVKSSPPPPAPVSSPPLTPKP 864

Query: 243 ARKPS-VGVPP---PASPSYPR-----AEPLTAPP 268
 A P+ V PP P++P P +EP ++PP
 Sbjct: 865 ASPPAHVSSPPEVVKPSTPPAPTTVISPPSEPKSSP 901

Score = 189 (28.4 bits), Expect = 1.0e-11, P = 1.0e-11
 Identities = 86/271 (31%), Positives = 112/271 (41%)

Query: 5 PPPEEAFFSVASPEPAGPSGSPEL-VSSP--AASSSSATALQIQPPG--SPDPPAP--- 56
 PPP A S P P S P + VSSP A SS A PP PPPAP
 Sbjct: 768 PPP--APLSSPPAPQVKSPPPVQVSSPPAPKSSPPLAPVSSPPQVEKTSPPAPLSS 825

Query: 57 PAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAP 116
 P AP SS P V P PV S PP V +P +TP V +P
 Sbjct: 826 PPLAPKSSPPHVVSPP--PVVKSS---PPAPVSSPPLTPKPASPPA--HVSSPPEVV 878

Query: 117 TPALGPSAPQKPLRRALSGRASVPVAPSSGLHAAVRLKAC-SLAASEGL---SSAQPN--- 169
 P+ P AP + ++SP P P S V+ ++ +S + SS P

Sbjct: 879 KPST-PPAPTTVISPPSEPKSSPPPTVSLPPPVIKSSPPPPAMVSSPPMTPKSSPPPVV 937

Query: 170 -NGPPEAEPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRLNVAELRSISEQRP 228
+ PP + PP + P S+ + P PE ++ V+ + P

Sbjct: 938 SSPPTVKSSPPAPVSSPPATPKSSPPAPVNL-PPEVKSSPPPTPVSSPPPAKSSP 996

Query: 229 PQAPKKSPKAPPPVARKPS---VGVPASPSPYPRAEPLTAPP 268
P AP SP PPP + P V PPP S P P+++PP

Sbjct: 997 PPAPMSSP--PPEVKSSPPAPVSSPPPVKSSPPAPVSSPP 1038

Score = 181 (27.2 bits), Expect = 8.8e-11, P = 8.8e-11

Identities = 73/277 (26%), Positives = 105/277 (37%)

Query: 3 DFPPEEAFSSVASPEPAGPSGSELVSSPAASSSSATALQIQPP---GSPDPP---PA 55
D+ PP V P S SP+ V PAAS+ + +++ PP GSP PP +

Sbjct: 469 DYVPPTTP---VPGKSPATSPSPQ-VQPPAASPPLVSLVLSPPQAPVGSPPPPVKTT 524

Query: 56 PPAPAPASSAPGHVAKL---PQKEPVGCSKGGPPREDVGAPLVTPLSLQMVRLRSVGA 111
PPAP + S P V+ + P K P + G PP + P P ++S

Sbjct: 525 PPAPIGSPSPPPVSVVSPPPVKSPPPPAPVGSPPPEKSPPPAPVASPPPPVKSPP 584

Query: 112 PG--GAPTALGPSAPQKPLRRA---LSGRASVPAPSSGLHAAVRLKACSLAASEGLSS 166
P +P P + P P+ + P P S A V + + +

Sbjct: 585 PTLVASPPPPVKSPPPPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPPMKSPPPPT 644

Query: 167 AQPNGPPEAEPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRLNVAELRSISEQ 226
PPE P PP PA + + ++ PE L+ +

Sbjct: 645 VSSPPPEKSP-PPPPAKSTPPPEEYPTPTS VKSSPPPEKSLP-PPTLIPSPPPQEK 702

Query: 227 RPPQAPKKSPKAPP-PVARKPSVGVPASPSPYPRAEPLTAPP 268
PP P K P +P P K V PP S P P+++PP

Sbjct: 703 TFPSTPSKPPSPPEKSPPEKPVSSPPQTPKSSPPAPVSSPP 745

Score = 177 (26.6 bits), Expect = 2.6e-10, P = 2.6e-10

Identities = 78/264 (29%), Positives = 105/264 (39%)

Query: 5 PPPEEAFSSVASPEPAGP---SGSELVSSPAASSSSATALQIQPPGSP--DPPAP-- 56
PPP +P+PA P S PE+V P+ + T I PP P PPP P

Sbjct: 850 PPPAPVSSPPLTPKASPPAHVSSPPEVVK-PSTPPAPTIV--ISPPSEPKSSPPPTV 906

Query: 57 -PAPAPASSAPGHVAKLPQKEPVGCSKGGPPREDVGAPLVTPLSLQMVRLRSVGA 115
P P SS P + P P PP V +P P++ V +P

Sbjct: 907 LPPPIVKSSPPAMVSSPPMTPKS-----SPPPVVSSP--PPTVKSSPPAPVSSPPAT 959

Query: 116 PTPALGPSAPQKPLRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEA 175
P + P+ P ++SP P P S A + S +SS P PPE

Sbjct: 960 PKSSPPAPVNLPPPEV---KSSPPPTPVSSPPAPK---SSPPAPMSSP-P--PPEV 1009

Query: 176 EPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRLNVAELRSISEQRPQAPKKS 235
+ PP +P S+ + P P ++ V+ + PP AP S

Sbjct: 1010 KSPPPAPVSSPPPPVKSPPPPAPVSSP-PPPVKSPPPPAPVSSPPPPVKSPPPPAPISS 1068

Query: 236 PKAPPPVARKPS---VGVPASPSPYPRAEPLTAPP 268
P PPPV P V PPP S P P+++PP

Sbjct: 1069 P--PPPVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP 1102

Score = 177 (26.6 bits), Expect = 2.6e-10, P = 2.6e-10

Identities = 82/267 (30%), Positives = 110/267 (41%)

Query: 17 PEPAG-PSGSELVSSPAASS---SSATALQIQPPGSPDPPAP---PAPAPASSAPGHV 69
P P G P SP + PAAS+ S T + P P+P P P P P P +P

Sbjct: 410 PTPGGGPPSSP-VPGKPAASAPMPSPTPPDVSPELPEPSVPAPAPMMPMPTPHSPPAD 468

Query: 70 AKLPQKEPV-GCSKGGPPREDVGAPLVTPLSLQMVRLRSVGA 128
+P PV G S P V P + +V+L AP G+P P + ++P P

Sbjct: 469 DYVPPTTPVPGKSPATSPSPVOVPPAASPPLVSLVLSPPQAPVGSPPPPVKTTSPAP 528

Query: 129 LRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSPASTAS 188
+ G SP P P S + +K+ A G + P PPE P PP AS

Sbjct: 529 I-----GSPSP-PPVSVVSSPPPPVKSPPPPAPVG---SPP--PPEKSPPPAPVASPP 577

Query: 189 FIFSKGSRKLQLERPV---SPETQADLQRLNVAELRS-----ISEQRPQA-----PK 233
+ S L P SP A + + ++S ++ PP P

Sbjct: 578 PVKSPPPTLVASPPPPVKSPPPPAPVA-SPPPPVKSPPPTPVASPPPPAPVASSPPPM 636

Query: 234 KSPKAPPPVARKP---SVGVPPASPSPYPRAEPLTAPPTN 270
KSP P PV+ P PPP + S P E PPT+

Sbjct: 637 KSPPTPVSSPPPEKSPPPPPAKSTPPPEEYPTPTS 676

Score = 170 (25.5 bits), Expect = 1.6e-09, P = 1.6e-09

Identities = 78/279 (27%), Positives = 108/279 (38%)

Query: 5 PPPEEAFSSVASPEPAGPSGSELVSSPAASSSSATALQIQPPGSPDPPPPAPPAPAPASS 64
 PP S S + P +P + P SS A+ PP +P +PP P SS
 Sbjct: 883 PPAPTTVISPPSEPKSSPPPTPVSLPPPIVKSSPPPPAMVSSPMTPKS--SPP-PVVVSS 939

Query: 65 APGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPLSLQMVRLRSVGAPG--GAPTALGP 122
 P V P PV PP +P P L ++S P +P PA
 Sbjct: 940 PPPTVKSSPPAPVS-----SPPATPKSSPPAPVNLPPPEVKSSPPPTPVSSPPPPAPKS 994

Query: 123 SAPQKPLRRALSG--RASVPAPSSGLHAAVRLKACSLAASEGLSSAQNGPPEAEPRPP 180
 S P P+ ++ P PAP S V+ S ++S P PP + PP
 Sbjct: 995 SPPAPMSSPPPEVKSSPPPPAPVSSPPPPVK----SPPPPAPVSS--P--PPFVKSPPP 1046

Query: 181 QSPASTASFIFSKGSRKLQLERPVSPETQADLQRLVAELRSISEQRPPQAPKSPKAPP 240
 +P S+ + P P ++ V+ + PP AP SP PP
 Sbjct: 1047 PAPVSSPPPPVKSPPPAPISSP-PPPVKSPPPAPVSSPPPPVKSPPPAPVSSP--PP 1103

Query: 241 PVARKPS---VGVPASP---PSYPRAEPLTAPPTNGLPHTQDRTKREL 283
 P+ P V PPPA PS P P+++PP P + ++ L
 Sbjct: 1104 PIKSPPPAPVSSPPAPVKPPSLPPAPVSSPPPVVTPAPPKKEEQL 1152

Score = 169 (25.4 bits), Expect = 2.1e-09, P = 2.1e-09
 Identities = 75/266 (28%), Positives = 104/266 (39%)

Query: 3 DFPPEEAFSSVASPEPAGPSGSELVSSPAASSSSATALQIQPP----GSPDPP---PA 55
 D+ PP V P S SP+ V PAAS+ + +++ PP GSP PP +
 Sbjct: 469 DYVPPTFP---VPGKSPATSPSQ-VQPPAASPPPSLVKLSPPQAPVGSPPPPVKTT 524

Query: 56 PPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPLSLQMVRLRSVGAPGGA 115
 PPAP + S P V+ + PV PP VG+P P V +P
 Sbjct: 525 PPAPIGSPSPPPVSVVSSPPPPVKSP----PPAPVGSPP--PPPEKSPPPAPVASP--- 575

Query: 116 PTPALGPSAPQKPLRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSAQNGPPEA 175
 P P P P ++ P PAP + V+ S ++S P P +
 Sbjct: 576 PPPVKSPPPPTLVASPPPEVKSPPPAPVASPPPPVK----SPPPTPVASPPPPAPVAS 631

Query: 176 EPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRLVAELRSISEQRPPQAPKKS 235
 P P +SP K P P S+ PP+
 Sbjct: 632 SPPPMKSPPPPTPVSSPPPEKSP--PPPPAKSTPPPEEYPTPTSVKSSPPPEKSLPP 689

Query: 236 PK---APPPVARK--PSVGVPASPSPYPRA--EPLTAPP 268
 P +PPP + PS PP+SP P EP+++PP
 Sbjct: 690 PTLIPSPPPQEKPTPSTPSKPPSSPEKSPPEKPVSSPP 729

Score = 168 (25.2 bits), Expect = 2.7e-09, P = 2.7e-09
 Identities = 75/267 (28%), Positives = 102/267 (38%)

Query: 2 ADFPPPEEAFSSVASPE-PAGPSGSELVSSPAASSSSATALQIQPPGSPDPP-PAPPAP 59
 A PPP + ++ P+ P G P +SP A S + SP PP +PP P
 Sbjct: 496 ASTPPP--SLVKLSPPQAPVGSPPPPVKTTSPAPIGSPSPPPVSVVSSPPPPVKSPPPP 553

Query: 60 APASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPLSLQMVRLRSVGAPGGAPTPA 119
 AP S P P PV PP + P + S V+ AP +P P
 Sbjct: 554 APVGSPPPEKSPPPPPAPVASPP--PPVKSPPPPTLVASPPPPVKSPPPPPAPVASPPPP 610

Query: 120 LGPSAPQKPLRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSAQNGPPEAEPR 178
 + P P+ + P PAP + ++ +S P PP A+
 Sbjct: 611 VKSPPPPTPVA-----SPPPPAPVASSPPPMKSPPPPTPVSSPPPEKSPPPPPAKST 664

Query: 179 PP--QSPASTASFIFSKGSRKLQLERPV--SPETQADLQRLVAELRSISEQRPPQAPK 233
 PP + P S S K L P SP Q S ++P +P
 Sbjct: 665 PPPEEYPTPTSVKSSPPPEK-SLPPPTLIPSPPPQEKPTPSTPSKPPSSPEKP--SPP 721

Query: 234 KSPKAPPVARKPSVGVPASPSPYPRAEPLTAPP 268
 K P + PP K S PPPA S P P+++PP
 Sbjct: 722 KEPVSSPPQTPKSS---PPAPVSSPPPTPVSSPP 753

Score = 166 (24.9 bits), Expect = 4.6e-09, P = 4.6e-09
 Identities = 81/268 (30%), Positives = 108/268 (40%)

Query: 5 PPPEEAF---FSVASPEPAGPSGSE-LVSSPAASSSS---ATALQIQPPGSPDPP-- 54
 PPPE++ VASP P S P LV+SP S A PP PPP
 Sbjct: 560 PPPEKSPPPAPVASPPPPVKSPPPPTLVASPPPPVKSPPPAPVASPPPPVKSPPPPTP 619

Query: 55 --APPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPLSLQMVRLRS 108
 +PP PAP +S+P + P PV K PP ++S
 Sbjct: 620 VASPPPPAPVASPPPMKSPPPPTLVSSPPPEKSPPPPPAKSTPPPEEYPTPTSVKS 679

Query: 109 VGAPGGA-PTPALGPSAPQKPLRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSA 167
 P + P P L PS P P + + ++P PSS + S SS
 Sbjct: 680 SPPPEKSLPPPTLIPSP--PQEKPTPSTPSKPPSSPEKSPPEKPVSSPPQTPKSSP 736

Query: 168 QPNGPPEAEPRPPQSPASTASFIFSKGSRKLQLERVSPETQADLQRLNVAELRSISEQR 227
 P P P SP + A + S S K P + P + + + +
 Sbjct: 737 PPAPVSSPPPTPVSSPPALAP-VSSPPSVKSS--PPAPLSSPPAPQVKSSPPPVQVSS 793

Query: 228 PPQAPKKSPPKAPPPVARKPSVGVPPPPASPSYPRAEPLTAPP 268
 PP APK SP P+A P V PP + P PL++PP
 Sbjct: 794 PPPAPKSSP----PLA--P-VSSPPQVEKTSPPAPLSSPP 827

Score = 165 (24.8 bits), Expect = 6.0e-09, P = 6.0e-09
 Identities = 79/264 (29%), Positives = 105/264 (39%)

Query: 5 PPPEEAFFSVASPEPAG-PSGSP--ELVSSPAASSSSATALQIOPPGSPDPPP-APPAPA 60
 PPP + + + P P G PS P +VS P S P GSP PP +PP PA
 Sbjct: 517 PPPVK---TTSPPAPIGSPSPPPPVSVSSPPPVKSPPPPA---PVGSPPPPEKSPPPPA 570

Query: 61 PASSAPGHVAKLPQKEPVGCSKG---GGPPREDVGAP---LVTPSLLQMVRLRSVGAPGG 114
 P +S P V P V PP V +P + +P V AP
 Sbjct: 571 PVASPPPVKSPPPTLVASPPPPVKSPPPPAPVASPPPVKSPPPTPVASPPPPAPVA 630

Query: 115 APTPALGPSAPQKPLRRALSGRASVPAP---SSGLHAAVRLKACSLAASEGLSSAQPNG 171
 + P + P P+ SP P P S+ S+ +S + P
 Sbjct: 631 SSPPPMKSPPPPTPVSSPPPEKSPPPPPAKSTPPPEEYPTPTS VKSSPPPEKSLP-- 688

Query: 172 PPEAEPRPPQSPASTASFIFSKGSRKLQLERVSPETQADLQRLNVAELRSISEQRPPQA 231
 PP P PP T SK P SPE + + V+ + PP A
 Sbjct: 689 PPTLIPSPPPQEKPTPPSTPSKP-----PSSPEKPS-PKEPVSSPPQTPKSSPPPA 739

Query: 232 PKKSPKAPPPVARKPSVGV--PPPASPSYPRAEPLTAPP 268
 P SP P PV+ P++ PP+ S P PL++PP
 Sbjct: 740 PVSSPP-PTPVSSPPALAPVSSPPSVKSSPPAPLSSPP 777

Score = 162 (24.3 bits), Expect = 1.3e-08, P = 1.3e-08
 Identities = 76/272 (27%), Positives = 99/272 (36%)

Query: 2 ADFPPPEEAFFSVASPEPAG-PSGSP-ELVSSPAASSSSATALQIOPPGSPDPPPAPPAPA 60
 A P P SPEP PS P P + S A PP P P +PPA +
 Sbjct: 427 ASAPMPSHTPPDVSPLEPEPSVPAPAPMPMPTPHSPADDYVPPTPPVVGKSPPTAS 486

Query: 61 PASSAPGHVAKLPQKEPVGCSKGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPT-- 118
 P+ A P V S PP+ VG+P P V+ S AP G+P+P
 Sbjct: 487 PSPQVQPPAASTPPPSLVKLS----PPQAPVGSPP--PPP----VKTTSPPAPIGSPSPPP 536

Query: 119 ---ALGPSAPQK-PLRRALSGRASVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPE 174
 + P P K P A G SP P S A S + + PP
 Sbjct: 537 PVSVSPPPPVKSPPPPAPVG--SPPPPEKSPPPAPVASPPPPVKSPPPTLVASPPPP 594

Query: 175 AEPRPPQSPASTASFIFSKGSRKLQLERVSPETQADLQRLNVAELRSISEQRPPQAPKK 234
 + PP +P ++ + P P A + + PP P+K
 Sbjct: 595 VKSPPPPAPVASPPPPVKSPPPTPVASPPPPAPVASSPPPMKSPPPPTPVSSPPPP-PEK 653

Query: 235 SPKAPPPVARKPSVGVPPPPASPSYPRAEPLTAPPTNGLP 273
 SP PPP P PP P+ P + + PP LP
 Sbjct: 654 SPPPPPPAKSTP---PPEEYPTPTS VKSSPPPEKSLP 688

Score = 159 (23.9 bits), Expect = 2.8e-08, P = 2.8e-08
 Identities = 77/264 (29%), Positives = 103/264 (39%)

Query: 5 PPPEEAFFSVASPEPAGPSGSP-ELVSSPAASSSSATALQIOPPGSP--DPPAP---PAP 59
 PPP V+SP P P SP P SS ++ PP +P PP P P P
 Sbjct: 916 PPPA---MVSSP-PMTPKSSPP---PVVVSSPPPTVKSSPPAPVSSPPATPKSSPP 966

Query: 60 APASSAPGHVAKLPQKEPVGCSKGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPT 119
 AP + P V P PV S P AP+ +P + V+ AP +P P
 Sbjct: 967 APVNLPPPEVKSSPPPTPVSS-SPPPAPKSSPPAPMSSPPPPPE-VKSPPPPAPVSSPPPP 1024

Query: 120 LGPSAPQKPLRRALSG-RASVPAPSSGLHAAVRLKACSLAASEG---LSSAQPNGPPEA 175
 + P P+ ++ P PAP S V+ S + S P P +
 Sbjct: 1025 VKSPPPPAPVSSPPPPVKSPPPPAPVSSPPPPVKSPPPPAPISSPPPPVKSPPPPAPVSS 1084

Query: 176 EPRPPQSPASTASFIFSKGSRKLQLERVSPETQADLQRLNVAELRSISEQRPPQAPKKS 235
 P P +SP A S ++ P P A + A ++ S PP AP S
 Sbjct: 1085 PPPPVKSPPPPAPV---SSPPPIKSPPPP---APVSSPPAPVKPPS--LPPPAPVSS 1135

Query: 236 PK--APPPVARKPSVGVPPPA-SPSYPRAEPLTAPP 268
 P P +K +PPA S P + PP
 Sbjct: 1136 PPPVVTAPPKKEEQLPPPAESQPPPSFNDIILPP 1171

Score = 143 (21.5 bits), Expect = 1.8e-06, P = 1.8e-06
 Identities = 59/179 (32%), Positives = 77/179 (43%)

Query: 3 DFPPEEAEFFSVASPEP-AGPSGSELVSSPAASSSSATA-LQIQPPGSP--DPPP---A 55
 + PPPE S P P + P +P+ PA SS ++ PP +P PPP +
 Sbjct: 970 NLFPPEVK--SSFPPTPVSSPPAPKSSPPAPMSSPPPEVKSPPPAPVSSPPPPVKS 1027

Query: 56 PPAPAPASSAPGHVAKLPQKEPVGCSKGGPPREDVGAPLVTPLSLQMVRLRSVGAPGGA 115
 PP PAP SS P V P PV PP + P S V+ AP +
 Sbjct: 1028 PFPAPVSSPPPPVKSPPPPAPVSSPP--PPVKSPPPPAPISSPPPPVKSPPPPAPVSS 1084

Query: 116 PTPALGPSAPQKPLRRALSG-RASVPAPSSGLHAAVRLKACSLAASEGLSSAQPNPPE 174
 P P + P P+ ++ P PAP S A +K SL +SS P PP
 Sbjct: 1085 PFPVKSPPPPAPVSSPPPIKSPPPAPVSSPPAP-VKPPSLPPAPVSS--P--PPV 1139

Query: 175 AEPRPPQ 181
 P PP+
 Sbjct: 1140 VTPAPPK 1146

Score = 133 (20.0 bits), Expect = 2.3e-05, P = 2.3e-05
 Identities = 50/132 (37%), Positives = 59/132 (44%)

Query: 1 MADFPPEEAEFFSVASPEPAGP-SGSELVSSP---AASSSSATALQIQPPGSP--DPPP 54
 M+ PPPE V SP P P S P V SP A SS ++ PP +P PPP
 Sbjct: 1001 MSSPPPE-----VKSPPPPAPVSSPPPPVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP 1055

Query: 55 ---APPAPAPASSAPGHVAKLPQKEPVGCSKG---GGPPREDVGAPLVTPLSLQMVRLRS 108
 +PP PAP SS P V P PV PP V +P P +
 Sbjct: 1056 PVKSPPPPAPISSPPPPVKSPPPPAPVSSPPPPVKSPPPPAPVSSP--PPPIKSPPPAP 1113

Query: 109 VGAPGGAPT--PALGPSAP 125
 V +P AP P+L P AP
 Sbjct: 1114 VSSPPAPVKKPSSLPPAP 1132

Score = 110 (16.5 bits), Expect = 8.0e-03, P = 8.0e-03
 Identities = 41/121 (33%), Positives = 49/121 (40%)

Query: 5 PPPEEAEFFS---VASPEPAGP-SGSELVSSP---AASSSSATALQIQPPGSP--DPPP 54
 PPP S V SP P P S P V SP A SS ++ PP +P PPP
 Sbjct: 1060 PFPAPISSPPPPVKSPPPPAPVSSPPPPVKSPPPPAPVSSPPPIKSPPPAPVSSPP 1119

Query: 55 AP-----PAPAPASSAPGHVAKLPQKEPVGCSKGGPPREDVGAPLVTPLSLQMVRLRS 108
 AP P PAP SS P V P K+ + PP E P +L +
 Sbjct: 1120 APVKPPSLPPAPVSSPPPVTPAPPKKE--EQSLPPAESQPPSFNDIILPPIMANK 1176

Query: 109 VGAP 112
 +P
 Sbjct: 1177 YASP 1180

Score = 108 (16.2 bits), Expect = 1.3e-02, P = 1.3e-02
 Identities = 46/155 (29%), Positives = 67/155 (43%)

Query: 114 GAPTPALGPSAPQKPLRRALSGRASVPAPSSGLHAAVR-LKACS-LAASEGLSSAQPNG 171
 G PTP GP + P + A S +P+P+P + L S + A + P+
 Sbjct: 408 GYPTGGGGPPSSPVGKPAAS---APMPSHTPPDVSPEPLPEPSPVPAPAPMPMPTPHS 464

Query: 172 PPEAEPRPPQSPASTASFIFSKGSRKQLERPVSPETQ---ADLQRNLVAELRSISEQR 227
 PP + PP P S + S ++Q +P + Q + + +
 Sbjct: 465 PPADDYVPTPPVPGKSPPATSPSPQVPPAASTPPPSLVKLSPPQAPVGSPPPPVKTS 524

Query: 228 PPQAPKKSPPKAPPPVARKPSVGVPPPASPSYPRAEPLTAPP 268
 PP AP SP PPPV SV PPP S P P+ +PP
 Sbjct: 525 PP-APIGSPSPPPV---SVVSPPPVKSPPPPAPVGSPP 560

Pedant information for DKFZphmcf1_lc23, frame 1

Report for DKFZphmcf1_lc23.1

[LENGTH] 311
 [MW] 31534.58
 [pI] 9.48
 [KW] All_Alpha
 [KW] LOW_COMPLEXITY 38.59 %

SEQ MADFPPEEAEFFSVASPEPAGPSGSELVSSPAASSSSATALQIQPPGSPDPPPPAPPAPA
 SEGXXXXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXX
 PRD CCC

SEQ PASSAPGHVAKLPQKEPVGCSKGGPPREDVGAPLVTPLSLQMVRLRSVGAPGGAPTPAL
 SEG XXXXXX.....XXXXXXXXXXXXXXXXXXXX

(No Pfam data available for DKFZphmcf1_1c23.1)

DKF2phmcf1_1e15

group: transmembrane protein

DKF2phmcf1_1e15 encodes a novel 454 amino acid protein with similarity to *C. elegans* proteins and transporter proteins.

The novel protein is similar to the PTR2 family of proton/oligopeptide symporter proteins and the D-xylose-proton symporter. Thus, the protein is a transporter of a so far unknown compound.

The new protein can find application as a new transporter in eukaryotic cells, e.g. in drug transport into cells.

similarity to D-XYLOSE TRANSPORTER
membrane regions: 9

complete cDNA, complete cds, EST hits
matches cDNA encoding cell growth inhibiting factor (E12646)

Sequenced by DKFZ

Locus: unknown

Insert length: 1957 bp

Poly A stretch at pos. 1947, polyadenylation signal at pos. 1929

```
1 GGTGCAGCGC CCGGGCTGAG CGACAGCAAG TGCAGCGGGC TCCTACCCCG
51 GGTGAGGGGT GGCCTCCGCG TGGGATCGTG CCTCTTCAG CCCGCTCCTG
101 TCCCCGACAT CACGTGTATT CCGCACGTCC CTTCCGCGCT GTGTGTCTAC
151 TGAGACGGGG AGGCGTGACA GGGCCCGGGT CCTTCTCAG TGTTGTCTCTG
201 TGCTTCAGGG CAAGCTCCCC GTCTCCGGGC GCACTTCCCT CGCCTGTGTT
251 CGGTCCATCC TCCTTTCTCC AGCCTCCTCC CTTGCGAGGT GGGATCGTCG
301 GTGGGACCGG AGCGCGGGCG GCGCGGGCCC CCGGGACCA TGGCCGGGTC
351 CGACACCGCG CCTTTCCTCA GCCAGGCGGA TGACCCGGAC GACGGGCCAG
401 TGCTTGGCAC CCGGGGGTTG CCAGGGTCCA CGGGGAACCC GAAGTCCGAG
451 GAGCCCGAGG TCCCGGACCA GGAGGGGCTG CAGCGCATCA CCGGCCTGTC
501 TCCCGGGCGT TCGGCTCTCA TAGTGGCGGT GCTGTGCTAC ATCAATCTCC
551 TGAACATCAT GGACCGCTTC ACCGTGGCTG TGTTCATCTC CAGTTACATG
601 GTGTTGGCAC CTGTGTTTGG CTACCTGGGT GACAGGTACA ATCGGAAGTA
651 TCTCATGTGC GGGGGCATTG CCTTCTGGTC CCTGGTGACA CTGGGGTCAT
701 CCTTCATCCC CGAGAGCAT TTCTGGCTGC TCCTCCTGAC CCGGGGCTG
751 GTGGGGGTGC GGGAGGCCAG TTATTCCACC ATCGCGCCA CTCTCATGTC
801 CGACCTCTTT GTGGCCGACC AGCGGAGCCG GATGCTCAGC ATCTTCTACT
851 TTGCCATTCC GGTGGGCAGT GGTCTGGGCT ACATTGCAGG CTCCAAAGTG
901 AAGGATATGG CTGGAGACTG GCACTGGGCT CTGAGGGTGA CACCGGGTCT
951 AGGAGTGGTG GCCGTTCTGC TGCTGTTTCT GGTAGTGGCG GAGCCGCCAA
1001 GGGGAGCCGT GGAGCGCCAC TCAGATTTCG CACCCCTGAA CCCACCTCG
1051 TGGTGGGCAG ATCTGAGGGC TCTGGCAAGA AATCTCATCT TTGGACTCAT
1101 CACCTGCTCG ACCGGAGTCC TGGGTGTGGG CCTGGGTGTG GAGATCAGCC
1151 GCCGGGCTCG CCACTCCAAC CCGGGGGCTG ATCCCTGGT CTGTGCCACT
1201 GGCCTCCTGG GCCTGCACC CTTCCTCTTC CTGTCCCTTG CCTGCGCCCG
1251 TGGTAGCATC GTGGCCACTT ATATTTTCAT CTTTATTGGA GAGACCTCC
1301 TGTCCATGAA CTGGGCCATC GTGGCCGACA TTCTGCTGTA CGTGGTGATC
1351 CCTACCCGAC GCTCCACCGC CGAGGCCCTC CAGATCGTGC TGTCCACCT
1401 GCTGGGTGAT CCTCGGACCC CTAACCTCAT TGGCCTGATC TCTGACCGCC
1451 TGCGCCGGAA CTGGCCCCCC TCCTTCTTGT CCGAGTTCCG GGTCTGCGAG
1501 TTCTCGCTCA TGCTCTGCGC GTTTGTTGGG GCACTGGGCG GCGCAGCCTT
1551 CCTGGGCACC GCCATCTTCA TTGAGGCCGA CCGCCGGCGG GCACAGCTGC
1601 ACGTGCAGGG CCTGCTGCAC GAAGCAGGGT CCACAGACGA CCGGATTGTG
1651 GTGCCCCAGC GGGGCCGCTC CACCCGCGTG CCGGTGGCCA GTGTGCTCAT
1701 CTGAGAGGCT GCCGCTCACC TACCTGCACA TCTGCCACAG CTGGCCCTGG
1751 GCCCACCCCA CGAAGGGCCT GGGCCTAACC CCTTGGCCTG GCCCAGCTTC
1801 CAGAGGGACC CTGGGCCGTC TGCCAGCTCC CAGACACTAC ATGGGTAGCT
1851 CAGGGGAGGA GGTGGGGGTC CAGGAGGGG ATCCCTCTCC ACAGGGGCG
1901 CCCCAAGGGC TCGGTGCTAT TTGTAACGGA ATAAAATTG TAGCCAGAAA
1951 AAAAAAA
```

BLAST Results

Entry E12646 from database EMBL:
cDNA encoding cell growth inhibiting factor.
Score = 3046, P = 2.2e-131, identities = 640/659

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 340 bp to 1701 bp; peptide length: 454
 Category: similarity to known protein

```

1 MAGSDTAPFL SQADDPDDGP VPGTPGLPGS TGNPKSEEP VPDQEGLQRI
51 TGLSPGRSAL IVAVLCYINL LNYMDRFTVA VFISYMYVLA PVFGYLGDRY
101 NRKYLKCGGI AFWSLVTLGS SFIPGEHFWL LLLTRGLVGV GEASYSTIAP
151 TLIADLFVAD QRSRMLSIFY FAIPVGSGLG YIAGSKVKDM AGDWHWALRV
201 TPGLGVVAVL LLFLVVREPP RGAVERHSDL PPLNPTSWWA DLRALARNLI
251 FGLITCLTGV LGVGLGVEIS RRLRHSNPRA DPLVCATGLL GSAPFLFLSL
301 ACARGSIVAT YIFIFIGETL LSMNWAIVAD ILLYVVIPT RSTAEAFQIV
351 LSHLLGDAGS PYLIGLISDR LRRNWPPSFL SEFRALQFSL MLCAFVGALG
401 GAAFLGTAIF IEADRRRAQL HVQGLLHEAG STDDRIVVPQ RGRSTRVPVA
451 SVLI

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphmcfl_le15, frame 1

TREMBL:CEC13C4_1 gene: "C13C4.5"; Caenorhabditis elegans cosmid C13C4,
 N = 3, Score = 441, P = 5.2e-76.

TREMBL:CEC39E9_10 gene: "C39E9.10"; Caenorhabditis elegans cosmid
 C39E9, N = 2, Score = 449, P = 8.2e-69

TREMBL:CEF09A5_1 gene: "F09A5.1"; Caenorhabditis elegans cosmid F09A5,
 N = 3, Score = 413, P = 9.1e-60

TREMBL:ATF6H11_18 gene: "F6H11.180"; product: "predicted protein";
 Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII
 project), N = 3, Score = 193, P = 2.5e-24

SWISSPROT:XYLT LACBR D-XYLOSE-PROTON SYMPORT (D-XYLOSE TRANSPORTER)., N
 = 1, Score = 180, P = 7.9e-11

>TREMBL:CEC39E9_10 gene: "C39E9.10"; Caenorhabditis elegans cosmid C39E9
 Length = 488

HSPs:

Score = 449 (67.4 bits), Expect = 8.2e-69, Sum P(2) = 8.2e-69
 Identities = 88/204 (43%), Positives = 125/204 (61%)

```

Query: 58 SALIVAVLCYINLLNYMDRFTVAVFISSYMYVLA PVFGYLGDRYNRKYLKCGGIAFWSLVT 117
      + ++ V Y N + + + VF+ S+MV +PV GYLGD+NRK++M G+ W
Sbjct: 29 AGVLTQVQTYYNISDSLGLLIQTVFLISFMVFPVCGYLGDRFNKRWIMIGVGIWLGAV 88

```

```

Query: 118 LGSSFIPGEHFWL LLLTRGLVGVGEASYSTIAPT LIADLFVADQRSRMLSIFYFAIPVGS 177
      LGSSF+P HFWL L+ R VG+GEASYS +AP+LI+D+F +RS + IFYFAIPVGS
Sbjct: 89 LGSSFVPANHFWLFLVLRSEVIGIGEASYSNVAPSLISDMFNGQKRSTVFEMIFYFAIPVGS 148

```

```

Query: 178 GLGYIAGSKVKDMAGDWHWALRVTPGLGVVAVLLFLVVREPPRGAVR---HSDLPL 233
      GLG+I GS V + G W W +RV+ G++ ++ L L EP RGA ++ D+
Sbjct: 149 GLGFIVGSNVATLTGHWQWGI RVSATAGLIVMIALVLFTYEPERGAADKAMGESKD VVVT 208

```

```

Query: 234 NPTSWADLRALARNLIFGLITCLTG 259
      T++ DL L + L+ C G
Sbjct: 209 TNTTYLEDLVILLKTPT--LVACTWG 232

```

Score = 267 (40.1 bits), Expect = 8.2e-69, Sum P(2) = 8.2e-69
 Identities = 74/212 (34%), Positives = 113/212 (53%)

```

Query: 249 LIFGLITCLTGVGLGVEISRR-----RHSNPRA DPLVCATGLLGSAPFLFLSL 300
      L FG IT G++GV G +S+ L R RA PLV G L +APFL + +
Sbjct: 277 LYFGAITTAGGLIGVIFGSMLSKWL VAGWGPFRRLQTDRAQPLVAGGALLAAPFL LIGM 336

```

```

Query: 301 ACARGSIVATYIFIFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGDAGS 360

```

Score = 70 (10.5 bits), Expect = 5.9e-24, Sum P(2) = 5.9e-24
Identities = 25/89 (28%), Positives = 41/89 (46%)

Report for DKFZphmcf1_1e15.1

```
[BLOCKS]          BL01022D
[PROSITE]        MYRISTYL          11
[PROSITE]        CAMP_PHOSPHO_SITE  1
[PROSITE]        CK2_PHOSPHO_SITE   3
[PROSITE]        PROKAR_LIPOPROTEIN 1
[PROSITE]        GLYCOSAMINOGLYCAN  1
[PROSITE]        PKC_PHOSPHO_SITE   4
[KW]             TRANSMEMBRANE      8
[KW]             LOW COMPLEXITY     15.42 %
```

SEQ HVOGLLHEAGSTDDRI VVPQGRGRSTRVPVASVLI

SEG
PRD hhhhhhhhhcccccccccccccccccccccccc
MEM MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

Prosite for DKFZphmcf1_1e15.1

PS00002	177->181	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	340->344	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	270->273	PKC_PHOSPHO_SITE	PDOC00005
PS00005	339->342	PKC_PHOSPHO_SITE	PDOC00005
PS00005	368->371	PKC_PHOSPHO_SITE	PDOC00005
PS00005	444->447	PKC_PHOSPHO_SITE	PDOC00005
PS00006	11->15	CK2_PHOSPHO_SITE	PDOC00006
PS00006	342->346	CK2_PHOSPHO_SITE	PDOC00006
PS00006	431->435	CK2_PHOSPHO_SITE	PDOC00006
PS00008	26->32	MYRISTYL	PDOC00008
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	52->58	MYRISTYL	PDOC00008
PS00008	139->145	MYRISTYL	PDOC00008
PS00008	176->182	MYRISTYL	PDOC00008
PS00008	252->258	MYRISTYL	PDOC00008
PS00008	262->268	MYRISTYL	PDOC00008
PS00008	266->272	MYRISTYL	PDOC00008
PS00008	288->294	MYRISTYL	PDOC00008
PS00008	305->311	MYRISTYL	PDOC00008
PS00008	397->403	MYRISTYL	PDOC00008
PS00013	292->303	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphmcf1_1e15.1)

DKFZphmcf1_lg13

group: mammary carcinoma derived

DKFZphmcf1_lg13 encodes a novel 573 amino acid protein with very weak similarity to the human KIAA0543 protein and Musca domestica hermes transposase.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of mammary carcinoma-specific genes.

similarity to KIAA0766

complete cDNA, complete cds, few EST hits
on genomic level encoded by AC005020, no splicing, genomic?

Sequenced by DKFZ

Locus: unknown

Insert length: 2210 bp

Poly A stretch at pos. 2200, polyadenylation signal at pos. 2176

```
1 GAAACCTGAT CTCATAAAAC CTAGGTCACA AAGGACAGCC CTGCAAAACA
51 GACCCCTATTT GGATCAAGTG AGCCAGTTCC TGGAACCTGA ATAATGACTC
101 CTGAATCAAG GGATACTACA GATTGTCTC CAGGGGTAC CCAGGAGATG
151 GAAGGCATCG TGATAGTGAA GGTGGAGGAG GAAGATGAAG AAGACCATT
201 TCAAAAGGAA AGAAACAAAG TAGAGTCATC GCCACAAGT CTCAGTCGCT
251 CTACAACATAT GAATGAGAGA GCCTTATTGT CATCGTATTT AGTTGCATAT
301 AGAGTGGCAA AAGAGAAAAT GGCTCACACA GCGGCTGAAA AAATTATCCT
351 TCCAGCATGT ATGGACATGG TACGGACAAT TTTTGATGAC AAATCAGCTG
401 ATAACTAAG AACTATACCT CTTAGTGATA ATACAATATC TCGTCGAATC
451 TGTACGATTG CAAAACATTT GGAAGCAATG CTTATTACAC GGCTGCAGTC
501 CGGTATAGAC TTGCAATCC AACTCGATGA GAGCACTGAT ATTGCAAGTT
551 GTCCCACT CTGGTTTAT GTCAGATATG TGTGGCAAGA TGATTTTGTA
601 GAGGATCTCT TATGTTGTTT AAATTTAAAT TCACATATAA CTGGATTAGA
651 TTTATTTACT GAATTAGAAA ACTGCCTTCT TGGTCAGTAT AAATTAAGT
701 GGAAACATTG TAAAGGAATT TCAAGTGATG GAACAGCAA TATGACCGGA
751 AAACACAGCA GACTTACTGA AAAATTGTTA GAAGCAACCC ACAACAATGC
801 TTTTGGGAA CACTGTTTGA TTTCATCGAGA AGCTTTGGTA TCCAAAGAAA
851 TTTCACCAAG TCTGATGGAT GTATTGAAAA ATGCAAGTGAA AACTGTTAAT
901 TTTATTAAGG GAAGCTCACT GAATAGCCGA CTTCTCGAAA TATTTGTTT
951 AGAGATTGGA GTGAACCACA CCCACTTATT GTTTCATACA GAAGTTCGTT
1001 GGCTTTCTCA AGGAAAAGTA TTGAGCAGAG TATATGAAC CAGGAACGAG
1051 ATTTACATTT TTCTCGTTGA AAAGCAATCT CATTGGCAA ATATTTTGA
1101 AGACGACATT TGGGTAACAA AATTGGCATA TTTAAGTGAT ATTTTGGCA
1151 TTCTTAATGA ATTAAGCCTG AAAATGCAGG GGAACAAACA TGATATATTT
1201 CAGTATCTTG AACATATTTT AGGATTCCAA AAGACGTTAT TATTGTGGCA
1251 AGCAAGACTT AAAAGTAACC GCCCTAGCTA CTATATGTTT CCAACATTAT
1301 TGCAACACAT CGAAGAGAAC ATTATTAATG AAGACTGCTT AAAAGAAATA
1351 AAATTAGAGA TATTGTTGCA TCTCACTTCT TTGTTCAAAA CTTTAAATTA
1401 TTACTTTCCG GAAGAGAAAT TTGAATCATT AAAGGAAAT ATTTGGATGA
1451 AAGATCCATT TGCTTTTCAA AACCCAGAAT CAATAATTGA GTTAAACTTG
1501 GACCCCTGAAG AAGAGAAATGA ATTATTGCAG CTCAGTTCAT CATTACACT
1551 AAAGAATTAT TATAAGATAT TAAGTTTATC AGCATTTTGG ATTAAGATTA
1601 AAGATGACTT TCCACTGCTA AGTAGGAAGA GTATATTGCT GTTACTACCA
1651 TTCACAACATA CATATTTGTG TGAAGTAGGA TTTTCAATCT TGACACGGTT
1701 AAAAACAAG AAGAGAAATA GGCTCAATAG TGCACCAGAT ATGCGGGTAG
1751 CATTATCTTC ATGTGTTTCT GACTGGAAGG AACTTATGAA CAGACAAGCA
1801 CACCCATCAC ATTAAATACA AACTTTACAA AATTCTGTGT ATAGCCAGGT
1851 GTGGTGGCTT ACGCCTGTAA TCCCAGCAGT GGGAGACCGA GGTGGGCAGA
1901 TCACTTGAGT TCAAGACCAG CCTGGCCAAC ATGGTGAAAC CCCATCTCTA
1951 CTAAAAATAG AACCTTAGC CAGGCGTGGT GGCACATGCC TGCAGTCCCA
2001 GTTACTTGGG TGCCTGAGGC AGGAGAATCT CTTAAACCAG GAAGGCAGAG
2051 ATTGCAGTGA GCTGAGATAA TCCCAGTGCA TTCCAGCCTG GGCAACAGCG
2101 TGAGACTTCA TCTCAAAAAA AAAAAATTGT ATTTGTAATT TTAAGGGAT
2151 TTTGCAATAT GTTGTAGTTA AACGTTAATA AAATTATATT TGTAATTAGG
2201 AAAAAA
```

BLAST Results

Entry AC005020 from database EMBL:

Homo sapiens clone GS259H13; HTGS phase 1, 4 unordered pieces.

Score = 9110, P = 0.0e+00, identities = 1822/1822

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 94 bp to 1812 bp; peptide length: 573
 Category: similarity to unknown protein

```

1 MTPESRDSTD LSPGGTQEME GIVIVKVEEE DEEDHFQKER NKVESSPQVL
51 SRSTTMNERA LLSSYLVAIR VAKEKMAHTA AEKIILPACM DMVRTIFDDK
101 SADKLRTIPL SDNTISRRIC TIAKHLEAML ITRLQSGIDF AIQLDESTDI
151 ASCPTLLVYV RYVWQDDFVE DLLCCNLNLS HITGLDLFTE LENCLLGQYK
201 LNWKCKKGIS SDGTANMTGK HSRLTEKLE ATHNNAVWNH CFHREALVS
251 KEISPSLMDV LKNAVKTVMF IKGSSLSNRL LEIFCSEIGV NHTHLLFHTF
301 VRWLSQGVKL SRVYELRNEI YIFLVEKQSH LANIFEDDIW VTKLAYLSDI
351 FGILNELSLK MQGKNNDIFQ YLEHILGFQK TLLWQARLK SNRPSYMF
401 TLLQHIENI INEDCLKEIK LEILLHLTSL SQTFNYYFPE EKFESEKNI
451 WMKDPFAFQN PESIIEINLE PEEENELLQL SSSFTLNYY KILSLSAFWI
501 KIKDDFPLLS RKSILLPLPF TTYLCELGF SILTRLKTKK RNLNSAPDM
551 RVALSSCVDP WKELMNRQAH PSH

```

BLASTP hits

Entry AC004877_3 from database TREMBLNEW:
 gene: "WUGSC:H_DJ0751H13.2"; product: "KIAA0543 protein"; Homo sapiens
 PAC clone DJ0751H13 from 7q35-qter, complete sequence.
 Score = 86, P = 4.4e-03, identities = 46/179, positives = 78/179

Entry MD36211_1 from database TREMBL:
 product: "Hermes transposase"; Musca domestica Hermes transposase
 gene, complete cds.
 Score = 105, P = 3.0e-02, identities = 101/465, positives = 202/465

Alert BLASTP hits for DKFZphmcf1_lg13, frame 1

TREMBL:AB018309_1 gene: "KIAA0766"; product: "KIAA0766 protein"; Homo sapiens mRNA for KIAA0766 protein, complete cds., N = 1, Score = 300, P = 1.1e-23

>TREMBL:AB018309_1 gene: "KIAA0766"; product: "KIAA0766 protein"; Homo sapiens mRNA for KIAA0766 protein, complete cds.
 Length = 607

HSPs:

Score = 300 (45.0 bits), Expect = 1.1e-23, P = 1.1e-23
 Identities = 120/485 (24%), Positives = 229/485 (47%)

```

Query: 89 CMD-MVRTIFDDKSADKLRTIPLSDNTISRRICTIAKHLEAMLITRLQSGIDFAIQLDES 147
      CM+ ++R + + L+ + LS + +RI +I ++L L R + +++ LD+
Sbjct: 124 CMEVLLREVLPFH-VSVLQGVLDSPDITRQRILSIDRNLRNQLFNRRARDFKAYSLALDDQ 182

Query: 148 TDIASCPDLLVYVRYVWQD-DFVEDLLCCNLNLSHIT-GLDLFTELENCLLGQYKLNWKH 205
      +A LLV++R V + + EDLL +NL H + G + LE+ L L+ +
Sbjct: 183 AFVAYENYLLVFIRGVGPELEVQEDLLTIINLTHHFSVGALMSAILES--LQTAGLSLQR 240

Query: 206 CKGISSDGTANMTGKHSRLTEKLEATHNNAVWN--HC--FIHREALVSKEISPSLMDVL 261
      G+++ T M G++S L + E + WN H F+H E L S ++ + ++
Sbjct: 241 MVGLTTTHTLRMIGENSGLVSYMREKAVSPNCWNVHYSGLHLELLSSYDQVDVN--QII 298

Query: 262 KNAVKTVMFIKGSSLSNRLLEIFCSEIGVNHHTHLLFHTFVR-WLSQGVLSRVYELRNEI 320
      + + IK + + +E H + + WL +GK L ++ LR E+
Sbjct: 299 NTISEWIVLIKTRGVRRPEFQTLTTESESEHGERVNGRCLNNWLRGKTLKLIFSLRKEM 358

Query: 321 YIFLVEKQSHLANIFEDDIWVTKLAYLSDIFGILNELSLKMQGKNNDIFQYLEHILGFQK 380
      FLV + + F D W+ +L DI L ELS +++ +HI F+
Sbjct: 359 EAFLVSVGATTVH-FSDKQWLCDFGLVDIMEHLRELSEELRVSKVFAAAAFDHICTFEV 417

```

Score = 290 (43.5 bits), Expect = 1.5e-22, P = 1.5e-22
Identities = 120/485 (24%), Positives = 228/485 (47%)

Query:	89	CMD-MVRTTIDDKSADKLRTIPLSDNTISRRICTIAKHLAEMLLITRLOSQSIDFAIQDLES	147
Sbjct:	124	CMV+ ++R + + L+ + LS + +RI +I ++L L R + +++ LD+	182
Query:	148	TDIASCPDLLVYVRYVWQD-DFVEDLLCCLNLNSHIT-GLDLFTELENCLLGQYKLNWKH	205
Sbjct:	183	+A LLV++R V + + EDLL +NL H + G + Le+ L L+ +	240
Query:	206	CKGISSDGTANMTGKHSRLTEKLEATHNNNAVWNHCFIHREALVSKEISPSLMDV-LKNA	264
Sbjct:	241	G+++ T MG++S L + E + WN IH + E+ S DV +	297
Query:	265	VKTVN----FIKGSSLSRLLLEIFCSEIGVNHTLLFHTEVR-WLSQGVLSRVYELRNE	319
Sbjct:	298	+ T++ IK + + +E H + + WL +GK L ++ LR E	357
Query:	320	IYIFLVEKQSHLANIFEDDIWVTKLAYLSDIFGILNELSLKMQGKNNDIFOYLEHILGFQ	379
Sbjct:	358	+ FLV + + F D W+ +L DI L ELS +++ +HI F+	416
Query:	380	MEAFVLSVSGATTVH-FSDKQWLCDGFLVDIMEHLRELSEELRVSKVFAAAAFDHICTFE	435
Sbjct:	417	KTLLWQARLKSNRPSYMFPTLLQHIENIINEDCLKEIL----EILLHTLSLSQTFN	472
Query:	436	L L+Q ++ + EP L ++E + + ++ K+ + + L + F	494
Sbjct:	473	YYPPEEKFESLKENIWM-KDPFAFQNPESIEINLEPEEENLQLSSFTLKNNYKILS	524
Query:	495	+F ++ +F +K+++ + PF F+ + I + +E L +L ++ L N Y+I	550
Sbjct:	525	RHFKDLRF--IKKDLELFSNPFNFKEPEYAPISVRVE-----LTKLOANTNLWNEYRIKD	584
Query:	551	LSAFWIKIK-DDFPLLSRKSILLLPFTTTYLCELGFISILTRLTKTKRNRNLNSA---PDM	584
Sbjct:	585	L F+ + + +P++ + + F + +CE FS LTR + L	
Query:	551	RVALSSCVPDWKELMNRQAHPH	573
Sbjct:	585	RVA + P W +L+ R+ + S+	606
Query:	551	RVATTEMEPGWDDLV-RERNESN	606

Pedant information for DKFZphmcf1 lq13, frame 1

Report for DKFZphmcf1 lg13.1

```

[LENGTH]      573
[MW]           66276.85
[pI]           5.82
[HOMOL]        TREMBL:AB018309_1 gene: "KIAA0766"; product: "KIAA0766 protein"; Homo sapiens
mRNA for KIAA0766 protein, complete cds. 1e-18
[PROSITE]      MYRISTYL 3
[PROSITE]      CK2_PHOSPHO_SITE 10
[PROSITE]      TYR_PHOSPHO_SITE 1
[PROSITE]      PKC_PHOSPHO_SITE 9
[PROSITE]      ASN_GLYCOSYLATION 2
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY 8.90 %

SEQ  MTPESRDTTDLSPGGTQEMEGIVIVKVEEEDDEEDHFQKERNKVESSPQVLSRSTTMNERA
SEG  .....xxxxxxxx.....
PRD  cccccccccccccccccceeeeeeecccccchhhhhhhhhccccceeecccchhhh

SEQ  LLSSYLVAYRVAKEKMAHTAAEKIILPACMDMVRTIFDDKSADKLRTIPLSDNTISRRIC

```

Prosites for DKFZphmcf1 1g13.1

(No Pfam data available for DKFZphmcf1_1g13.1)

DKFZphtes3_14g5

group: testes derived

DKFZphtes3_14g5 encodes a novel 379 amino acid protein with strong similarity to murine cell growth regulating nucleolar protein LYAR.

The novel protein is very similar to murine Ly-1 antibody reactive clone protein (LYAR). It contains a ATP/GTP-binding site motif A (P-loop, interacts with one of the phosphate groups of a ATP/GTP nucleotide), but not the zinc finger motif and and nuclear localization signals of lyar.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

strong similarity to cell growth regulating nucleolar protein LYAR, of mouse

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 1503 bp

Poly A stretch at pos. 1467, polyadenylation signal at pos. 1440

```
1 CCCAGAGGTC CGACCTGGGA GGCTGGGGCT CAGAGAGCAA TGTTTGCTGT
51 CTTCCATTGG AGTGACTGAA TTTCTACATG ACGGCTTTTT GACAAGACTT
101 AAAACCTGTC TTGGATAGAG AATATTTAGC CATTACCTA AAAATGGTAT
151 TTTTACATG CAATGCATGT GGTGAATCAG TGAAGAAAAT ACAAGTGGAA
201 AAGCATGTGT CTGTTTGCAG AAAGTGTGAA TGCCTTTCTT GCATTGACTG
251 CGGTAAAGAT TTCTGGGGCG ATGACTATAA AAACCACGTG AAATGCATAA
301 GTGAAGATCA GAAGTATGGT GGCAAAGGCT ATGAAGGTAA AACCACAAAA
351 GGCAGATCA AACAGCAGGC GTGGATTGAG AAAATTAGTG AATTAATAAA
401 GAGACCCAAT GTCAGCCCCA AAGTGAGAGA ACTTTAGAG CAAATTAGTG
451 CTTTTGACAA CGTTCCCAGG AAAAAGGCAA AATTCAGAA TTGGATGAAG
501 AACAGTTTAA AAGTTCATAA TGAATCCATT CTGGACCAGG TGTGGAATAT
551 CTTTTCTGAA GCTTCCAACA GCGAACCAGT CAATAAGGAA CAGGATCAAC
601 GGCCACTCCA CCCAGTGGCA AATCCACATG CAGAAATCTC CAACAAGGTT
651 CCAGCCTCCA AAGTGAAAGA CGCCGTGGAA CAGCAAGGGG AGGTGAAGAA
701 GAATAAAAGA GAAAGAAAGG AAGAACGGCA GAAGAAAAGG AAAAGAGAAA
751 AGAAAGAACT AAAGTTAGAA AACCACCAGG AAAACTCAAG GAATCAGAAG
801 CCTAAGAAGC GCAAAAAGGG ACAGGAGGCT GACCTTGAGG CTGGTGGGGA
851 GGAAGTCCCT GAGGCCAATG GCTCTGCAGG GAAGAGGAGC AAGAAGAAGA
901 AGCAGCGCAA GCAGACGCC AGTGAGGAAG AGGCACGCGT GGGCGCAGG
951 AAGAGGAAGC GGAGGCACTC GGAAGTTGAA ACAGATTCTA AGAAGAAAAA
1001 GATGAAGCTC CCAGAGCATC CTGAGGGCGG AGAACCAGAA GACGATGAGG
1051 CTCCTGCAA AGGTAAATTC AACTGGAAGG GAACTATTAA AGCAATTCTG
1101 AAACAGGCCC CAGACAATGA AATAACCATC AAAAAGCTAA GGAAAAAGGT
1151 TTTAGCTCAG TACTACACAG TGACAGATGA GCATCACAGA TCCGAAGAGG
1201 AACTCCTGGT CATCTTAAAC AAGAAAATCA GCAAGAACCC TACCTTTAAG
1251 TTATTAAGAG ACAAAGTCAA GCTTGTGAAA TGAACATTG TGTATTTAAA
1301 AATTGAATCC ATTCTGCTGA CTTCTTCCTT TCACTGCTGT TTATAAAATG
1351 TGTAATGAAT TCTAACAAC CAAATTTTGC TTTTGAAGC TGTATTTTAA
1401 AGTTAAGAAA ATATATTTTT GGTATAACTT TTATGAGAAA AATAAAATAT
1451 ATTCTGGTCC AAACCTCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1501 AAA
```

BLAST Results

No BLAST result

Medline entries

93259460:

LYAR, a novel nucleolar protein with zinc finger DNA-binding motifs, is involved in cell growth regulation.

Peptide information for frame 3

ORF from 144 bp to 1280 bp; peptide length: 379
 Category: strong similarity to known protein
 Classification: Cell division
 Prosite motifs: ATP_GTP_A (60-68)

```

1 MVFFTCNACG ESVKKIQVEK HVSVCNCEC LSCIDCGKDF WGGDYKNHVK
51 CISEDQKYGG KGYEGKTHKG DIKQQAUIQK ISELIKRPNV SPKVRELLEQ
101 ISAFDNVPRK KAKFQNMWKN SLKVHNESIL DQVWNIFSEA SNSEPVNKEQ
151 DQRPLHPVAN PHAEISTKVP ASKVKDAVEQ QGEVKKNKRE RKEERQKRRK
201 REKKELKLEN HQENSRNQKP KKRKKGQEAD LEAGGEEVPE ANGSAKGRSK
251 KKKQRKDSAS EEEARVGAGK RKRHRSEVET DSKKKMKMLP EHPEGGEPEP
301 DEAPAKGKFN WKGTIKAILK QAPDNEITIK KLRKKVLAQY YTVTDEHHRS
351 EEELLVIFNK KISKNPFTKL LKDKVKLVK

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_14g5, frame 3

PIR:A40683 cell growth regulating nucleolar protein LYAR - mouse, N = 1, Score = 1410, P = 2.7e-144

SWISSPROT:YQ58_CAEEL HYPOTHETICAL 28.5 KD PROTEIN C16C10.8 IN CHROMOSOME III., N = 1, Score = 381, P = 2.9e-35

TREMBL:AC003058 18 gene: "F27F23.18"; product: "putative RNA-binding protein"; Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence., N = 3, Score = 139, P = 4e-15

PIR:S70049 nucleic acid-binding protein YCR087c-a - yeast (Saccharomyces cerevisiae), N = 1, Score = 164, P = 1.4e-11

>PIR:A40683 cell growth regulating nucleolar protein LYAR - mouse
 Length = 388

HSPs:

Score = 1410 (211.6 bits), Expect = 2.7e-144, P = 2.7e-144
 Identities = 275/388 (70%), Positives = 317/388 (81%)

```

Query:      1 MVFFTCNACGESVKKIQVEKHVSVCNCECLSCIDCGKDFWGGDYKNHVKCISEDQKYGG 60
            MVFFTCNACGESVKKIQVEK VS CRNCECLSCIDCGKDFWGGDYK+HVKCISE QKYGG
Sbjct:      1 MVFFTCNACGESVKKIQVEKQVSNCRNCECLSCIDCGKDFWGGDYKSHVKCISEGQKYGG 60

Query:     61 KGYEGKTHKGDIKQQAUIQKISELIKRPNVSPKVRELLEQISAFDNVPRKKAKFQNMWKN 120
            KGYE KTHKGD KQQAUIQKI+ELIK+PNVSPKVRELL+QISAFDNVP KAKFQNMWKN
Sbjct:     61 KGYEAKTHKGDAKQQAUIQKINELIKKPNVSPKVRELLQQISAFDNVPIKKAKFQNMWKN 120

Query:    121 SLKVHNESILDQVWNIFSEASNSEPVNKEQDQRPLHPVANPHAEIS-TKVPASKVKDAVE 179
            SLKVH++S+L+QVW+IFSEAS+SE ++Q Q P H A PHAE+ TKVP++K E
Sbjct:    121 SLKVHSDSVLEQVWDIFSEASSSE---QDQQQPPSH-TAKPHAEMPITKVPSAKTNGTTE 176

Query:    180 QQGEVKKNKRRERKEERQKRRKREKKELKLENHQENSRNQKPKRRKKGQEADLEAGGEEVP 239
            +Q E KKNKRRERKEERQK RK+EKKELKLENHQEN R QKPKRRKK QEA EA GE+
Sbjct:    177 EQTEAKKNKRRERKEERQKNRKKKEKKELKLENHQENLRGQKPKRRKKNQEAGHEAAGEDGA 236

Query:    240 EANG-----SAGKRSKKKKQRKDSASEEEA----RVGAGKRRK-RHSEVETDSKKKKM 287
            + +G      G+ S++ R E+ A + AGKRRK +HS E+ KKKKM
Sbjct:    237 DSGGPPEKKKAQGGQASEGADRNGGPGEDRAEGQTAKTAAGKRRKPKHSGAESGYKKKKM 296

Query:    288 KLPEHPEGGEPEDEAPAKGKFNWKGTIKAILKQAPDNEITIKLRKKVLAQYYTVTDEH 347
            KLPE PE GE +D EAP+KGKFNWKGTIKA+LKQAPDNEI++KKL+KKV+AQY+ V ++
Sbjct:    297 KLPEQPEEGEAKDHEAPSKGKFNWKGTIKAVLKQAPDNEISVKKLKKKKVIAQYHAVMNDT 356

Query:    348 HRSEELLVIFNKKISKNPFTKLLKDKVKLVK 379
            EEELL IFN+KIS+NPTFK+LKD+VKL+K
Sbjct:    357 SHHEELLAIFNRKISRNPFTKVLKDRVKLLK 388

```

Pedant information for DKFZphtes3_14g5, frame 3

Report for DKFZphtes3_14g5.3

[LENGTH] 379
 [MW] 43634.03
 [pI] 9.59
 [HOMOL] PIR:A40683 cell growth regulating nucleolar protein LYAR - mouse le-122
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YCR087c-a] 2e-11
 [BLOCKS] BL00603D Thymidine kinase cellular-type proteins
 [BLOCKS] BL00530C
 [PROSITE] ATP_GTP_A 1
 [KW] All_Alpha
 [KW] LOW_COMPLEXITY 18.73 %

```

SEQ  MVFFTCNACGESVKKIQVEKHVSVCNRNCECLSCIDCGKDFWGDDYKNHVKCISEDQKYGG
SEG  .....
PRD  cccccccccccccchhhhhhhheeeccccceeeccccccccccccccccccccccccccccccccc

SEQ  KGYEGKTHKGDIKQQAWIQKISELIKRPNVSPKVRELLEQISAFDNVPRKKAKFQNWMMKN
SEG  .....
PRD  cccccccccchhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhccccchhhhhhhhhhhhh

SEQ  SLKVHNESILDQVWNIFSEASNSEPVNKEQDQRPLHPVANPHAEISTKVPASKVKDAVEQ
SEG  .....
PRD  cccccchhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhccccccccccccccccccccccccchhhhh

SEQ  QGEVKKNKRERKEERQKRRKREKKELKLENHQENSARNQPKRRKKGQEADLEAGGEEVPE
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccchhhhhchhhhhcccccccc

SEQ  ANGSAKRSKSKKKQKRDSEEEARVGAGKRRRHSEVETDSKKKKMKLPEHPEGGEPE
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  cccccccchhhhhhhhhccchhhhhhhhhccccccccccccccccccccchhhhhcccccccccccc

SEQ  DEAPAKGKFNWKGTIKAILKQAPDNEITIKLRKKVLAQYYTVDDEHHRSEEEELLVIFNK
SEG  xxxxx.....
PRD  cccccceeehhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhh

SEQ  KISKNPFTKLLKDKVKLVK
SEG  .....xxxxxxxxxxxxx
PRD  cccccchhhhhhhhhhhccccc

```

Prosites for DKFZphtes3_14g5.3

PS00017 60->68 ATP_GTP_A PDOC00017

(No Pfam data available for DKFZphtes3_14g5.3)

DKFZphtes3_14h21

group: nucleic acid management

DKFZphtes3_14h21 encodes a novel 648 amino acid protein with strong similarity to mus musculus RNA helicase and several RNA-dependent ATPases from the DEAD box family.

RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. The novel protein contains a DEAD-box and a ATP/GTP-binding site motif A (P-loop) and is a new member of this subgroup.

The new protein can find application in modulating RNA metabolism and gene expression.

strong similarity to RNA helicases

start at Bp 33 matches Kozak consensus ACNAtg

Sequenced by BMFZ

Locus: unknown

Insert length: 2200 bp

Poly A stretch at pos. 2166, polyadenylation signal at pos. 2140

```
1 CAACGACGTC GGACGCGCCC CTTCTTGGA CAATGTCCCA CCACGGAGGA
51 GCTCCCAAGG CCTCTACGTG GGTCTTGCT AGTCGGCGAA GCTCGACAGT
101 GTCCCGAGCG CCAGAGAGGA GGCCGGCGGA GGAGTTGAAT CGAACAGGTC
151 CTGAGGGATA TAGTGTCGGC AGAGGTGGTC GCTGGAGAGG CACCTCTAGG
201 CCCCAGGAGG CCGTGCCGCG TGGTCACGAG GAACTGCCCG TGTGTTTTGC
251 TTTGAAGAGC CACTTTGTTG GCGCGGTAAT CGGTCTGGT GGGTCAAAAA
301 TAAAGAATAT ACAAAGTACA ACAAACACCA CAATCCAAAT AATACAAGAA
351 CAACCGAAT CATTAGTCAA AATTTTGGC AGCAAGGCAA TGCAAAACGAA
401 AGCAAAAGCA GTGATAGACA ATTTTGTTAA AAAGCTAGAA GAAAATTACA
451 ATTCAGAATG CGGAATTGAT ACTGCATTCC AACCTTCTGT TGGAAAAGAT
501 GGAAGCACAG ATAACAATGT TGTTCAGGA GATCGGCCAT TGATAGATTG
551 GGATCAAATT AGAGAGGAAG GTTTGAAATG GCAAAAAACA AAGTGGGCAG
601 ATTTACCACC AATTAAAGAAA AACTTTTATA AAGAGTCCAC TGCCACAAGT
651 GCCATGTCAA AAGTAGAAGC AGATAGTTGG AGGAAAGAAA ATTTAATAT
701 AACGTGGGAT GACTGAAGG ATGGGGAGAA ACGACCTATC CCCAATCCTA
751 CCTGCACATT TGATGACGCC TTTCAATGTT ATCCTGAGGT TATGGAAGAC
801 ATTAAGAGAG CAGGTTTTTA AAAGCCAACA CCTATTCACT CACAGGCATG
851 GCCCATTTGT TTGCAAGGAA TAGATCTTAT AGGAGTAGCC CAGACTGGAA
901 CAGGAAAGAC ATTGTGTTAT TTAATGCCTG GATTATTATCA TCTGGTCCTT
951 CAACCCAGCC TTAAGAGTCA AAGGAATAGA CCCGGCATGT TAGTTCTAAC
1001 TCCCACTCGG GAATTAGCAC TTCAAGTAGA AGGAGAATGT TGCAAAATAT
1051 CATATAAAGG GCTTCGGAGT GTTTGTGTAT ATGGTGGTGG AAATAGAGAT
1101 GAACAAATAG AAGAGCTTAA AAAAGGTGTA GATATCATAA TTGCAACTCC
1151 CGGAAGATTG AATGATCTGC AAATGAGTAA CTTCTGCAAT CTGAAGAATA
1201 TAACCTACTT GGTTTTAGAT GAAGCAGACA AGATGTTGGA CATGGGATTT
1251 GAACCCAGCA TAATGAAGAT TTTGTTAGAT GTCCGCCAGC ATAGGCAGAC
1301 AGTTATGACC AGTGCTACAT GGCCTCATTC AGTTCATCGC CTCGCACAAT
1351 CTTATTTGAA AGAACCAATG ATTGTCTATG TTGGTACATT GGATCTAGTT
1401 GCTGTAAGTT CAGTGAAGCA AAATATAATT GTAACCACCG AGGAAGAGAA
1451 ATGGAGTCAC ATGCAAACTT TTCTACAGAG TATGTCATCC ACAGACAAAG
1501 TCATTGCTTT CGTTTCTCGA AAAGCTGTTG CGGATCATT ATCAAGTGAC
1551 CTAATACTTG GAAATATATC AGTAGAGTCT CTGCATGGAG ATAGAGAACA
1601 GAGAGATCGG GAGAAAGCAT TAGAGAACTT TAAAACAGGC AAAGTGAGAA
1651 TACTAATTGC AACTGATCTA GCCTCTAGAG GACTTGATGT CCATGACGTT
1701 ACACATGTCT A'AAATTTTGA CTTTCCACGG AATATTGAAG AATACGTACA
1751 CCGAATAGGG CGCACGGGAA GAGCAGGGAG GACTGGTGT TCCATTACAA
1801 CTTTGACTAG AAATGATTGG AGGGTTGCCT CTGAATTGAT TAATATTCTG
1851 GAAAGAGCAA ATCAGAGTAT TCCAGAGGAG CTGTATCAA TGCTGAGAG
1901 GTTTGAGGCA CATCAACGGA AAAGGGAAT GGAAGAGAAA ATGGAAGAGC
1951 CTAAGGAAG GCCCAAGGAG TTTCATTAAT GTCTTCTGTA CTAGTGGGGT
2001 AGAGAATTCA AGATTTTTTA GAAATATAGT AAGACAGAAG TATTGGACAT
2051 GTTGGCAGTA TGAAGAGACC GGACTGATTT GACTGATTCT TAAAATAATA
2101 GTGTTTGAAA ATATAGAATC CAGTGTTTAA TACTTTCTTT AATAAAAAATA
2151 GAAGTATTTA AACTTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 33 bp to 1976 bp; peptide length: 648
 Category: strong similarity to known protein
 Classification: Nucleic acid management
 Prosite motifs: ATP_GTP_A (286-294)
 DEAD_ATP_HELICASE (394-403)

```

1 MSHHGAPKA STWVVASRRS STVSRAPERR PAEELNRTGP EGYSVGRGGR
51 WRGTSRPPEA VAAGHEELPL CFALKSHFVG AVIGRGGSKI KNIQSTNTT
101 IQIIQEQPES LVKIFGSKAM QTKAKAVIDN FVKKLEENYN SECGIDTAFQ
151 PSVGKDGSTD NNVVAGDRPL IDWDQIREEG LKWQTKWAD LPPIKKNFYK
201 ESTATSAMSK VEADSWRKEN FNITWDDLKD GEKRPIPNPT CTFDDAFQCY
251 PEVMENIKKA GFQKPTPIQS QAWPIVLOGI DLIGVAQTGT GKTLCYLMPG
301 FIHLVLQPSL KGQRNRPGLM VLTPTRELAL QVEGECCCKYS YKGLRSVCVY
351 GGGNRDEQIE ELKKGVDDII ATPGRNLNLO MSNFVNLKNI TYLVLEADK
401 MLDMGFEPQI MKILLDVRPD RQTVMTSATW PHSVHRLAQS YLKEPMIVYV
451 GTLDDLAVSS VKQNIIVTTE EEKWSHMQTF LQSMSSTDKV IVFVSRKAVA
501 DHLSSDLILG NISVESLHGD REQRDREKAL ENFKTGKVR I LIATDLASRG
551 LDVHDVTHVY NFDFFRNIEE YVHRIGRTGR AGRTGVSITT LTRNDWRVAS
601 ELINILERAN QSIPEELVSM AERFEAHQOK REMERKMERP QGRPKKFH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_14h21, frame 3

TREMBL:CEY54G11A_9 gene: "Y54G11A.3"; Caenorhabditis elegans cosmid
 Y54G11A, N = 1, Score = 1008, P = 1.1e-101

TREMBL:SPBP8B7_16 gene: "dbp2"; "SPBP8B7.16c"; product: "p68-like
 protein."; S.pombe chromosome II pl p8B7., N = 1, Score = 971, P =
 9.1e-98

PIR:S13757 RNA helicase DBP2 - yeast (Saccharomyces cerevisiae), N = 1,
 Score = 970, P = 1.2e-97

PIR:S14048 RNA helicase dbp2 - fission yeast (Schizosaccharomyces
 pombe), N = 1, Score = 961, P = 1e-96

PIR:A57514 RNA helicase HEL117 - rat, N = 2, Score = 888, P = 7.8e-91

>TREMBL:CEY54G11A_9 gene: "Y54G11A.3"; Caenorhabditis elegans cosmid
 Y54G11A
 Length = 504

HSPs:

Score = 1008 (151.2 bits), Expect = 1.1e-101, P = 1.1e-101
 Identities = 211/473 (44%), Positives = 298/473 (63%)

```

Query: 174 DQIREEGLKWQTKWADLPPIKKNFYKESTATSAMSKVEADSWRKENFNITWDDLKDGEK 233
      D++++E W K PI ++ YK +S + + ++
Sbjct: 23 DRLKDENFSWMK-----PIVRDLYKIPNEQKNLSPEQLQELYTNGGVMKVYPFEEST 75

Query: 234 RPIPNPTCTFDDAFQCYPEVMENIKKAGFQKPTPIQSQAAPIVLQIDLIGVAQTGTGKT 293
      IP P +F+ AF +M I+K GF+KP+PIQSQ WP++L G D IGV+QTG+GKT
Sbjct: 76 VKIPPPVNSFEQAFGSNASIMGEIRKNGFEKPSPIQSQMWPPLLSGQDCIGVSQTGSGKT 135

Query: 294 LCYLMPGFIHLVLQPSL-----KGQRNRPGLMVLTPPTRELALQVEGECCCKYSYKGLRSVC 348
      L +L+P +H+ Q + + Q+ P +LVL+PTRELA Q+EGE KYSY G +SVC
Sbjct: 136 LAFLLPALLHIDAQLAQYEKNDDEQKPSPFVLVLSPTRELAQQIEGEVKKYSYNGYKSV 195

Query: 349 VYGGGNRDEQIEELKKGVDDIIATPGRNLNLOMSNFVNLKNITYLVLEADKMLDMGFEP 408

```

+YGGG+R EQ+E + GV+I+IATPGRL DL ++L ++TY+VLDEAD+MLDMGFE
 Sbjct: 196 LYGGGSRPEQVEACRGGVEIIVATPGRLTDLSDNGVISLASVTYVVLDEADRMLDMGFEV 255
 Query: 409 QIMKILLDVRPDRQTVMTSATWPHSVHRLAQSYLKPMIVYVGTLDLVAVSSVKQNIIVT 468
 I +IL ++RPDR +TSATWP V +L Y KE ++ G+LDL + SV Q
 Sbjct: 256 AIRRILFEIRPDRLVALTSATWPEGVRKLTDKYTKEAVMAVNGSLDLTCKSVTQFFEFV 315
 Query: 469 TEEKW---SHMQTFLQSMSSTD-KVIVFVSRKAVADHLSSDLILGNISVESLHGDREQR 524
 + ++ + FL + + K+I+V K +ADHLSSD + I+ + LHG R Q
 Sbjct: 316 PHDSRFLRVCEIVNFLTAAHGQNYKMIIFVKSKVMADHLSSDFCMKGINSQGLHGGRSQS 375
 Query: 525 DREKALENFKTGKVRILIAITDLASRGDLVDVHTVYNFDFPRNIEEYVHRIGRTGRAGRT 584
 DRE +L ++G+V+IL+ATDLASRG+DV D+THV N+DFP +IEEYVHR+GRTGRAGR
 Sbjct: 376 DREMSLNLRSGEVQILVATDLASRGIDVDPDITHVLNYDFPMIDIEEYVHRVGRTRGRGRK 435
 Query: 585 GVSITTLTRNDWRVASELINILERANQSIPEELVSMARFEAHQRKREMERKMERPPQGRP 644
 G +++ L ND LI ILE++ Q +P+L AE++ K + R RP R
 Sbjct: 436 GEAMSFLWWNDRSNFEGLIQILEKSEQEVPDQLRRDAEKYRL---KCQSGRDGPRPSFRN 492
 Query: 645 KK 646
 K
 Sbjct: 493 NK 494

Pedant information for DKFZphtes3_14h21, frame 3

Report for DKFZphtes3_14h21.3

[LENGTH] 648
 [MW] 72873.51
 [pI] 8.84
 [HOMOL] TREMBL:CEY54G11A_9 gene: "Y54G11A.3"; Caenorhabditis elegans cosmid Y54G11A 1e-101
 [FUNCAT] 04.01.04 rna processing [S. cerevisiae, YNL112w] 2e-97
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YNL112w] 2e-97
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPL119c] 4e-72
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR204w] 2e-70
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YOR204w] 2e-70
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YBR237w] 1e-61
 [FUNCAT] 1 genome replication, transcription, recombination and repair [H. influenzae, HI0892] 2e-49
 [FUNCAT] j mrna translation and ribosome biogenesis [H. influenzae, HI0231 RNA] 1e-48
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YDL160c] 9e-45
 [FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YMR290c] 3e-44
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YJL033w] 2e-36
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YOR046c] 7e-32
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YDR194c] 2e-28
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL064c] 5e-10
 [FUNCAT] 11.10 cell death [S. cerevisiae, YMR190c] 2e-08
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YMR190c] 2e-08
 [FUNCAT] r general function prediction [M. jannaschii, MJ1401] 1e-07
 [BLOCKS] BL00039D DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039C DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039B DEAD-box subfamily ATP-dependent helicases proteins
 [BLOCKS] BL00039A DEAD-box subfamily ATP-dependent helicases proteins
 [PIRKW] nucleus 4e-96
 [PIRKW] RNA binding 3e-87
 [PIRKW] DEAD box 5e-50
 [PIRKW] transmembrane protein 4e-27
 [PIRKW] DNA binding 3e-67
 [PIRKW] recF recombination pathway 3e-10
 [PIRKW] ATP 4e-96
 [PIRKW] purine nucleotide binding 5e-50
 [PIRKW] P-loop 4e-96
 [PIRKW] hydrolase 9e-45
 [PIRKW] protein biosynthesis 5e-50
 [PIRKW] ATP binding 1e-61
 [SUPFAM] WW repeat homology 8e-88
 [SUPFAM] DEAD/H box helicase homology 4e-96
 [SUPFAM] unassigned DEAD/H box helicases 7e-87
 [SUPFAM] ATP-dependent RNA helicase DBP1 4e-96
 [SUPFAM] ATP-dependent RNA helicase DHH1 2e-43
 [SUPFAM] recQ protein 3e-10
 [SUPFAM] Bloom's syndrome helicase 5e-07
 [SUPFAM] translation initiation factor eIF-4A 5e-50
 [SUPFAM] recQ helicase homology 3e-10
 [SUPFAM] tobacco ATP-dependent RNA helicase DB10 8e-88
 [PROSITE] DEAD_ATP_HELICASE 1

```

[PROSITE]      ATP_GTP_A      1
[PFAM]         Helicases conserved C-terminal domain
[PFAM]         KH domain family of RNA binding proteins
[PFAM]         DEAD and DEAH box helicases
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY      8.49 %

SEQ      MSHGGGAPKASTWVVASRRSSTVS RAPERRPAEELNRTGPEGYSVGRGGRWRGTSRPPEA
SEG      .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD      cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      VAAGHEELPLCFALKSHFVGAVIGRGGSKIKNIQSTNTTTIQUIEQEPESLVKIFGSKAM
SEG      .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD      cccccccccchhhhhccccceeeccccccccccccccccccccccccccccccccccccchh

SEQ      QTKAKAVIDNFVKLEENYNSECIDTAFQPSVGKDGSTDNVNVAGORPLIDWDQIREEG
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccc

SEQ      LKWQKTKWADLPPIKKNFYKESTATSAMSKEADSWRKENFNITWDDLKDGEKRPIPNPT
SEG      .....
PRD      chhhhhhhccccccccccccccccccccccccchhhhhhhhhhhhhhhheeecccccccccccccc

SEQ      CTFDADFQCYPEVMENIKKAGFQKPTPIQSQAWPVLQIGIDLIGVAQTGTGKTLCYLMPG
SEG      .....
PRD      cccccccccchhhhhhhhhhhccccccccccccccccccccccccccccccccccccccccce

SEQ      FIHLVLQPSLKGQRNRPGLVLTPTRELALQVEGECCCKYSYKGLRSVCVYGGGNRDEQIE
SEG      .....
PRD      eeeccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhh

SEQ      ELKKGVDIIATPGRLNDLQMSNFVNLKNITYLVLEADKMLDMGFEPQIMKILLDVRPD
SEG      .....
PRD      hhhhhceeeccccccccchhhhhhhccccccccccccccccccccccccchhhhhhhhhhhcccc

SEQ      RQTVMTSATWPHSVHRLAQSYLKEPMIVYVGTLDLVAVSSVKQNIIVTTEEEKWSHMOTF
SEG      .....
PRD      ceeeeeeccccchhhhhhhhhhhhhheeeccccccccccccccccccccchhhhhchhhhhhhhh

SEQ      LQMSSTDKIVFVSRKAVADHLSSDLILGNISVESLHGDREQRDREKALENFKTGKVRI
SEG      .....
PRD      hhhhhccccccccccccchhhhhhhhhhhhhccccccccccccccccchhhhhhhhhhhccccce

SEQ      LIATDLASRGLDVHDVTHVYNFDFPRNIEEYVHRIGRTGRAGRTGVSITTLTRNDWRVAS
SEG      .....
PRD      eeehhhhhhccccccccccccccccccccccccccccccccccccccccccccccccchhh

SEQ      ELINILERANQSIPEELVSMARFEAHQRKREMERKMERPOGRPKKFH
SEG      .....
PRD      hhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccc

```

Prosites for DKFZphtes3_14h21.3

```

PS00017      286->294      ATP_GTP_A      PDOC00017
PS00039      394->403      DEAD_ATP_HELICASE      PDOC00039

```

Pfam for DKFZphtes3_14h21.3

```

HMM_NAME      DEAD and DEAH box helicases

HMM            *gLpPWILRnIyeMGFEKPTPIQQqAIPiILeGRDVMACAQTGSGKTAAF
Query          248      QCYPEVMENIKKAGFQKPTPIQSQAWPVLQIGIDLIGVAQTGTGKTLCY      296

HMM            LIPMLQHDIdwPWPqpPQd..PrALILAPTRELAMQIEEcRkFgkHMNg
Query          297      LMPGFIHLVLQP-SLKGQRNRPGLVLTPTRELALQVEGECCCKYSYK-G-      343

HMM            IRImcIYGGtnMRdQMRmLeRgPpHIVIATPGRLIDHIERgtldLDRIeM
Query          344      LRSVCVYGGGNRDEQIEELKKGv-DIIATPGRLNDLQMSNFVNLKNITY      392

HMM            LVMDEADRMMLDMGFIDQIRrIMrQIPMpwnRQTMFSATMPdeIqELARr
Query          393      LVLDEADKMLDMGFEPQIMKILLDVR--PDRQTVMTSATWPHSVHRLAQs      440

```

```

HMM          FMRNPiRInId.MdElTtnEnIkQwYiyVerEMWKfdclcrLIE*
          +++++P + ++ D + + + +KQ +I+ E++K + + + +
Query        441 YLKEPMIVYVGTLDLVAVS-SVKQNIIVTT-EEEKWSHMQTFLO 482

HMM_NAME     KH domain family of RNA binding proteins

HMM          *rIiIPedhMGMIIGKGGsNIRqIREEYgvrINIPdecCeDstdRIITit
          + + + + +G++IG+GGS I++I++ + + + I I++E+ + + + I
Query        71 CFALKSHFVGAVIGRGGSKIKNIQSTTNTTIQIIQEQ-P---ESLVKIF 115

HMM          G*
          G
Query        116 G 116

HMM_NAME     Helicases conserved C-terminal domain

HMM          *EileeWLknl....GirvmYIHGdMpQeERdeImddFNnGEynVLicTD
          + + + L+ + +I+V.++HGD++Q++R+++++F++G+ ++LI+TD
Query        497 KAVADHLSSDLILGNISVESLHGDREQRDREKALENFKTGKVRILIATD 545

HMM          VggRGIDIPdVNHVINYDMPWNPEqYIQRIGRTgRIG*
          + + +RG+D+ DV HV+N+D+P+N+E Y++RIGRTGR+G
Query        546 LASRGLDVHDVTHVYNFDFPRNIEEYVHRIGRTGRAG 582

```


DKFZphtes3_14p14

group: testes derived

DKFZphtes3_14p14 encodes a novel 159 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, few EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 3969 bp

Poly A stretch at pos. 3948, polyadenylation signal at pos. 3927

```
1 GAAGCCCAGG CTCTCCTTAG TTGACTGTGT GTTAATCACC CAGCAATTTTC
51 ATTACTCAAC AGCTCTCCAG AGTTGCACAT TACAGCTGGG GTAGAAATTG
101 GGTGCTGAAG GCCAGGCAGA GCATTTGGCT GTAGGGAGGC CGATCCTCCT
151 CGGGCCTGTT ACCGCGGGT CTTTGTCTT AGACCTGGGG TTCTTGGCCT
201 CACGGATTCC AAGGAATGGA ACGTTGGGCC ATGCGTGTGA ACGAGCTCTA
251 TGTCGATGAC CCAGACAAGG ACAGCGGTGG CAAGATCGAC GTCAGTCTGA
301 ACATCAGTTT ACCCAATCTG CACTGCCAGT TGGTTGGGCT TGACATTCAG
351 GATGAGATGG GCAGGCACGA AGTGGGCCAC ATCGACAAC CCATGAAGAT
401 CCCGCTGAAC AATGGGGCAG GCTGCCGCTT CGAGGGGCAG TTCAGCATCA
451 ACAAGGTATG GAAGCCCTGC CTCAGCCCTT TCTACCTGCT CCCCTTTCCT
501 GCTGTCTCCC CGTCCCTGG AAACCTGGTTG TGGAGGCACT CACTCGACCT
551 GACCCTGACA CAGCCCCCAG CAAGCGAGGG TTCGTGTCCA GCTGCCTGGC
601 CTTTCCCTGT AGAATCTGG ATGGGGGTCC AGGCTCCCTG GGGTTTAAAG
651 CCCCTGATGG CTGGTTCAGG AAGGAGCTAC TCTTCTCTCC AGTGAGGGGG
701 ACAATGATGA GAAGACCTGA GGATTGTCAG CCCCCAGCCC TGGGTTCAAG
751 TCCCAGCTCT ACCCTTCTT GGCCCTTACA AGTCACTTGA CCCATCTTAG
801 GCTGAGGGTG TGATGGCGAT AATAGTATCA CGATACCACC CACTTCACAA
851 AGTTTGTGTG GGGATTAAAT GAGCTAATGC AGATTCATC ATTCAGAAAA
901 ATTTTGAATG GGCACGTTCT GTGTTCAGG GTCGGTGATA GCGCTCGGGG
951 CAGCGTTCCT GGCTGGTGG GGCTCCCAT CTGGTAGAGG GAGACAGTCT
1001 ACAAACCCAG AAGCATCAGG GATGCTAAGT GCAGTGATGA GGAATAAAGC
1051 CAAGGGGAGT GAGATGAGG GGGCTTGAAA GTACCTTGTC CGCTCAAGG
1101 GACCATTCAA GGTTCACGTG TGTTTGTGCC TCAGAACCAG GAGCTTCAGA
1151 TCCTAAGTCA AGTGGGTGAA CGCACTGCC TTGGGAGGGC CGAGGCCACC
1201 GGTGGCAGCT GGCAGGGTTT TGCTCAGCAC GTGCCGGCCT TCCTCGAAGC
1251 TCGGTACTGT CACAGTGGAG CCTCTCAACA ACCTGTGTAG GCAGCACCAT
1301 TTGACAGGTT AGGATGCTGG GGCCAGAGA GGTAAAGTGT CTTGCCCGAG
1351 GTCACACAGC TATCTGCATG TCCCACAAC CCCTTCCCA GCCCCAGCCA
1401 AACTGAGCCA CTGGCCACTC CTGGCTTCTC CTGTCCCTC CTGCAGCCTC
1451 TGCTCAGAAC GGCCTTCTC CAGACCCTGA CACCTGAGT GGGGTGCGAA
1501 AGTCACTGGC CACATCCAGC CCAAAGATAA ATTTTGTGTT TCCAGTATAG
1551 CATTTAACTG CATCAGAAC AGTATGAAAA GACCAGGAAT CCAGATTTCT
1601 GGCTTTTAAA AGTCAGAGGC TCTCACTACA CTGGGTCCGT GTTCCCGCTA
1651 TGACAATGAC CTGGCACCAA TGGGCAGTGT TCCCCTTTAG AGAGGGTGTG
1701 TGCTGTCCCT TCCCACAGTC CCTGGCAGGC GGCTGGAAGG CCAGGCCTGG
1751 TCATCTGTCA AGCAGGGTGG ACTTCTTACG TGACAGTTCA GGGCTCCCTT
1801 AAGTGCTAAA GCAGAAGCTG CAAGGCTTTC TTAAGGTTTC GAGTGTGCT
1851 GGGAGAAATC TGCTGCATGT TGTGGGTAA AGGGAGTCTC TCACCAGCCC
1901 AGGCCCTCAG GAGGAGGAGA TACCAGGAGG CAGGGATGCT GGGGGTCGTG
1951 GTTCACTGGG GGCTCTCTCT GCCCATGAGC TGCCACACAG CACCTTTGCC
2001 ATGCCCCGTA ATTTGGATTT TATGGTGGTT GTGATGGAAG GCCATTTGAG
2051 GGTTTTGAAC AGGGAGGCAA TGTAAATCAGA TTTATGCCCT AGAACTGGAC
2101 TATCCAATAG GTTGCCACCA GCCACATAAG GCTATTTAAA TTAATTCAAA
2151 TTAATGTGAC AATTCACTCA CTCAATCTCA TCAACCACAT TTCAAGTGCT
2201 CAAAGCCACG TGCTGGCTAG GGGCCACAGC GTTAGACAGT GCAGAGAGAA
2251 AGCACTTCCA TCGCTGAGGA AAGTTCTGCT GGACCGCACA CCCTTAGAAG
2301 GATGGCTCTG GTGGCCGGGC GCGGTGGCTC AAACCTGTAA TCCCAGCACT
2351 TTGGGAGGCC GAGTGGGTG GATCACGAGG TCAGGAGATC GAGACCATCC
2401 CGGCTAACAT GGTGAAACCC TGCTCTACT AAAAATACAA AAAAAACAA
2451 AATTAGCCGG GCGTGGTTGC GGGCACCTGT AGTCCAGCT ACTCAGGAGG
2501 CTGAGCGCGG AGAATGGCAT GAACCCGGGA GGTGGAGCTT GCAGTGAGCC
2551 AAGATCGTAC CACTGCACTC CAGTCTGGGC GACAGAGTGA GACTCCATCT
2601 CAAAACAAAC AAAAAAGGA TGGGGCTGGG CTGGAGAGGG TGGCAGGCAG
2651 TGATTGTGGC AGTGGAGCTG GGGAGATGTG GTCGGATTAG GGAGGTAGAA
2701 TCAATAAGAC TCAGTGAAGA ATCGCATGTG GGGGTAAGGG CACATGTGGA
```

```

2751 AGCAAAGAAA CCTTTGACGT CTTTGTCTTG ACAACCGGGT GGTCTGTGTT
2801 CTAGACATGG AAGCTTAGAA AAGCCTGGAG TCTGTGGGAA GTAGGTAGGG
2851 CTGGGCACTG GTCATTCCAC TCTGGTTTCC TTTGGGGTTC CCATTAGGTG
2901 TCTACAGGGA GAGGTGAAAT TGGAGTTGG AGGTGTGGAG AGTTCAGGAG
2951 AGGGTTCTGG ACCACAGATG TTGAGGTGGG AGTCATTAGT GAATAGATGA
3001 TGTGGAAGT CATGGGTCCT CAGAGTGGGG GCTCCTTAAG CCTCCAGGCC
3051 AGCAGCATCA GCATCACCTG GGAGATTGTT AGGAATGCAG ATTCTCAGGC
3101 CCCCCTAAGA CCCACCGACT CTGTGCTAGA ACAAGCGCCC CTCAGAGATT
3151 CTGATGCCAC TGAAGTTTGA GGAGCATTGG TTTAAGCAAG ATTACCTACG
3201 GAGAGGCTGT AGATCCGTGT TCTAAACCTG GGGTCCACAG ACACCCCCAA
3251 GAAGAGCGGA TTGAATGCAA GAGATCTATG AAGTTGGATG GGGGAAAAAT
3301 TGACATCTTT ATTTTGTGTA AACTCGATCT AAAGTTTAGC ATTTCCATCT
3351 GCGATGAATG TAGGCCACAA ACCACAGTAG TATTAGCAGT GCCTGGGACC
3401 TCCTCAACAA CAGAAATTGC CGGTATTTAT AGCACGTTAC AGTTGTTGCA
3451 GATAATTTCC AGAGACTGTT TATATGCACC ACTGTTTAA AATTACGGTG
3501 ATTGCCAGG TGCACTGGCT CACACCTGTA ATCCAGCAC TTTGGGAGGC
3551 CAAAGTGGGT GGATCACTG AGGAGTTCAA GACCAGCCTG GTCAACATGT
3601 CAAAACCTG TATCTACAAA AAAATACAAA AGTTAACCAA GCCTATGCTT
3651 GTAGTCACAG CTACTCGGGA GGCCGAGGTG GGAGGGTCTT CTGAGCCCAG
3701 GGAGGTAGAG GCTTCAGTGA GCTGAGATCG CACCACCACA CTCCAGCCTG
3751 GGTGACAGAG TGAACCCCTT AATCAATCAG TCAATAAAAA TTACAGTAAT
3801 TATTAGACCC ACCACTAGGT CATCTTATT GATGCATCAG TAAAGCAGCA
3851 TATTCAAATG TGGATTTTAA AATATTTTAA TTACTATTTA AATATCTCTT
3901 TACTTTGTAA TCCTATGCAT TTTACGCATT AAAACATTTT AAGCATTTAA
3951 AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 216 bp to 692 bp; peptide length: 159
 Category: putative protein
 Classification: no clue

```

1 MERWAMRVNE LYVDDPKDS GKKIDVSLNI SLPNLHCELV GLDIQDEMGR
51 HEVGHIDNSM KIPLNNGAGC RFEGQFSINK VWKPCLSFY LLPFPAVSPL
101 PGNWLWRHSL DLTLTQPPAS EGSCPAWPF LLRIWMGVQA PWGFKPLMAG
151 SGRSYSSLQ

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_14p14, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_14p14, frame 3

Report for DKFZphtes3_14p14.3

```

(LENGTH)      159
(MW)           17778.55
(pI)           5.74
(FUNCAT)       99 unclassified proteins      [S. cerevisiae, YAL042w] 5e-04
(KW)           Alpha_Beta

```

```

SEQ  MERWAMRVNELYVDDPKDSGGKKIDVSLNISLPNLHCELVGLDIQDEMGRHEVGHIDNSM
PRD  ccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc
SEQ  KIPLNNGAGCRFEGQFSINKVWKPCLSFYLLPFPAPVSPPLGNWLWRHSLDLTLTQPPAS
PRD  eeeeeeeeeeeeecccccccccccccccccccccccccccccccccccccccccccccccccc

```

SEQ EGSCPAAWPFLRLIWMGVQAPWGFKPLMAGSGRSYSSLQ
 PRD cccccchhhhhhhhhhhcccccccccccccccccccccccc

(No Prosite data available for DKFZphtes3_14p14.3)

(No Pfam data available for DKFZphtes3_14p14.3)

DKFZphtes3_14p7

group: testes derived

DKFZphtes3_14p7 encodes a novel 702 amino acid protein with very weak similarity to kinesin associated protein KAP3.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

weak similarity to kinesin associated protein KAP3

complete cDNA, complete cds, few EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 2497 bp

Poly A stretch at pos. 2424, polyadenylation signal at pos. 2400

```
1 GGAATCCAAA GAAACAGTTA TGATGGGGGA CTCTATGGTG AAAATAAATG
51 GGATTTATTT AACAAAATCA AATGCTATTT GCCACTTAAA GAGTCACCCA
101 CTTCAGCTAA CTGATGATGG AGGCTTCAGT GAAATAAAGG AGCAAGAAAT
151 GTTCAAAGGA ACAACATCTT TACCATCTCA TCTCAAGAAT GGAGGGGACC
201 AGGGGAAGAG ACATGCGAGG GCCTCATCAT GCCCCAGTAG CTCAGACCTG
251 AGCAGGCTGC AAACCAAAGC AGTCCCAAAA GCTGACCTGC AAGAAGAGGA
301 CGCAGAAATA GAAGTAGACG AAGTCTTTTG GAATACAAGG ATTGTACCGA
351 TTTTGCCTGA ATTAGAAAAG GAAGAAAACA TTGAACGGT TTGTGCTGCT
401 TGCACACAAC TTCATCATGC TTTAGAGGAA GGAAACATGC TTGGAATAAA
451 ATTTAAGGGA AGAAGTATTC TCCTGAAGAC CCTGTGTAAG CTAGTTGATG
501 TTGTTTCAGA CTCGCTCAGC CTTAAACTTG CAAAAATAAT TCTAGCACTT
551 AAAGTGAGTA GAAAGAATCT TCTTAATGTC TGCAAACTTA TATTTAAAT
601 TAGCAGGAAT GAGAAGAATG ATTCTTTGAT TCAAAATGAC AGCATTCTGG
651 AATCATTATT GGAGGTACTA AGAAGTGAAG ACCTGCAAAAC TAACATGGAA
701 GCTTTTTTAT ACTGTATGGG GTCTATAAAG TTCATTCTG GAAATCTGGG
751 ATTTCTTAAT GAAATGATCA GCAAAGGTGC TGTGGAATA CTGATAAATT
801 TGATAAAACA AATAAATGAG AACATCAAGA AATGTGGTAC ATTTTGCCT
851 AATTCGGGCC ACTTGCTAGT CCAGGTGACT GCTACATTGA GAAACTTGTT
901 TGATTCATCA TTAGTAAGAA GTAAGTTCCCT AAACATCAGT GCCCTTCCCC
951 AGCTCTGCAC GGCAATGGAA CAGTACAAGG GTGACAAGGA CGTCTGTACC
1001 AATATTGCCA GAATATTGAG CAAACTTACT TCTTACCGTG ACTGCTGCAC
1051 AGCCTTGGCC AGCTATTCCA GATGTTATGC CTTATTTCTG AATCTAATTA
1101 ACAAATACCA GAAGAAGCAG GATTTAGTCG TCCGTGTTGT TTTTATTCTT
1151 GGCAACCTGA CGGCAAAAAA TAACCAAGGCT CGTGAACAAAT TTTCCAAAGA
1201 GAAAGGGAGC ATCCAAACTC TGCTGTCATT ATTCAGACG TTCCATCAGC
1251 TGGATCTGCA TTCCAGAAAG CCGGTGGGCC AACGAGGCGA GCAGCACAGG
1301 GCGCAGAGGC CGCCGTCAGA GGCAGAGGAC GTGCTCATCA AGCTGACTCG
1351 TGTGCTGGCC AACATTGCCA TCCACCCGGG CGTGGGCCCG GTGCTGGCCG
1401 CCAACCCGGG GATAGTGGGC CTGCTCCTGA CCACGCTGGA ATACAAGTCA
1451 CTTGATGATT GTGAGGAGCT GGTGATCAAT GCTACAGCGA CAATCAACAA
1501 TTTATCTTAC TACCAAGTGA AGAATTCCAT AATCAAGAC AAAAAGCTAT
1551 ATATTGCTGA ATTGCTCTTA AAGCTTCTTG TCAGTAACAA CATGGATGGA
1601 ATCCTGGAGG CTCTGCGTGT TTTCGGAAAT CTCTCCCAGG ACCATGATGT
1651 CTGCGATTTC ATTGTGCAGA ACAATGTCCA CAGGTTTCATG ATGGCGCTGC
1701 TGGATGCTCA GCATCAGGAT ATCTGCTTTT CTGCCTGTGG TGTCTCCTC
1751 AATCTCACTG TGGATAAAGA CAAGCGTGTG ATCTTGAAG AAGGAGGTGG
1801 CATTAATAAG TTAGTGGACT GTTAAAGAGA TTTGGGTCCT ACTGATTGGC
1851 AGCTGGCCTG CTGCTTTGT AAAACTTTAT GGAACCTCAG TGAAAACATC
1901 ACTAATGCTT CGTCATGTTT TGGAAATGAA GACACCAACA CACTCTTACT
1951 CTTGCTCTCA TCATTTTGTAG ATGAAGAACT AGCACTGGAT GGCAGTTTGT
2001 ATCCAGACCT AAAAAACTAT CACAAACTCC ATTGGGAAAC AGAATTCAAA
2051 CCTGTGGCAC AGCAGCTTCT AAACCGAATT CAGAGACATC ACACCTTCCT
2101 GGAACCCCTG CCCATTCCCT CTTTCTAACA TGATGCAGAT TAACAGTAGA
2151 AACGAGAACT CACGTCTCCC TCATTCTTAA GAACTGGTAA CAAACGTGAA
2201 CATTTTTTTC AGCATTAAACA AATGTGGAAA GTTTTTCAAG AACTGGTTTT
2251 AGTGAGTAGC TGAAGTATTT TTTAAATTA AGCATTCTT CTGTGTTAGT
2301 ATTATGAAAA AATGAATATA CACATTATAT TTCCTGTTGA GAGAAATGTA
2351 AGATGAAAAA ATGTGCATTT TCAAGTAAAT GACTTTTTCT TCTATTCTCT
2401 ATTAACAAT TTAGTTCTAG TCTTAAAAAA AAAAAAATAA AAAAAAATAA
2451 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 20 bp to 2125 bp; peptide length: 702
 Category: putative protein

```

1 MMGDSMVKIN GIYLTGSNAI CHLKSHPLQL TDDGGFSEIK EQEMFKGTTS
51 LPSHLKNGGD QGKRHARASS CPSSSLSRL QTKAVPKADL QEEDAEIEVD
101 EVFWNTRIVP ILRELEKEEN IETVCAACTQ LHHALEEGNM LGNKFKGRSI
151 LLKTLCKLVD VGSDSLKL AKIILALKVS RKNLLNVCKL IFKISRNEKN
201 DSLIQNDSIL ESLLVLRSE DLQTNMEAFI YCMGSIKFIS GNLGFLNEMI
251 SKGAVEILIN LIKQINENIK KCGTFLPNSG HLLVQVTATL RNLVDSSLVR
301 SKFLNISALP QLCTAMEQYK GDKDVCTNIA RIFSKLTSYR DCCTALASYS
351 RYALFLNLI NKYQKKQDLV VRVVFILGNL TAKNNQAREQ FSKEKGSIQI
401 LLSLFQTFHQ LDLHSQKPVG QRGEQHRQR PPSEAEVLI KLTRVLANIA
451 IHPGVGPVLA ANPGIVGLLL TTLEYKSLDD CEELVINATA TINNLSYYQV
501 KNSIIQDKKL YIAELLLKLL VSNMMDGILE AVRVEGNLSQ DHQVCDFFIVQ
551 NNVHRFMAL LDAHQDICEF SACGVLLNLT VDKDKRVILK EGGGIKKLVD
601 CLRD LGPTDW QLACLVCCTL WNFSENITNA SSCFGNEDTN TLLLLSSFL
651 DEELALDGSF DPDLKNYHKL HWETEFPKVA QOLLNRIQRH HTFLEPLPIP
701 SF

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFzptes3_14p7, frame 2

TREMBL:MMD367_1 product: "KAP3B"; Mus musculus mRNA for KAP3B,
 complete cds.; N = 2, Score = 97, P = 0.00039

>TREMBL:MMD367_1 product: "KAP3B"; Mus musculus mRNA for KAP3B, complete
 cds.

Length = 772

HSPs:

Score = 97 (14.6 bits), Expect = 3.9e-04, Sum P(2) = 3.9e-04
 Identities = 45/163 (27%), Positives = 77/163 (47%)

Query: 442 LTRVLANIAIHPGVGPVLAANPGIVGLLLTTLEYKSLDDCEELVINATATINNLSYYQVK 501
 L +++ NI+ H G P VG L + S D+ EE VI T+ NL+ +
 Sbjct: 483 LMKMIRNISQHDG--PTKNLFIDYVGDIAAQI---SSDEEEFVIECLGTLANLTIPDLD 537

Query: 502 -NSIIQDKKLYIAELLLKLLVSNMMDG-ILEAVRVFGNLSQDHQVCDFFIVQNNVHRFMMA 559
 +++++ KL + L KL D +LE V + G +S D + + + + ++
 Sbjct: 538 WELVLKEYKL-VPFLKDKLKPAAEDDLVLEVIMIGTVSMDDSCAALLAKSGIIPALIE 596

Query: 560 LLDAQHQDICEFSACGVLL---NLTVDKDKR-VILKEGGGIKKLVDCLRD 604
 LL+AQ +D F C ++ + + R VI+KE L+D + D
 Sbjct: 597 LLNAQQEDEF-VCQIIYVFYQMFVHQATRDVIKETQAPAYLIDLMD 644

Score = 77 (11.6 bits), Expect = 3.9e-04, Sum P(2) = 3.9e-04
 Identities = 42/178 (23%), Positives = 82/178 (46%)

Query: 169 KLAKIILALKVSRKNLLNVCK-LIFKISRNEKNDSLIQNDSILESLLVLRSEDLQTNME 227
 K K L V ++ LL V L+ ++ + + + ++N +I+ L+ L + N E
 Sbjct: 263 KTFKKYQGLVVKQEQLLRVALYLLNLAEDTRTELKMRNKNIVHMLVKALDRD----NFE 318

Query: 228 AFLYCMGSIKFISGNLGLFNEMISKGAVEILINLIKQINENIKKCGTFLPNSCHLLVQVT 287
 + + +K +S + N+M+ VE L+ +I +E++ L + +
 Sbjct: 319 LLILVVSFLKKLSIFMENKNDMVEMDIVEKLVKMIPCEHEDL-----LNITLR 366

Query: 288 ATLRLNVDSLVRSKFLNISALPQLCTAM--EQYKGDKDVCT--NIARI--FSKLTSYRD 341
 L D+ L R+K + + LP+L + E YK +C +I+ F + +Y D
 Sbjct: 367 LLLNLSFDTGL-RNKMVQVGLLPKLTALLGNENYK-QIAMCVLYHISMDDRFSMFAYTD 424

Query: 342 CCTAL 346
C L
Sbjct: 425 CIPQL 429

Score = 69 (10.4 bits), Expect = 2.6e+00, Sum P(2) = 9.2e-01
Identities = 35/146 (23%), Positives = 70/146 (47%)

Query: 512 IAELLKLLVSNMMDGILEAVRVFGNLSQDHDVCD FIVQNNVHREMMALLDAQHQDICFS 571
I +L+K L +N + ++ V LS + + +V+ ++ ++ ++ +H+D+
Sbjct: 304 IVHMLVKALDRDNFELLILVVSFLKKLSIFMENKNDMVEMDIVEKLVKMIPCEHEDLLNI 363

Query: 572 ACGVLLNLTVDKDKRVILKEGGGIKKLVDCRLDGLPTDW-QLACLVCCKTLWNFSENITNA 630
+LLNL+ D R + + G + KL L G ++ Q+A +C L++ S +
Sbjct: 364 TLRLLNLSFDTGLRNKMVQVGLLPKLTALL---GNENYKQIA--MC-VLYHISMD-DRF 416

Query: 631 SSCFGNEDT-NTLLLLSSFLDEELALD 657
S F D L+ +L DE + L+
Sbjct: 417 KSMFAYTDCIPQLMKMLFECSDERIDLE 444

Score = 68 (10.2 bits), Expect = 3.2e-03, Sum P(2) = 3.2e-03
Identities = 18/58 (31%), Positives = 30/58 (51%)

Query: 190 LIFKISRNEKN-DSLIQND SILESLEVL RSE-----DLQTNMEAFLYCMGSIK FISC 241
LI +++RN N + L+ N++ L +L VLR + +L TN+ +C S G
Sbjct: 155 LILQLARNPDNLEELLNLTALGALARVLRDQKQSVELATNIIYIFFCFSSFSHFHG 212

Score = 65 (9.8 bits), Expect = 6.4e+00, Sum P(2) = 1.0e+00
Identities = 26/122 (21%), Positives = 53/122 (43%)

Query: 283 LVQVTATLRNL----VDSSLVRSKFLNISALPQLCTAMEQYKGDQDVCTNIARIFSKLTS 338
+++ TL NL +D LV ++ +P L ++ +D+ + I S
Sbjct: 521 VIECLGTLANLTIPDLWELVLKEY---KLVPFLKDKLPGAAEDDLVLEV V-IMIGTVS 576

Query: 339 YRDCCTALASYSRCYALFLNLINKYQKKQDLVVRVVFILGNLTAKNNQAREQFSKEK GSI 398
D C AL + S + L+N Q+ + V +++++ + + R+ KE +
Sbjct: 577 MDDSCAALLAKSGIIPALIELLNAQQEDDEFVCQIIYVFYQMV F-HQATRDVIKETQAP 635

Query: 399 QTL LSL 404
L+ L
Sbjct: 636 AY LIDL 641

Score = 65 (9.8 bits), Expect = 6.4e+00, Sum P(2) = 1.0e+00
Identities = 44/177 (24%), Positives = 79/177 (44%)

Query: 481 CE-ELVINATATIN-NLSYYQ-VKNSIIQDKKLYIAELLKLLVSNMMDGILEAVRVFGN 537
CE E ++N T + NLS+ ++N ++Q + + L LL + N I A+ V +
Sbjct: 355 CEHEDLLNITLRLLNLSFDTGLRNKMVQ---VGLLPKLTALLGNENYKQI--AMCVLYH 409

Query: 538 LSQDHDVCD-FIVQNNVHREMMALLDAQHQDICFSACGVLLNLTVDKDKRVILKEGGGIK 596
+S D F + + + M L + + I +NL +K ++ EG G+K
Sbjct: 410 ISMDDRFKSMFAYTDCIPQLMKMLFECSDERIDLELISFCINLAANKRNVQLICEGNGLK 469

Query: 597 KLVDCRLDGLPTDWQLACLVCCKTLWNFSENITNASSCFGNEDTNTLLLLSSFLDEELAL 656
L+ R L D L+ K + N S++ + F + L +SS +EE +
Sbjct: 470 MLMK--RALKLD---PLMKMIRNISQHDGPTKNLF-IDYVGDLAAQISSDEEEEFVI 522

Query: 657 D 657
+
Sbjct: 523 E 523

Score = 61 (9.2 bits), Expect = 1.6e-02, Sum P(2) = 1.6e-02
Identities = 20/66 (30%), Positives = 34/66 (51%)

Query: 304 LNISALPQLCTAM-EQYKGDQDVCTNIARIFSKLTSYRDCCTALASYSRCYALFLNLINK 362
LN +AL L + E +K ++ TNI IF +S+ + Y + AL +N+I+
Sbjct: 171 LNETALGALARVLRDQKQSVELATNIIYIFFCFSSFSHFHGLITHY-KIGALCMNIIDH 229

Query: 363 YQKKQDL 369
K+ +L
Sbjct: 230 ELKRHEL 236

Pedant information for DKF2phtes3_14p7, frame 2

Report for DKF2phtes3_14p7.2

[LENGTH] 708
[MW] 79266.35
[pI] 6.57

[FUNCAT] 30.25 vacuolar and lysosomal organization [S. cerevisiae, YEL013w] 3e-04
 [FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YEL013w] 3e-04
 [FUNCAT] 09.25 vacuolar and lysosomal biogenesis [S. cerevisiae, YEL013w] 3e-04
 [BLOCKS] BL00923F Aspartate and glutamate racemases proteins
 [BLOCKS] BL00288B Tissue inhibitors of metalloproteinases proteins
 [PROSITE] MYRISTYL 9
 [PROSITE] AMIDATION 1
 [PROSITE] CK2_PHOSPHO_SITE 12
 [PROSITE] PKC_PHOSPHO_SITE 7
 [PROSITE] ASN_GLYCOSYLATION 11
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 7.49 %

SEQ ESKETVMGDSMVKINGIYLTKSNAICHLKSHPLQLTDDGGFSEIKEQEMFKGTTSLPSH
 SEG
 PRD ccc

SEQ LKNGGDQGRHARASSCPSSSDLSRLQTKAVPKADLQEDAEIEVDEVFWNTRIVPILRE
 SEGxxxxxxxxxxxxx.....
 PRD cccccccchhhhhhhccccccccchhhhhhhccccchhhhhhhhhhhhhccccccccceehhhhhhh

SEQ LEKEENIETVCAACTQLHHALEEGNMLGNFKGRSILLKTLCKLVDVGSLSLKLAKII
 SEGxxxxxxxxxxxxx.....
 PRD hhhhhcchhhhhhhhhhhhhhhhhhhhhccccccccccccccccchhhhhheeeccccchhhhhhhhh

SEQ LALKVSRKNLLNVCKLIFKISRNEKNDLSLQNDLSILESLLVLRSEDLTQNMFAFLYCMG
 SEGxxxxx.....
 PRD hhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccchhhhhhhhhhhhhccchhhhhhhhhhhcc

SEQ SIKFISGNLGLNEMISKGAVEILINLIKQINENIKKCGTFLPNSGHLVQVTATLRNLV
 SEG
 PRD ceeeeccccchhhhhhhcchhhhhhhhhhhhhccccccccccccccccceeeehhhhhhhhh

SEQ DSSLVRSKFLNISALPQLCTAMEQYKGDQDVCTNIARIFSKLTSYRDCCTALASYSRCYA
 SEG
 PRD ccchhhhhheeeccccchhhhhhhhhhhccccceeeehhhhhhhhhhhccccchhhhhhhhhhhhh

SEQ LFLNLINKYQKKQDLVVRVVFILGNLTAKNNQAREQFSKEKGSIQTLLSLFQTFHQDLH
 SEG
 PRD hhhhhhhhhhhhhhhhhheeeccccccccccccchhhhhhhhhhhhhchhhhhhhhhhhhhhhhhcc

SEQ SQKPVGQRGEQHRAQRPPSEADVLIKLTRVLANIAIHPGVGPVLAANPGIVGLLLTTLE
 SEG
 PRD cccccccccccccccccccccchhhhhhhhhhhhhhhccccccccceeeccccchhhhhhhhh

SEQ YKSLDDCEELVINATATINNLSYYQVKNSIIQDKKLYIAELLKLLVSNMMDGILEAVRV
 SEGxxxxxxxxxxxxx.....
 PRD hhccccchhhhhhhhhheeeccccccccceeeehhhhhhhhhhhhhhhccccchhhhhhhhh

SEQ FGNLSQDHDVDCFIVQNNVHRFMALLDAQHQDICFSACGVLLNLTVDKDKRVILKEGGG
 SEG
 PRD cccccccccceeeccccchhhhhhhhhhhhhccccceeeccccceeeccccceeecccc

SEQ IKKLVDCLRDGLPTDWQLACLVKTLWNFSENITNASSCFGNEDNTLLLLSSFLDEEL
 SEGxxxxxxxxxxxxx.....
 PRD hhhhhhhhhccccccccchhhhhhhhhccccccccccccccccccccceeeehhhhhhhhh

SEQ ALDGSFDPDLKNYHKLHWETEFKPVAAQQLNRIQRHHTFLEPLPIPSF
 SEGxxx.....
 PRD hhccccccccchhhhhhhhhhhchhhhhhhhhhhhhhhheeecccccc

Prosites for DKFZphtes3_14p7.2

PS00001	206->210	ASN_GLYCOSYLATION	PDOC00001
PS00001	212->216	ASN_GLYCOSYLATION	PDOC00001
PS00001	311->315	ASN_GLYCOSYLATION	PDOC00001
PS00001	385->389	ASN_GLYCOSYLATION	PDOC00001
PS00001	493->497	ASN_GLYCOSYLATION	PDOC00001
PS00001	500->504	ASN_GLYCOSYLATION	PDOC00001
PS00001	543->547	ASN_GLYCOSYLATION	PDOC00001
PS00001	584->588	ASN_GLYCOSYLATION	PDOC00001
PS00001	628->632	ASN_GLYCOSYLATION	PDOC00001
PS00001	632->636	ASN_GLYCOSYLATION	PDOC00001
PS00001	635->639	ASN_GLYCOSYLATION	PDOC00001
PS00005	173->176	PKC_PHOSPHO_SITE	PDOC00005
PS00005	186->189	PKC_PHOSPHO_SITE	PDOC00005
PS00005	241->244	PKC_PHOSPHO_SITE	PDOC00005

PS00005	295->298	PKC_PHOSPHO_SITE	PDOC00005
PS00005	344->347	PKC_PHOSPHO_SITE	PDOC00005
PS00005	387->390	PKC_PHOSPHO_SITE	PDOC00005
PS00005	421->424	PKC_PHOSPHO_SITE	PDOC00005
PS00006	79->83	CK2_PHOSPHO_SITE	PDOC00006
PS00006	201->205	CK2_PHOSPHO_SITE	PDOC00006
PS00006	214->218	CK2_PHOSPHO_SITE	PDOC00006
PS00006	218->222	CK2_PHOSPHO_SITE	PDOC00006
PS00006	230->234	CK2_PHOSPHO_SITE	PDOC00006
PS00006	320->324	CK2_PHOSPHO_SITE	PDOC00006
PS00006	344->348	CK2_PHOSPHO_SITE	PDOC00006
PS00006	439->443	CK2_PHOSPHO_SITE	PDOC00006
PS00006	477->481	CK2_PHOSPHO_SITE	PDOC00006
PS00006	483->487	CK2_PHOSPHO_SITE	PDOC00006
PS00006	654->658	CK2_PHOSPHO_SITE	PDOC00006
PS00006	698->702	CK2_PHOSPHO_SITE	PDOC00006
PS00008	17->23	MYRISTYL	PDOC00008
PS00008	64->70	MYRISTYL	PDOC00008
PS00008	144->150	MYRISTYL	PDOC00008
PS00008	384->390	MYRISTYL	PDOC00008
PS00008	402->408	MYRISTYL	PDOC00008
PS00008	473->479	MYRISTYL	PDOC00008
PS00008	533->539	MYRISTYL	PDOC00008
PS00008	580->586	MYRISTYL	PDOC00008
PS00008	641->647	MYRISTYL	PDOC00008
PS00009	67->71	AMIDATION	PDOC00009

(No Pfam data available for DKF2phtes3_14p7.2)

DKFZphtes3_15a13

group: testes derived

DKFZphtes3_15a13 encodes a novel 387 amino acid protein with weak similarity to *S.cerevisiae* Hop1.

No informative BLAST results; No predictive prosite, pfam or SCOP motifs.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to *S.cerevisiae* Hop1

complete cDNA, complete cds, potential start codon at Bp 116, 3 EST hits

S.cerevisiae Hop1p is a meiosis-specific protein

Sequenced by GBF

Locus: unknown

Insert length: 1848 bp

Poly A stretch at pos. 1766, no polyadenylation signal found

```
1  GGAAAGCGCA  TCGCGTCCG  GCACAGCGCG  TGCAGCCTCG  TGCAGCTCTT
51  CTGGTCTCCG  GCGCCCGCCC  CTCAGACGTA  ATGTTGAATT  AAAGAAAATA
101  CTTTATCAGA  AGAAGATGGC  CACTGCCAG  TTGCAGAGGA  CTCCCATGAG
151  TGCACCTGGT  TTCCCAATA  AGATATCAAC  TGAACACCAG  TCTTTGGTGT
201  TAGTGAAGAG  GCTTCTAGCA  GTTTCAGTAT  CCTGTATCAC  GTATTGAGG
251  GGAATATTCC  CAGAATGCGC  TTATGGAACA  AGATATCTAG  ATGATCTTTG
301  TGTCAAAATA  CTGAGAGAAG  ATAAAAATTG  CCCAGGATCT  ACACAGTTAG
351  TGAAATGGAT  GCTAGGATGT  TATGATGCTT  TACAGAAAAA  ATATGTATAC
401  ACAAACCCAG  AAGATCCTCA  GACAATTTCA  GAATGTTACC  AATTCAAATT
451  CAAATACACC  AATAATGGAC  CACTCATGGA  CTTTATAAGT  AAAAACCAAA
501  GCAACGAATC  TAGCATGTTG  TCTACTGACA  CCAAGAAAGC  AAGCATTCTC
551  CTCATTCCGA  AGATTTATAT  CCTAATGCAA  AATCTGGGGC  CTTTACCTAA
601  TGATGTTTGT  TTGACCATGA  AACTTTTTTA  CTATGATGAA  GTTACACCCC
651  CAGATTACCA  GCCTCCCGGT  TTTAAGGATG  GTGATTGTGA  AGGAGTTATA
701  TTTGAAGGGG  AACCTATGTA  TTTAAATGTG  GGAGAAGTCT  CAACACCTTT
751  TCACATCTTC  AAAGTAAAAG  TGACCACTGA  GAGAGAACGA  ATGGAAAATA
801  TTGACTCAAC  TATACTATCA  CCAAAACAAA  TAAAACACCC  ATTTCAAAAA
851  ATCCTGAGGG  ACAAAGATGT  AGAAGATGAA  CAGGAGCATT  ATACAAGTGA
901  TGATTTGGAC  ATTGAAACTA  AAATGGAAGA  ACAGGAAAAA  AACCTGTCAT
951  CTTCTGAAC  TGAAGAACCA  AGTTTAGTTT  GTGAGGAAGA  TGAAATTATG
1001  AGGTCTAAAG  AAAGTCCAGA  TCTTCTATT  TCTCATTCTC  AGGTTGAGCA
1051  GTTAGTCAAT  AAAACATCTG  AACTTGATAT  GTCTGAAAGC  AAAACAAGAA
1101  GTGGAAAAAG  CTTTCAGAA  AAAATGGCAA  ATGGAAATCA  ACCAGTAAAA
1151  TCTTCCAAAG  AAAATCGGAA  GAGAAGTCAA  CATGAATCTG  GGAGAATAGT
1201  CCTCCATCAC  TTTGATTCTT  CTAGTCAAGA  GTCAGTGCCA  AAAAGGAGAA
1251  AGTTTAGTGA  ACCAAAGGAA  CATATATAAA  AATTATTTTT  GTTCTGCAGG
1301  CTTGCAGAGT  TCTTCTCACC  ATTTAACTG  AAGGACCCTA  TATTATATTT
1351  CCCTAACTCT  GAAGATGTAT  ATGTAGTTTA  AAGCAGTTTG  TACATAAAA
1401  CTAAGTTTTT  GGCTGACTGT  CATATTGTGG  TCCTTAATCT  TGAGATAAAT
1451  CCAATAGAAC  TTTTGAATAA  AAGCAAAAGT  ACAAATGTCA  TAATTGATTC
1501  GGTAATAAGT  AAAATTTCAA  AATTGATTTT  GTTCATTACC  TACTTAATAT
1551  TTCCTTTAAA  TATATACTAA  CTGTTAAGGC  CCTCTAATGC  CATTTTCTA
1601  AACAGTAATG  TTTACTTTGG  TATTAAAATT  TGGTATGGAT  TCACCTTTTA
1651  CTTATGTTAA  AATTATACCA  TTTAACTGGC  TCTTTTGTC  TTGTGCTGTT
1701  ATTAATAAC  TGTTCTTCAA  TATTTTGACA  TAATGTATTA  ACATTTTAAT
1751  ATATAATGTA  CAATTTAAAA  AAAAAAAAAA  AAAAAAAAAA  AAAAAAAGG
1801  GCGGCGCGCT  CTAGAGGATC  CAAGCTTACC  TACAAAAAAA  AAAAAAAGG
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 116 bp to 1276 bp; peptide length: 387
Category: similarity to known protein

```

1 MATAQLQRTP MSALVFPNKI STEHQSLVLV KRLLAVSVSC ITYLRGIFPE
51 CAYGTRYLDD LCVKILREDK NCPGSTQLVK WMLGCDALQ KKYVYTNPED
101 PQTISECYQF KFKYTNNGPL MDFISKQSN ESSMLSTDTK KASILLIRKI
151 YILMQLNGPL PNDVCLTMKL FYYDEVTPPD YQPPGFKDGD CEGVIFEGEP
201 MYLNVGEVST PFHIFKVKVT TERERMENID STILSPKQIK TPFQKILRDK
251 DVEDEQEHYT SDDLDIETKM EEQKNPASS ELEEPSLVCE EDEIMRSKES
301 PDLSSISHSQV EQLVNKTSEL DMSESKTRSG KVFQNMANG NQPVKSSKEN
351 RKRSQHESGR IVLHHFDSSS QESVPKRRKF SEPKEHI

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_15a13, frame 2

TREMBL:ATAC2130_3 product: "F1N21.3"; The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence., N = 1, Score = 274, P = 5.7e-22

TREMBL:SC9877_9 gene: "hop1"; S.cerevisiae chromosome IX cosmid 9877., N = 2, Score = 126, P = 7.1e-09

PIR:A34691 meiosis-specific protein HOP1 - yeast (Saccharomyces cerevisiae), N = 2, Score = 126, P = 7.8e-08

>TREMBL:ATAC2130_3 product: "F1N21.3"; The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence.
Length = 562

HSPs:

Score = 274 (41.1 bits), Expect = 5.7e-22, P = 5.7e-22
Identities = 84/290 (28%), Positives = 145/290 (50%)

```

Query: 22 TEHQSLVLVKRLLAVSVSCITYLRGIFPECAYGTRYLDDLCVKILREDKNCPGSTQLVKW 81
      TE SL+L + LL +++ I+Y+RG+FPE + + + L +KI + S +L+ W
Sbjct: 11 TEQDSLLLTRNLLRIAIFNISYIRGLFPEKYFNOKSVPALDMKIKKLMPMDAESRRLIDW 70

Query: 82 M-LGCYDALQKKYVYT-----NPEDPQTISECYQFKFKYTNNGP--LMDFISK--NQSN 130
      M G YDALQ+KY+ T D I E Y F F Y+++ +M I++ N+ N
Sbjct: 71 MEKGVYDALQRYLKTLMFSICETVDGPMIEE-YSFSSYSQSDSDQVMMNINRTGNKKN 129

Query: 131 ESSMLST-----DTKKASILLIRKIYILMQLNGPLPNDVCLTMKLFYYDEVTPPDYQPP 184
      ST + ++ ++R + LM+ L +P++ + MKL YYD+VTPPDY+PP
Sbjct: 130 GGIFNSTADITPNQMRSSACKMVRTLVQLMRTLDKMPDERTIVMKLLYYDDVTPPDYEP 189

Query: 185 GFKD--GDCEGVIFEGEPMYLNVGEVSTPFHIFKVKVT-----ERERMENIDSTILS 235
      F+ D ++ P+ + +G V++ + +KV + E + M++ D +
Sbjct: 190 FFRGCTEDEAQYVWTKNPLRMEIGNVNSKHLVLTLLKVKSVLDPCEDENDDMQD-DGKSIG 248

Query: 236 PKQIKTPFQKILRDKDVEDEQEHY-----TSDDLDIETKMEEQKNPASSE 281
      P + Q D ++ QE+ DD D E ++ ++PA +E
Sbjct: 249 PDSVHDD-QPSDSDSEISQTQENQFIVAPVEKQDDDDGEVDEDDNTQDPAENE 300

```

Pedant information for DKFZphtes3_15a13, frame 2

Report for DKFZphtes3_15a13.2

```

[LENGTH] 387
[MW] 44417.64
[pI] 5.57
[HOMOL] TREMBL:ATAC2130_3 product: "F1N21.3"; The sequence of BAC F1N21 from
Arabidopsis thaliana chromosome 1, complete sequence. 9e-23
[FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YIL072w] 7e-11
[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YIL072w] 7e-11
[FUNCAT] 03.13 meiosis [S. cerevisiae, YIL072w] 7e-11
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YIL072w] 7e-11
[PIRKW] nucleus 2e-09
[PIRKW] zinc finger 2e-09

```

[PIRKW] DNA binding 2e-09
 [PROSITE] MYRISTYL 1
 [PROSITE] CAMP_PHOSPHO_SITE 3
 [PROSITE] CK2_PHOSPHO_SITE 12
 [PROSITE] PKC_PHOSPHO_SITE 7
 [PROSITE] ASN_GLYCOSYLATION 3
 [KW] Alpha_Beta

SEQ MATAQLQRTPMALVFPNKISTEHQSLVLVKRLAVSVSCITYLRGIFPECAYGTRYLDD
 PRD cccccccccccccccccchhhhhhhhhhhhhhhhhheeeecccccccccchh
 SEQ LCVKILREDKNCPGSTQLVKWMLGCYDALQKKYVYTNPEDPQTISECYQFKFYTNNGPL
 PRD hhhhhhccccccccccccccccchhhhhhhhhhhccccccccchhhheeeeccccce
 SEQ MDFISKQSNSSMLSTDTKKASILLIRKIYILMQNLGPLPNDVCLTMKLFYYDEVTPPD
 PRD eeeecccccccccccccchhhhhhhhhhhhhhhhhccccccccceeeeeeecccccc
 SEQ YQPPGFKDGDCEGVIFEGEPMYLNVGEVSTPFHIFVKVVTTEREREMENIDSTILSPKQIK
 PRD cccccccccccccceeeccccceeeccccccccceeeccccchhhhhccccccccchhh
 SEQ TPFQKILRDKDVEDEQEHTSDLDIETKMEEQEKNPASSELEEPSLVCEEDEIMRSKES
 PRD hhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhccccccccccccchhhhhhhhhcc
 SEQ PDLISHSQVEQLVNKTSELDMSSEKTRSGKVFNQNMANGNPVKSSKENRKRSQHESGR
 PRD cccccchhhhhhhhhhhccccccccccccccccceeeccccccccchhhhhhhhhccccce
 SEQ IVLHHFDSSSQESVPKRRKFSEPKHEI
 PRD eeeecccccccccccccccccccccccccc

Prosite for DKFZphtes3_15a13.2

PS00001	127->131	ASN_GLYCOSYLATION	PDOC00001
PS00001	130->134	ASN_GLYCOSYLATION	PDOC00001
PS00001	315->319	ASN_GLYCOSYLATION	PDOC00001
PS00004	140->144	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	351->355	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	378->382	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	139->142	PKC_PHOSPHO_SITE	PDOC00005
PS00005	167->170	PKC_PHOSPHO_SITE	PDOC00005
PS00005	221->224	PKC_PHOSPHO_SITE	PDOC00005
PS00005	235->238	PKC_PHOSPHO_SITE	PDOC00005
PS00005	329->332	PKC_PHOSPHO_SITE	PDOC00005
PS00005	346->349	PKC_PHOSPHO_SITE	PDOC00005
PS00005	358->361	PKC_PHOSPHO_SITE	PDOC00005
PS00006	96->100	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	177->181	CK2_PHOSPHO_SITE	PDOC00006
PS00006	221->225	CK2_PHOSPHO_SITE	PDOC00006
PS00006	260->264	CK2_PHOSPHO_SITE	PDOC00006
PS00006	268->272	CK2_PHOSPHO_SITE	PDOC00006
PS00006	280->284	CK2_PHOSPHO_SITE	PDOC00006
PS00006	308->312	CK2_PHOSPHO_SITE	PDOC00006
PS00006	318->322	CK2_PHOSPHO_SITE	PDOC00006
PS00006	346->350	CK2_PHOSPHO_SITE	PDOC00006
PS00006	354->358	CK2_PHOSPHO_SITE	PDOC00006
PS00006	369->373	CK2_PHOSPHO_SITE	PDOC00006
PS00008	84->90	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_15a13.2)

DKF2phtes3_15c24

group: metabolism

DKF2phtes3_15c24 encodes a novel 404 amino acid protein with strong similarity to 2-hydroxyacid dehydrogenases.

The novel protein contains a D-isomer specific 2-hydroxyacid dehydrogenases signature. Proteins with such a signature have similar enzymatic activities: D-lactate dehydrogenase (EC 1.1.1.28), catalyzes the reduction of D-lactate to pyruvate. D-glycerate dehydrogenase (EC 1.1.1.29) catalyzes the reduction of hydroxypyruvate to glycerate. 3-phosphoglycerate dehydrogenase (EC 1.1.1.95), catalyzes the oxidation of D-3-phosphoglycerate to 3-phosphohydroxypyruvate. Therefore the novel protein is a new 2-hydroxyacid dehydrogenase.

The new protein can find application in modulation of 2-hydroxyacid dehydrogenases-dependent pathways and as a new enzyme for biotechnologic production processes.

strong similarity to C.elegans T03F1.1

potential start at Bp 55 matches kozak consensus PyCCatgG

Sequenced by GBF

Locus: unknown

Insert length: 1956 bp

Poly A stretch at pos. 1929, polyadenylation signal at pos. 1903

```
1 CGAAGGCGGC GCGGAAGGCC CGGGCTGGGA GCGTTGGCGG CCGGAGTCCC
51 AGCCATGGCG GAGTCTGTGG AGCGCCTGCA GCAGCGGGTC CAGGAGCTGG
101 AGCGGGAACT TGCCCAGGAG AGGAGTCTGC AGGTCCCCGAG GAGCGGCGAC
151 GGAGGGGCGG GCCGGGTCCG CATCGAGAAG ATGAGCTCAG AGGTGGTGGA
201 TTCGAATCCC TACAGCCGCT TGATGGCATT GAAACGAATG GGAATTGTAA
251 GCGACTATGA GAAAATCCGT ACCTTTGCCG TAGCAATAGT AGGTGTTGGT
301 GGAGTAGGTA GTGTGACTGC TGAATGCTG ACAAGATGTG GCATTGGTAA
351 GTTGCTACTC TTTGATTATG ACAAGGTGGA ACTAGCCAAT ATGAATAGAC
401 TTTTCTTCCA ACCTCATCAA GCAGGATTAA GTAAAGTTCA AGCAGCAGAA
451 CATACTCTGA GGAACATTAA TCCTGATGTT CTTTTGAAG TACACAACCTA
501 TAATATAACC ACAGTGGAAA ACTTTCAACA TTTTCATGGAT AGAATAAGTA
551 ATGGTGGGTT AGAAGAAGGA AAACCTGTTG ATCTAGTTCT TAGCTGTGTG
601 GACAATTTTG AAGCTCGAAT GACAATAAAT ACAGCTTGTA ATGAACCTGG
651 ACAACATGGG ATGGAATCTG GGGTCAGTGA AAATGCAGTT TCAGGGCATA
701 TACAGCTTAT AATTCTCTGA GAATCTGCTT GTTTTGCGTG TGCTCCACCA
751 CTTGTAGTTG CTGCAATAT TGAAGAAAG ACTCTGAAAC GAGAAGGTGT
801 TTGTGCAGCC AGTCTTCCTA CCACTATGGG TGTGGTTGCT GGGATCTTAG
851 TACAAAACGT GTTAAAGTTT CTGTTAAATT TTGGTACTGT TAGTTTTTAC
901 CTTGGATACA ATGCAATGCA GGATTTTTTT CTTACTATGT CCATGAAGCC
951 AAATCCTCAG TGTGATGACA GAAATGCAG GAAGCAGCAG GAGGAATATA
1001 AGAAAAAGGT AGCAGCACTG CCTAAACAAG AGGTTATACA AGAAGAGGAA
1051 GAGATAATCC ATGAAGATAA TGAATGGGGT ATTGAGCTGG TATCTGAGGT
1101 TTCAGAAGAG GAACTGAAAA ATTTTTCAGG TCCAGTTCCA GACTTACCTG
1151 AAGGAATTAC AGTGGCATAC ACAATTCCAA AAAAGCAAGA AGATTCTGTG
1201 ACTGAGTTAA CAGTGGAAGA TTCTGGTGAA AGCTTGGAAG ACCTCATGGC
1251 CAAAATGAAG AATATGTAGA TAATGGACTG GGATATATTG TATTCTCAT
1301 GTTAAAGCCT CTTCCCTTGA AATTAAGAAA AAATTTTAACT TGATAAACT
1351 TAGGGCAACA TTAATTAATG TATATTCTTA CCTGAATTGT TATACTTTTT
1401 GAAAATCCTG TGACTTGCCT GTTCTCCCC GCTCCAACGA AATCATTAAC
1451 TCTCCTAAAA TGTGTTTCAT TCTAGTAAGA AAACCTCAAA GGATATTGTA
1501 GGATATAAAT CTTACTTGAA AACATAGCTG TTGAAATGTT TTGGCCTTTT
1551 GGAGTGGGGG AAGGACAAAT CTGATCCTGT AATCTTTTTC TTTCAGTAA
1601 TCCCTTGTGT CTGTTGCATG AGGACATGGA CAATAAGTA GTATATGATC
1651 CTCAGATACA GGGAGAAGGA CAAGGCATAC AGCTTATTGA TTAGAGCTGG
1701 CAAGCATCTG CTCATTATGT TTGGAATTGC TTTCTATAAG AAAATTGCC
1751 ACTACTACTA ACTTGATCAA CAATGAATTC AAAATAGTTA ACCTATGAAA
1801 TAACATCCTC TCAAAATGTT GCTGATGAAG TACAAGTTGA AATGTAGTTA
1851 TTGGAAGAGT CTGTAACCTG TGGATCATAT ATATTCAAAG TGAGACAAAG
1901 GCAATAAAAA AGCAGCTATT TTCATGAATA GACAAAAAAA AAAAAAAA
1951 AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 55 bp to 1266 bp; peptide length: 404
 Category: similarity to unknown protein
 Classification: Metabolism
 Prosite motifs: D_2_HYDROXYACID_DH_1 (76-105)

```

1 MAESVERLQQ RVQELERELA QERSLQVPRS GDGGGGRVRI EKMSSEVVDS
51 NPYSRLMALK RMGIVSDYEK IRTFAVAIVG VGGVGSVTAE MLTRCGIGKL
101 LLDYDKVEL ANMNRLFFQP HQAGLSKVQA AEHTLRNINP DVLFEVHNYN
151 ITTVENFQHF MDRISNGGLE EGKPVDLVLS CVDNFEARMT INTACNELGQ
201 TWMESEGVSEN AVSGHIQLII PGESACFACA PPLVVAANID ETKLKREGVC
251 AASLPTTMGV VAGILVQNVL KELLNFGTVS FYLGYNAMQD FFPTMSMKPN
301 PQCDNRNCRK QEEYKKKVA ALPKQEVQIE EEEIHHEDNE WGIELVSEVS
351 EEELKNFSGP VPDLPPEGITV AYTIPKKQED SVTELTVEDS GESLEDLMAK
401 MKNM

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_15c24, frame 1

TREMBL:CEUT03F1_11 gene: "T03F1.1"; Caenorhabditis elegans cosmid
 T03F1., N = 1, Score = 1204, P = 1.9e-122

TREMBL:ATAC98_3 gene: "YUP8H12.3"; Arabidopsis thaliana chromosome 1
 YAC yUP8H12 complete sequence., N = 1, Score = 733, P = 1.5e-72

PIR:A69319 thiamine biosynthesis protein (thiF) homolog - Archaeoglobus
 fulgidus, N = 1, Score = 218, P = 1.8e-17

TREMBL:AF022796_4 gene: "moeB"; product: "MoeB"; Staphylococcus
 carnosus molybdenum cofactor biosynthetic gene cluster, complete
 sequence., N = 1, Score = 220, P = 3.7e-16

>TREMBL:CEUT03F1_11 gene: "T03F1.1"; Caenorhabditis elegans cosmid T03F1.
 Length = 419

HSPs:

Score = 1204 (180.6 bits), Expect = 1.9e-122, P = 1.9e-122
 Identities = 241/367 (65%), Positives = 293/367 (79%)

```

Query:   37 RVRIEKMSSEVVDSNPYSRLMALKRMGIVSDYEKIRTFAVAIVGVGGVGSVTAEMLTRCG 96
          R +IEK+S+EVVDSNPYSRLMAL+RMGIV++YE+IR  VA+VGVGGSV AEMLTRCG
Sbjct:   48 RQIEKLSAEVVDSNPYSRLMALQRMGIVNEYERIREKTVAVVGVGGSVVAEMLTRCG 107

Query:   97 IGKLLFDYDKVELANMNRLFFQPHQAGLSKVQAAEHTLRNINPDVLFEVHNYNITTVEN 156
          IGKL+LFDYDKVE+ANMNRLF+QP+QAGLSKV+AA  TL ++NPDV  EVHN+NITT++N
Sbjct:  108 IGKLILFDYDKVEIANMNRLFYQPNQAGLSKVEAARDTLIHVNPDVQIEVHNFNITMDN 167

Query:  157 FQHFMDRISNGGLEEGKPVLDVLSCVDNFEARMTINTACNELGQTMESGVSENAVSGHI 216
          F F++RI  G L +GK +DLVLSVDNFEARM +N ACNE  Q WMESGVSENAVSGHI
Sbjct:  168 FDTFVNRIKGSGLTDGK-IDLVLSVDNFEARMAVNMACNEENQIWMESGVSENAVSGHI 226

Query:  217 QLIIPGESACFACAPPLVVAANIDEKTLKREGVCAASLPTTMGVVAGILVQNVLKFLNF 276
          Q I PG++ACFAC PPLVVA+ IDE+TLKR+GVCAASLPTTM VVAG LV N LK+LLNF
Sbjct:  227 QYIEPGKTACFACVPLVVASGIDERTLKRQGVCAASLPTTMVAVAGFLVMNTLKYLLNF 286

Query:  277 GTVSFYLGYNAMQDFFPTMSMKPNPQCDNRNCRKQEEYKKKVAALPKQ-EV-IQEEEEI 334
          G VS Y+GYN+ DFFP S+KPNP CDD +C ++Q+EY++KVA  P  EV + EEE +
Sbjct:  287 GEVSQYVGYNALSDFPRDSIKPNPYCDDSHCLQRQKEYEEKVANQPDLEVEVPEEETV 346

Query:  335 IHEDNEWGIELVSEVSEELKNFSGPVPDLPEGITVAYTIPKKQEDSVTELTVEDSGESL 394
          +HEDNEWGIELV+E SE  + S  +  G+ AY P K+ D+ TEL+  +  +
Sbjct:  347 VHEDNEWGIELVNE-SEPSAEQSSSL--NAGTGLKFAYE-PIKR-DAQTELSPAQA--AT 399

Query:  395 EDLMAKMKN 403

```

Sbjct: 400 D M +K+ HDEMKS IKD 408

Pedant information for DKFZphtes3_15c24, frame 1

Report for DKFZphtes3_15c24.1

```

[LENGTH] 404
[MW] 44863.36
[pI] 4.79
[HOMOL] TREMBL:CEUT03F1_11 gene: "T03F1.1"; Caenorhabditis elegans cosmid T03F1. 1e-115

[FUNCAT] h cofactor metabolism [H. influenzae, HI1449] 2e-08
[FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YDR390c UBA2 - E1-like]
4e-07
[FUNCAT] 04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S.
cerevisiae, YDR390c UBA2 - E1-like] 4e-07
[FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YDR390c UBA2 - E1-like]
4e-07
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YDR390c UBA2 - E1-like] 4e-07
[FUNCAT] 11.01 stress response [S. cerevisiae, YKL210w UBA1 - E1-like] 2e-06
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YKL210w UBA1 - E1-like]
2e-06
[BLOCKS] BL01042A Homoserine dehydrogenase proteins
[PIRKW] thiamine pyrophosphate 1e-07
[PIRKW] molybdenum 5e-07
[PIRKW] molybdopterin biosynthesis 5e-07
[SUPFAM] molybdopterin biosynthesis protein moeB 2e-12
{PROSITE} D_2_HYDROXYACID_DH_1 1
[KW] TRANSMEMBRANE 1
[KW] LOW COMPLEXITY 8.66 %

```

```

SEQ      MAESVERLQQRVQELERELAQERSLQVPRSGDGGGGRVRIEKMSSEVVDNSPYSRLMALK
SEG      .....
PRD      ccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccceeeccccccccccchhhhhhhc
MEM      .....

SEQ      RMGIVSDYEKIRTFAVAIVGVGGVGSVTAEMLTRCGIGKLLLFDYDKVELANMNRFFQP
SEG      .....xxxxxxxxx.....
PRD      cccccchhhhhhhheeeccccchhhhhhhhhhhccccceeeccccchhhhhhhhhhhc
MEM      .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.....

SEQ      HQAGLSKVQAAEHLTRNINPDVLFVHNYNITTVENFQHFMDRISNGGLEEGKPVDLVLS
SEG      .....
PRD      cccccchhhhhhhhhhhhhhhccccccccccccccccchhhhhhhhhhhccccccccccccceeee
MEM      .....

SEQ      CVDNFEARMTINTACNELGQTWMESGVSENAVSGHIQLIIPGESACFACAPPLVVAANID
SEG      .....
PRD      cccchhhhhhhhhhhhhhhccccccccccccccccccccceeecccccccccecccccccccccc
MEM      .....

SEQ      EKTCLKREGVCAASLPTTMGVVAGILVQNVLKFLNFGTVSFYLGYNAMQDFFPTMSMKPN
SEG      .....
PRD      cccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhccccceeecccccccccccccccccccc
MEM      .....

SEQ      PQCDNRNCRKQOEYKKKVAALPKQEVIEEEEEI IHEDNEWGIELVSEVSEELKNFSGP
SEG      .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccceeeeeeehhhhhhhhhhhc
MEM      .....

SEQ      VPDLPegITvAYtIPKkQEDSVtELtVEDSGESLEDLMakMkNM
SEG      .....
PRD      cccccccccceeeeeeehhhhhhhhhheeeccccchhhhhhhhhhhccc
MEM      .....

```

Prosite for DKFZphtes3_15c24.1

PS00065 76->105 D 2 HYDROXYACID DH 1 PDOC00063

(No Pfam data available for DKFZphtes3 15c24.1)

DKFZphtes3_15c6

group: transmembrane protein

DKFZphtes3_15c6 encodes a novel 118 amino acid protein without similarity to known proteins.

The novel protein contains 1 transmembrane region.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

unknown

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1283 bp

Poly A stretch at pos. 1264, no polyadenylation signal found

```
1 GAGACACTGA GCCCCGAGAC AGTGAGTGGT GGCCTCACTG CTCTGCCCCG
51 CACCCTGTCA CCTCCACTTT GCCTTGTGGT AAGTGACCCA GCCCCCTCCC
101 CTTCCATTCT CCCACCTGTT CCCCAGGACT CACCCAGGCC CTGCCTGCC
151 CTTGAGGAAG AAGAGGCACT CACCACTGAG GACTTTGAGT TGCTGGATCA
201 GGGGGGAGCTG GAGCAGCTGA ATGCAGAGCT GGGCTTGGAG CCAGAGACAC
251 CGCCAAACC CCCTGATGCT CCACCCCTGG GGGCCGACAT CCATTCTCTG
301 GTACAGTCAG ACCAAGAAGC TCAGGCCGTG GCAGAGCCAT GAGCCAGCCG
351 TTGAGGAAGG AGCTGCAGGC ACAGTAGGGC TTCCTGGCTA GGAGTGTTCG
401 TGTTCCTCTC TTTGCCCTACC ACTCTGGGGT GGGGCAGTGT GTGGGAAGC
451 TGGCTGTCGG ATGGTAGCTA TTCCACCCTC TGCCTGCCTG CCTGCCTGCT
501 GTCCTGGGCA TGGTGCAGTA CCTGTGCCTA GGATTGGTTT TAAATTTGTA
551 AATAATTTTC CATTTGGGTT AGTGGATGTG AACAGGGCTA GGAAGTCCT
601 TCCACAGGCC TGGCCTTGCC TCCCTGCCTC ATCTCTATTC TCATTCCACT
651 ATGCCCAAG CCCTGGTGGT CTGGCCCTTT CTTTTCTCTC CTATCCTCAG
701 GGACCTGTGC TGCTCTGCC TCATGTCCCA CTGGTTGTT TAGTTGAGGC
751 ACTTTATAAT TTTTCTCTTG TCTTGTGTTC CTTTCTGCTT TATTTCCCTG
801 CTGTGTCTTG TCCTTAGCAG CTCAACCCCA TCCTTTGCCA GCTCCTCCTA
851 TCCCGTGGGC ACTGGCCAAG CTTTAGGGAG GCTCCTGGTC TGGGAAGTAA
901 AGAGTAAACC TGGGGCAGTG GGTCAAGCCA GTAGTTACAC TCTTAGGTCA
951 CTGTAGTCTG TGTAACCTTC ACTGCATCCT TGCCCCATTC AGCCCGGCTT
1001 TTCATGATGC AGGAGAGCAG GGATCCCGCA GTACATGGCG CCAGCACTGG
1051 AGTTGGTGAG CATGTGCTCT CTCTTGAGAT TAGGAGCTTC CTTACTGCTC
1101 CTCTGGGTGA TCCAAGTGTA GTGGGACCCC CTACTAGGGT CAGGAAGTGG
1151 AACTAACAT CTGTGCAGGT GTTGACTTGA AAAATAAAGT GTTGATTGGC
1201 TAAAAAATAA AAAAAAATAA AAAAAAATAA AAGGGCGGCC GCTCTAGAGG
1251 ATCCAAGCTT ACCTAAAAAA AAAAAAATAA AAG
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 461 bp to 814 bp; peptide length: 118
Category: putative protein

```
1 MVAIPPSACL PACCPGHGAV PVPRIKFKFV NNFPEGLVDV NRAREVLPTA
51 CACLPASSLF SFHYAPSPG LALSFSYPQ GPVLLCPHVP LGCLVEALYN
101 FSLVLCSEFL YFPAVSCP
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_15c6, frame 2

PIR:S54250 ribosomal protein L2 - Arabidopsis thaliana, N = 1, Score = 76, P = 0.33

>PIR:S54250 ribosomal protein L2 - Arabidopsis thaliana
Length = 258

HSPs:

Score = 76 (11.4 bits), Expect = 4.0e-01, P = 3.3e-01
Identities = 30/91 (32%), Positives = 44/91 (48%)

Query: 15 PGHGAVPVPRIGFKFVNNFPFGLVDVNRAREVLPTACACLPASSLFSFHYAPSPGGLALS 74
PG GA P+ R+ F+ PF + +E+ A C P SSL+ A G L
Sbjct: 52 PGRGA-PLARVTFRH----PFRF---KKQKELFVAAEVCTPVSSLYCGKKATLVVGNVLP 103

Query: 75 FSSYPQGPVLLCP---HV-PLGCLVEALYNFSLVL 105
S P+G V+ C HV G L A ++++V+
Sbjct: 104 LRSIPEGAVV-CNVEHHVGDGRGLARASGDYAIVI 137

Pedant information for DKFZphtes3_15c6, frame 2

Report for DKFZphtes3_15c6.2

[LENGTH] 118
[MW] 12413.79
[pI] 7.53
[PROSITE] LEUCINE_ZIPPER 1
[PROSITE] MYRISTYL 1
[PROSITE] ASN_GLYCOSYLATION 1
[KW] TRANSMEMBRANE 1

SEQ MVAIPPSACLPAACPGHGAVPVPRIGFKFVNNFPFGLVDVNRAREVLPTACACLPASSLF
PRD ccc
MEM
SEQ SFHYAPSPGGLALSFSSYPQGPVLLCPHVPLGCLVEALYNFSLVLCFLLYFPAVSCP
PRD eeeeeeeeeeeeeeeeeeeeeeeeeeeeecccccccccccccccccccccccccccccccc
MEMMMMMMMMMMMMMMMMMMM.

Prosites for DKFZphtes3_15c6.2

PS00001	100->104	ASN_GLYCOSYLATION	PDOC00001
PS00008	70->76	MYRISTYL	PDOC00008
PS00029	84->106	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphtes3_15c6.2)

DKFZphtes3_15g14

group: testes derived

DKFZphtes3_15g14 encodes a novel 701 amino acid protein with weak similarity to *S. cerevisiae* hypothetical protein YOR243c.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to YOR243c

complete cDNA, complete cds, potential start codon at Bp 35, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 3495 bp

Poly A stretch at pos. 3462, no polyadenylation signal found

```
1 GCCTTCCACT GAACCGAGGC ACTGTTATAG AAGAATGGAA GAAGATACAG
51 ATTATAGAAT CAGGTTTAGT TCTTTGTGTT TCTTTAATGA TCACGTTGGA
101 TTTCATGGCA CTATAAAAAG CTCACCAAGT GACTTTATTG TTATTGAAAT
151 TGATGAACAG GGACAGTTAG TTAATAAGAC CATCGATGAG CCTATTTTCA
201 AGATTAGTGA AATACAACCTT GAGCCAAATA ATTTTCCCAA AAAACCAAAA
251 CTAGATCTTC AAAATCTGTC CTTAGAAGAT GGAAGAAACC AAGAAGTTCA
301 TACTTTGATT AAGTACACTG ATGGTGACCA AAATCATCAG TCTGGTTCAG
351 AAAAGGAAGA TACTATCGTT GATGGAACCT CCAAATGTGA AGAAAAAGCT
401 GATGTTTAA GCTCCTTTT GGATGAAAAA ACTCATGAGT TACTGAATAA
451 TTTTGCCTGT GATGTAAGAG AGAAGTGGCT TTCTAAAACA GAGCTAATTG
501 GACTACCTCC TGAATCTCA ATAGGCAGAA TCCTTGACAA AAACCAGAGG
551 GCTAGTTTAC ACAGTGCCAT TAGGCAGAAA TTTCCATTTT TAGTAACTGT
601 AGGAAAAAAC AGTGAAATTG TTGTAAAACC AAATCTTGAA TATAAAGAAC
651 TTTGTCAATT GGTATCTGAA GAGGAAGCAT TTGACTTTTT TAAATATTTG
701 GATGCCAAGA AAGAAAATTC CAAATTTACC TTTAAACCTG ATACAAACAA
751 AGACCACAGA AAAGCTGTCC ACCATTTTGT CAACAAAAAG TTTGGAAACC
801 TTGTGGAAAC CAAATCTTTT TCTAAAATGA ATTGCAGTGC TGGTAATCCG
851 AATGTGGTGG TAACAGTAAG ATTTCGGGAA AAAGCACACA AACGTGGGAA
901 AAGGCCTCTT TCTGAATGCC AAGAAGGAAA AGTTATATAT ACAGCTTTTA
951 CCCTACGAAA GGAAAACCTG GAAATGTTTG AAGCGATTGG TTTTTFAGCT
1001 ATCAAACCTG GTGTTATTCC TTCGGATTTT AGTTATGCAG GCCTTAAAGA
1051 CAAGAAAGCC ATCACCATATC AAGCAATGGT TGTTAGAAAA GTGACTCCAG
1101 AGAGGTTGAA AAATATTGAA AAAGAAATG AAAAGAAAAG AATGAATGTC
1151 TTTAATATTG GGTCTGTAGA TGATTCCCTG AGACTTGGTC AGCTCAAAGG
1201 AAATCACTTT GATATTGTCA TTAGAAATTT AAAAAACAA ATAAATGATT
1251 CTGCAACCTT GAGGGAGAGA ATTATGGAAG CAATAGAAAA TGTTAAGAAA
1301 AAAGGCTTTG TGAATTTACTA TGGACCACAG AGATTTGGA AGGGAAGGAA
1351 AGTTCACACA GACCAAATTG GACTAGCTTT GCTGAAGAAT GAAATGATGA
1401 AAGCCATAAA ATGTTTCTT ACACCAGAAG ACTTGGATGA TCCTGTAAAT
1451 AGAGCAAAAG AGTATTTCT TCAAAC TGAGCTAAAG GCACACTTTC
1501 ATTGATGCCT GAATTCAAAG TCGGTGAGAG AGCATTGTTG GAGGCATTGC
1551 ACCGCTTTGG CATGACCGAG GAAGGTTGTA TCCAGGCATG GTTCTCTTTA
1601 CCCCATTTCA TCGCATATT CTATGTTTAC GCATATACCA GCAAAATTTG
1651 GAATGAGGCA GTATCTTACA GACTTGAAAC CTATGGAGCA AGAGTAGTGC
1701 AGGGTGATTT GGTCTGTTG GATGAAGACA TTGATGACGA GAATTTCCCA
1751 AATAGTAAAA TTCACCTGGT AACTGAAGAG GAGGGATCAG CTAATATGTA
1801 TGCAATACAT CAGGTGGTTC TTCCAGTACT TGGATACAAT ATTCACTACC
1851 CGAAGAACAA AGTAGGGCAG TGGTACCATG ACATACTTAG CAGAGATGGA
1901 CTACAGACAT GTAGGTTTAA AGTACCTACT CTGAAACTGA ATATACCAGG
1951 TTGCTATAGA CAGATTTTGA AACATCCCTG TAATCTCTCA TACCAACTAA
2001 TGGAAGATCA TGACATTGAT GTCAAAACGA AAGGTTCCCA CATTGATGAA
2051 ACAGCTTTGT CTCTTTTGAT CTCTTTTGAT CTTGATGCTT CATGCTATGC
2101 TACCGTTTGT CTGAAGGAAA TAATGAAGCA TGACGTTTAA AACTGATACC
2151 CTTGGTATAA CCATATATAT GTCACCTTTT CCTGTTTTTG AAATTATTGA
2201 TCAGAACAAAT ATACAAGGGA AATGCCATAC CTCTGTTTGT GATAGATACC
2251 CCAGAGTAGT TATTACCTCT TTGTGAGATA AGTAATCTTT GATGAAGATT
2301 GAAATACAAT TTCTCATCCA ATTTTATAT CTGGGCATAC GCTGACCCTC
2351 TTGACCAATT TACTATTTT CATATTATCT AAAACAGGTG TTAGAGTCAG
2401 ACAGATTCAT TCTTAGATTG TAGCTCTGAC ACTTACTAGT GATTTTGAGT
2451 ATGTTGTTGA TTTTGTGTG TGTGGTTACT GATAGAATCA AGACAATTAC
2501 AACTTCATAA ATGACAAATA ATAGGATTAT CTCCACATTT TCTGTTGCTG
2551 GAGGAACAAA ACATTGTGCC CATTTGAAAA TTTTAATTTT TGTGTTGTTA
2601 ACTATCCCAC ATTATAAATC ATCCTTACC ATTTTATATC AGTTAAATAT
2651 GGGTGTGTTG GGGAGGAATG ACTGGCATGT AGACATGTAT TGATTTAGGA
2701 AGATCTGAGC ATTTCTTTCA TTGTTGGTAA GATATAATGA TGAAATTTAA
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2751 AAAGCAGTAT GGAGCATTAT ATATCAGTAA TGTGATATAT ATACTTAAGG
2801 CAGTTTAACC ATTTTGGGAA ATGTTAGCAT TAGGAAATAA AATCCAAAAG
2851 AAGGAAGAGA AGCTATATGC AATGCAAAAT TTGCTTATTG CAATATTTTC
2901 ATATACAGAC ACTAAAAACA GTTTTCAAAG TCCAGCATTG CGTAACTAAA
2951 GTAAGTAAAA TGATGTGTAT CAACTTGATG GTAAATATG TAGTTATTTA
3001 AAAAAGCAAT GAACAATTTA GTTTCATGAG AAAATGTTGC CCCCTAAAAG
3051 TAGAACACAT ATGTTACAAC TGCAATAATA CTCTGAATTC ATCTTTCACA
3101 AATAAGAGAC ATGTTAGCAT AGTGATTAAA AGCACAGATA TTGGAGACAA
3151 ACTAACCCAG TTTGAACCCT GGCCTGCCA CGTATAGCAC TGCAGCCTTG
3201 GGAAGTTAT TTAACATCAT GGGCTTCAGT TTCAACATCT GTAAAATGGG
3251 CATGTTAACA TTGCCTACCT CATAGGATTA CTGTGAGAAT TTTCTAAGTT
3301 AATATATGTA AAGCAACTTT AAAAAGTGCC TGGCACTTAG TTATTGTTAA
3351 GTAAGTGTCT GCAGATGCAA GTTTGGAAGA GAAAAGCAAA TAAATGAAAA
3401 TCCCTTCCCT TTAAGATGAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGGG
3451 CGGCCGCTCA AGATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAGG

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 35 bp to 2137 bp; peptide length: 701
 Category: similarity to unknown protein

```

1 MEEDTDYRIR FSSLCFFNDH VGFHGTIKSS PSDFIVIEID EQGQLVNKTI
51 DEPIFKISEI QLEPNNFPKK PKLDLQNLSL EDGRNQEVHT LIKYTDGDON
101 HQSGSEKEDT IVDGTSKCEE KADVLSSFLD EKTHELNMF ACDVREKWL
151 KTELIGLPPE FSGRILDKN QRASLHSAIR QKFPFLVTVG KNSEIVVKPN
201 LEYKELCHLV SEEEAFDFFK YLDAKKENSK FTFKPDNTNKD HRKAVHHEVN
251 KKEGNLVETK SFSKMNCASG NPNVVTVRF REKAHKGKRV PLSECQEGKV
301 IYTAFTLRKE NLEMFEAIGF LAIKLGVIPS DFSYAGLKDK KAITIYQAMVV
351 RKVTPERLKN IEKEIEKKRM NVFNIRSVDD SLRLGQLKGN HFDIVIRNLK
401 KQINDSANLR ERIMEAIENV KKKGFVNYG PQRFKGKRV HTDQIGLALL
451 KNEMMKAIKL FLTPEDLDDP VNRAKKYFLQ TEDAKGTLNL MPEFKVRERA
501 LLEALHRRFGM TEEGCIQAWF SLPHSMRIFY VHAYTSKIWN EAVSYRLETY
551 GARVVQGDV CLDEDIDDEN FPNSKIHLVT EEEGSANMYA IHQVVLPLVG
601 YNIQYPKNKV GQWYHDILSR DGLQTCRFKV PTLKLNIPGC YRQILKHPCN
651 LSYQLMEDHD IDVKTKGSHI DETALSLLIS FDLASCYAT VCLKEIMKHD
701 V

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_15g14, frame 2

TREMBL:SPBC1A45P_10 gene: "SPBC1A4.09"; product: "hypothetical protein"; S.pombe chromosome II cosmid clA4 left hand region 1-26184 bp
 Originates from chimeric cosmid., N = 3, Score = 511, P = 2.9e-57

PIR:S67136 hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae), N = 2, Score = 516, P = 7.3e-54

SWISSPROT:YQ4B_CAEEL HYPOTHETICAL 64.6 KD PROTEIN B0024.11 IN CHROMOSOME V., N = 2, Score = 386, P = 2.1e-34

>PIR:S67136 hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae)
 Length = 676

HSPs:

Score = 516 (77.4 bits), Expect = 7.3e-54, Sum P(2) = 7.3e-54
 Identities = 151/498 (30%), Positives = 245/498 (49%)

Query: 191 KNSEIVVKPNLEYKELCHLVSEEEAFDFFK-YLDAKKENSKFTFKPDNTNKDHRKAVHHEV 249
 + E V P L +L + EE+ Y A K + F+ +K R +H +

Sbjct: 109 RRQEFNVDPCLR-NQLVEIFGEEDVLKIESVYRTANKMETAKNFE---DKSVRTKIHQLL 164

Query: 250 NKKFGNLVETKSFSGMNCSSAGNPVNVVTVRFREKAHK-RGKRPLSECQEG-KVIYTAFTL 307
+ F N +E+ + N +EK ++ R + G + FTL

Sbjct: 165 REAFKNELESVTTDTNTFKIARSNRNRSTNKQEKINQTRDANGVENWGYGPKDFIHFTL 224

Query: 308 RKENLEMFEAIGFLAIKLGVIPSD-FSYAGLKDKKAITQAMVVRKVTPERLKNIKIEKE 366
KEN + EA+ + KL +PS YAG KD++A+T Q + + K+ +RL + + +

Sbjct: 225 HKENKDTMEAVNVIT-KLLRVPSRVIRYAGTKDORRAVTCQRVSSISKIGLDRNLNLRNL- 282

Query: 367 KKRNVNFNIRSVDDSLRLGQLKGNHFDIVIRNLKKQINDSANLRERIMEAIENVKKKGFV 426
K M + N D SL LG LKGN F +VIR++ N +L E + +++ + GF+

Sbjct: 283 -KGMIIGNYNFSDASLNLGDLKGNFVVVIRDVTG-NSEVSLEEIVSNGCKSLSENGFI 340

Query: 427 NYYGPRFGKGRKVHTDQIGLALLKNEMMKAIKFLTPEDLDDPVNR-AKKYFLQTEDAK 485
NY+G QRFG + T IG LL + KA +L L+ +D P ++ A+K + +T+DA

Sbjct: 341 NYFGMQRFGTTF-SISTHTIGRELLLSNWKKAELILSDQDNVLPKSKARKIWAETKDAA 399

Query: 486 GTLSLMPEFKVRERALLEALHRFGMTEEGCIQ--AWFS----LPHSMRIFYVHAYTSKIW 539
L MP + E ALL +L E+G A+++ +P ++R YVHAY S +W

Sbjct: 400 LALKQMPROCLAENALLYSLNQRKEEDGTYSENAYYTAIMKIPRNLRTMYVHAYQSYVW 459

Query: 540 NEAVSYRLETYGARVVOGDLVC-----LDEDIDDENFPNS-----KIHVTEEEGS 585
N S R+E +G ++V GDLV L IDDE+F + VT+E+

Sbjct: 460 NSIASKRIELHGLKLVVGDVIDTSEKSPGISGIDDEDFEDVREAQFIRAKAVTQEDID 519

Query: 586 ANMYAIHQVVLVPLGYNIQYPKNK-VGQWYHDILSRDGLQTCRFKVPTLKLNI PGCYRQI 644
+ Y + VVLP G+++ YP N+ + Q Y DIL D + + ++ G YR +

Sbjct: 520 SVKYTMEDVVLPSPGFDVLYPSNEELKQLYVDILKADNMDPFNMRRKVRDFSLAGSYRTV 579

Query: 645 LKHPCNLSYQLMEDHDIDVKTGSHID 671
++ P +L Y+++ D + + +D

Sbjct: 580 IQPKKSLEYRIIHYDDPSQQLVNTDLD 606

Score = 86 (12.9 bits), Expect = 3.2e-01, Sum P(2) = 2.8e-01
Identities = 40/160 (25%), Positives = 77/160 (48%)

Query: 22 GFHGTIKSSPSDFVIEIDEQGQLVNKTIDEPIFKISEIQLEPNNFPKKPKLDLQNLSE 81
GF G IK +DF+V EID++G++++ T D+ FK+ + +P K +++ + S E

Sbjct: 55 GFRGQIKQRYTDFLVNEIDQEGKVIHILT-DKG-FKMPK---KPQR--SKEEVNAEKES-E 106

Query: 82 DGRNQEVHTLIKYTGDQNHQSGS--EKEDTI-VDGTSKCEEKADVLSSFLDEKTHELLN 138
R QE + D + +Q +ED + ++ + K + +F D+ ++

Sbjct: 107 AARRQEFNV-----DPELRNQLVEIFGEEDVLKIESVYRTANKMETAKNFEDKSVRTKI 161

Query: 139 NFACDVREKWLSTKTELIGLPPE-FSIGRILDKNQRASLHSAIRQ 181
+RE + ++ E + F I R ++N R + I Q

Sbjct: 162 QL---LREAFKNELESVTTDTNTFKIARS-NRNRSTNKQEKINQ 201

Score = 58 (8.7 bits), Expect = 7.3e-54, Sum P(2) = 7.3e-54
Identities = 10/23 (43%), Positives = 17/23 (73%)

Query: 676 SLLISFDLDASCYATVCLKEIMK 698
++++ F L S YAT+ L+E+MK

Sbjct: 638 AVVLKFQLGTSAYATMALRELMK 660

Pedant information for DKFZphtes3_15g14, frame 2

Report for DKFZphtes3_15g14.2

[LENGTH] 701
[MW] 80700.96
[pI] 7.31
[HOMOL] PIR:S67136 hypothetical protein YOR243c - yeast (*Saccharomyces cerevisiae*) 2e-51
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR243c] 8e-53
[BLOCKS] BL01268C
[BLOCKS] BL01268B
[BLOCKS] BL01268A
[SUPFAM] hypothetical protein HI0701 3e-06
[PROSITE] MYRISTYL 7
[PROSITE] AMIDATION 2
[PROSITE] CAMP_PHOSPHO_SITE 1
[PROSITE] CK2_PHOSPHO_SITE 16
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] PKC_PHOSPHO_SITE 13
[PROSITE] ASN_GLYCOSYLATION 5
[KW] Alpha_Beta

```

SEQ  MEEDTDYRIRFSSLCFFNDHVGFGHTIKSSPSDFIVIEIDEQGQLVNKTIDEPIFKISEI
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  QLEPNNFPPKPKLQNLSDGRNQEVHTLIKYTDGQNHQSGSEKEDTIVDGTSKCEE
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  KADVLSSFLDEKTHELLNMFACDVREKWLKTELIGLPPEFSIGRILDKNQRASLHSAIR
PRD  hhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhheeeccccccccccccccccccccch

SEQ  QKFPFLVTVGKNSIIVVKPNLEYKELCHLVSEEEAFDFFKYLDACKENSÁFTFKPDTNKD
PRD  hhccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  HRKAVHHFVNKKFGNLVETKSFSSKMNCAGNPVNVTVRFREKAHKRGKRPLSECQEGKV
PRD  hhhhhhhhhhhhhhhhhhhhhheeeccccccccccccccccccccchhhhhhhhhhhhhhh

SEQ  IYTAFTLRKENLEMFEAIGFLAIKLGVI PSDFSAGLKDKKAITYQAMVVRKVTPERLKN
PRD  eeeeeccccccccchhhhhhhhhhhhhccccccccccccccccchhhhhhhheeeccccchhh

SEQ  IEKEIEKKRMNVFNIRSVDDSLRLGQLKGNHFDIVIRNLKKQINDSANLRERIMEAIENV
PRD  hhhhhhhhhhhheeeccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhh

SEQ  KKKGFVNYYGPGQRFKGRKVTQIGLALLKNEMMKAIKFLTPEDLDDPVNRAKKYFLQ
PRD  hhccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  TEDAKGTLSLMPEFKVRERALLEALHRFGMTEEGCIQAWFSLPHSMRIFYVHAYTSKIWN
PRD  hccccchhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhccccchhhhhhhhhhhhh

SEQ  EAVSYRLETYGARVVQGDVLCLEDDIDENFPNSKIHLVTEEEGSANMYAIHQVVLVPLG
PRD  hhhhhhhhhhhcceecccccccccccccccccccccccccccccccccccccccccccc

SEQ  YNIQYPKNKVGQWYHDILSRDGLQTCRFKVP TLKLNIPGCYRQILKHPCNLSYQLMEDHD
PRD  cccccccccchhhhhhhhhhhhhccccccccccccccccccccchhhhhhhhhccccchhhhhhh

SEQ  IDVKTKGSHIDETALLISFDLDASCYATVCLKEIMKHDV
PRD  ceccccccccchhhhhhhheeeccccccccchhhhhhhhhhhhhcc

```

Prosites for DKF2phtes3_15g14.2

PS00001	47->51	ASN_GLYCOSYLATION	PDOC00001
PS00001	77->81	ASN_GLYCOSYLATION	PDOC00001
PS00001	266->270	ASN_GLYCOSYLATION	PDOC00001
PS00001	404->408	ASN_GLYCOSYLATION	PDOC00001
PS00001	650->654	ASN_GLYCOSYLATION	PDOC00001
PS00004	351->355	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	105->108	PKC_PHOSPHO_SITE	PDOC00005
PS00005	115->118	PKC_PHOSPHO_SITE	PDOC00005
PS00005	232->235	PKC_PHOSPHO_SITE	PDOC00005
PS00005	237->240	PKC_PHOSPHO_SITE	PDOC00005
PS00005	277->280	PKC_PHOSPHO_SITE	PDOC00005
PS00005	306->309	PKC_PHOSPHO_SITE	PDOC00005
PS00005	381->384	PKC_PHOSPHO_SITE	PDOC00005
PS00005	525->528	PKC_PHOSPHO_SITE	PDOC00005
PS00005	535->538	PKC_PHOSPHO_SITE	PDOC00005
PS00005	544->547	PKC_PHOSPHO_SITE	PDOC00005
PS00005	625->628	PKC_PHOSPHO_SITE	PDOC00005
PS00005	632->635	PKC_PHOSPHO_SITE	PDOC00005
PS00006	30->34	CK2_PHOSPHO_SITE	PDOC00006
PS00006	49->53	CK2_PHOSPHO_SITE	PDOC00006
PS00006	79->83	CK2_PHOSPHO_SITE	PDOC00006
PS00006	95->99	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	110->114	CK2_PHOSPHO_SITE	PDOC00006
PS00006	116->120	CK2_PHOSPHO_SITE	PDOC00006
PS00006	127->131	CK2_PHOSPHO_SITE	PDOC00006
PS00006	150->154	CK2_PHOSPHO_SITE	PDOC00006
PS00006	211->215	CK2_PHOSPHO_SITE	PDOC00006
PS00006	237->241	CK2_PHOSPHO_SITE	PDOC00006
PS00006	377->381	CK2_PHOSPHO_SITE	PDOC00006
PS00006	463->467	CK2_PHOSPHO_SITE	PDOC00006
PS00006	580->584	CK2_PHOSPHO_SITE	PDOC00006
PS00006	668->672	CK2_PHOSPHO_SITE	PDOC00006
PS00007	537->546	TYR_PHOSPHO_SITE	PDOC00007
PS00008	25->31	MYRISTYL	PDOC00008
PS00008	43->49	MYRISTYL	PDOC00008
PS00008	114->120	MYRISTYL	PDOC00008

PS00008	326->332	MYRISTYL	PDOC00008
PS00008	385->391	MYRISTYL	PDOC00008
PS00008	514->520	MYRISTYL	PDOC00008
PS00008	622->628	MYRISTYL	PDOC00008
PS00009	287->291	AMIDATION	PDOC00009
PS00009	436->440	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_15g14.2)

DKFZphtes3_15h1

group: testes derived

DKFZphtes3_15h1 encodes a novel 672 amino acid protein with very weak similarity to several proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to Hsp70/Hsp90 organizing protein

complete cDNA, complete cds, no EST hits

Sequenced by GBF

Locus: unknown

Insert length: 2277 bp

Poly A stretch at pos. 2252, polyadenylation signal at pos. 2226

```
1 AAACCAGATA GAGGTTCTCC AGCTTTTCTT TGATTGTCTC TGCTTTAGCG
51 TCTCTAAATC CGGTCACCAT GTCGGACCCC GAAGGCGAGA CCTTGCGAAG
101 CACCTTTCCC TCTTATATGG CCGAAGGCGA GCGGCTCTAC CTGTGCGGGG
151 AATTTTCTAA AGCGCGCGAG AGCTTCAGCA ACGCTCTTTA CCTTCAGGAT
201 GGAGACAAGA ACTGCCTGGT TGCTCGCTCA AAGTGCTTCC TGAAGATGGG
251 AGACTTGGAG AGATCCCTGA AGGATGCTGA GGCTTCGCTC CAGAGTGACC
301 CAGCTTTCTG TAAGGGGATT TTGCAAAAGG CTGAGACACT GTACACCATG
351 GGAGACTTTG AGTTTGCCTT GGTATTCTAT CATCGAGGCT ACAAGCTGAG
401 GCCTGATCGG GAATTCAGAG TTGGCATTCA GAAAGCCCAG GAAGCCATCA
451 ACAACTCAGT GGGAAAGTCCT TCTTCCATTA AGCTGGAGAA CAAAGGGGAC
501 CTCTCCTTCT TAAGCAAGCA GGCTGAGAAT ATAAAAGCCC AGCAGAAGCC
551 TCAGCCCATG AAACACCTCT TACACCCAC CAAGGGAGAG CCCAAGTGGA
601 AGGCCTCGCT CAAGAGTGAG AAGACTGTCC GCCAGCTTCT GGGGGAGCTC
651 TACGTGGACA AAGAGTATT GGAGAAGCTC CTATGGATG AAGACCTGAT
701 CAAAGGCACC ATGAAGGGCG GCCTGACTGT GGAGGACCTC ATCATGACGG
751 GCATCAACTA CCTGGATACT CACAGCAACT TCTGGAGGCA GCAGAAGCCG
801 ATCTACGCCA GGGAGCGGGA CCGAAGCTG ATGCAAGAGA AATGGCTGCG
851 GGACCACAAA CGCCGTCCTT CACAGACAGC CCATTACATC CTCGAAGGCC
901 TGGAGGAGAT TGATATGTTG CTCACAAGTG GCAGTGTGTA AGGGAGTCTT
951 CAGAAAGCTG AGAAAGTGCT GAAGAAGGTA CTGGAATGGA ACAAGGAAGA
1001 GGTACCCAAC AAGGATGAAC TGGTTGGAAA CTTGTATAGC TGCATAGGGA
1051 ATGCCCAGAT TGAGCTGGGG CAGATGGAGG CAGCCCTGCA GAGCCACAGA
1101 AAGGACCTGG AGATCGCCAA GGAATATGAC CTTCTGTATG CAAAATCGAG
1151 AGCCCTTGAC AACATTGGCA GAGTTTTTGC CAGAGTTGGG AAATTCCAGC
1201 AAGCCATTGA CACGTGGGAA GAAAAGATCC CTCTGGCAAA AACCACCCTG
1251 GAGAAGACCT GGCTGTTCCA CGAGATCGGC CGCTGCTACT TGGAGCTGGA
1301 CCAGGCCTGG CAGGCCCAGA ATTATGGCGA GAAGTCCCAG CAGTGTGCCG
1351 AGGAGGAAGG GGACATTGAG TGGCAACTGA ATGCCAGTGT TCTGGTGGCC
1401 CAGGCACAAG TGAAGCTGAG AGACTTCGAG TCAGCCGTGA ACAATTTTGA
1451 GAAGGCCCTG GAGAGAGCAA AGCTTGTGCA TAACAACGAG GCGCAGCAGG
1501 CCATCATCAG TGCCCTGGAC GATGCCAACA AGGGTATCAT CAGAGAAGCTG
1551 AGGAAGACCA ACTACGTGGA GAATCTCAA GAAAAAGCG AGGGAGAAGC
1601 TTCACTGTAT GAAGATAGAA TAATAACAAG AGAGAAGGAC ATGAGGAGAG
1651 TGAGAGATGA GCCCGAGAAG GTGCTGAAGC AGTGGGACCA TAGTGAGGAT
1701 GAGAAAGAGA CAGATGAGGA CGATGAGGCT TTTGGGGAAG CTCTGCAGAG
1751 CCCAGCAAGC GGAAGCAGAG GTGTGGAAGC AGGAAAAGCC AGAAGCGATT
1801 TGGGAGCAGT TGCCAAGGGC CTGTCAGGAG AATTAGGCAC AAGATCAGGA
1851 GAAACAGGCA GGAAGCTACT AGAAGCTGGC AGAAGAGAGT CAAGAGAAAT
1901 TTATAGGAGG CCTTCGGGAG AATTAGAGCA AAGACTCTCA GGAGAATTCA
1951 GCAGACAGGA ACCAGAAGAA CTAAAGAAAC TTTCAGAAGT GGGCAGAAGA
2001 GAGCCAGAAG AACTGGGAAA AACACAATTT GGAGAAATAG GAGAAACGAA
2051 AAAAAACAGA AATGAGATGG AAAAGGAATA TGAATGAAGC CATCGGTAGA
2101 GATGAGGATC AGGAAGCTGG TGTTCAAGAG GATCATGGGA TTTTATTAAA
2151 CTGGATTTC AAGCGATTG TCTGTTATAG GAAAAATGAG GGTTTTACTT
2201 CTGTGCTTT CCACTACTAT TTTGCCATTA AATAGGTGTC TTTCACTCTT
2251 GCAAAAAAAA AAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

No Medline entry

Peptide information for frame 3

ORF from 69 bp to 2084 bp; peptide length: 672
Category: similarity to known protein

1	MSDPEGETLR	STFPSYMAEG	ERLYLCGEFS	KAAQSFSNAL	YLQDGDKNCL
51	VARSCKFLKM	GDERSLSKDA	EASLQSDPAF	CKGILQKAEAT	LYTMGDFEFA
101	LVFYHRGYKL	RPDREFRVGI	KQAQEAINNS	VGPSSSIKLE	NKGDLSFLSK
151	QAEINAKAQQK	RPDMKHLHP	TKGEPKKWAS	LKSEKTVRQL	LGELYVDKEY
201	LEKLLDLEDL	IKGTMKGGLT	VEDLIMTGIN	YLDTHSNFWR	QQKPIYAER
251	DRKMLQEWKL	RDHKRPSQT	ALYILSKLED	IMDLTLSGSA	EGSLQAKAEKV
301	LKKVLEWNKE	EVPNKDELVG	NHICISGNAQ	IELGQMEAL	QSHRKDELEIA
351	KEYDLPDAKS	RALDNIGRVF	ARVGKFQQAII	DTWEEKIPLA	KTTLEKTWLF
401	HEIGRCYLEL	DQAWQAQNYL	EKSQQCAEEE	GDIEWQLNAS	VLVAQAQVKL
451	RDFSFAVNFF	EKALERAQKL	HNNEAQAQAI	SALDDANKGI	IRELKRTNYN
501	ENLKEKSEGE	ASLYEDRIIT	REKDMRRVRD	EPEKVQKQWD	HSEDEKETDE
551	DDEAFGEALQ	SPASGQSQVE	AGKARSDLGA	VAKGLSGELG	TRSGETGRKL
601	LEAGRRESRE	IYRRPSGELE	QRLSGEFSRQ	EPEELKKLSE	VGRREPEELG
651	KTOFGEIGET	KKTGNEMEKE	YE		

BLASTP hits

Entry AF039202_1 from database TREMBL:
product: "Hsp70/Hsp90 organizing protein"; *Cricetulus griseus*
Hsp70/Hsp90 organizing protein mRNA, complete cds.
Score = 149, P = 5.3e-07, identities = 42/160, positives = 74/160

Entry AI09782_1 from database TREMBL:
product: "myosin heavy chain"; *Argopecten irradians* myosin heavy chain
mRNA, complete cds.
Score = 155, P = 6.1e-07, identities = 140/623, positives = 256/623

Entry S56658 from database PIR:
stress-induced protein stil - soybean
Score = 156, P = 9.7e-08, identities = 41/153, positives = 72/153

Alert BLASTP hits for DKFZphtes3 15h1, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_15h1, frame 3

Report for DKFZphtes3 15h1.3

```

[LENGTH]          672
[MW]               76655.61
[pI]              5.49
[HOMOL]           PIR:S56658 stress-induced protein stil - soybean 6e-10
[SUPFAM]          tetratricopeptide repeat homology 1e-07
[PROSITE]         MYRISTYL          7
[PROSITE]         AMIDATION         3
[PROSITE]         CAMP_PHOSPHO_SITE 4
[PROSITE]         CK2_PHOSPHO_SITE  15
[PROSITE]         TYR_PHOSPHO_SITE   1
[PROSITE]         PKC_PHOSPHO_SITE   11
[PROSITE]         ASN_GLYCOSYLATION  2
[KW]              All_Alpha
[KW]              LOW_COMPLEXITY      4.76 %

```

```

SEQ      MSDPEGETLRSTFPSYMAEGERLYLCGEFSKAAQSFSNALYLQDGDKNCLVARSKCF LKM
SEG
PRD      cccccccceeeccccccccccccccccccccchhhhhhhhhhhhhhhhhccccceehhhhhhhhhh

SEQ      GDLERSLKDAEASLQSDPAFCKGILQKAETLYTMGDFEFALVFYHRYGKLRPDREFRVGI
SEG
PRD      hcchhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccchhhhhh

```

```

SEQ      QKAQEAINNSVGSPSSIKLENKGDLSFLSKQAENIKAQQKPQPMKHLLHPTKGEPKWKAS
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhccchhhhhhhchhhhhhhccchhhhhhhccccccccchhh

SEQ      LKSEKTVRQLLGELYVDKEYLEKLLDEDLIKGTMKGGLTVEDLIMTGINYLDTHSNFWR
SEG      .....XXXXXXXXXXXXXXXXXXXXX.....
PRD      hhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhcccccccccccccc

SEQ      QQKPIYARERDRKLMQEKWLRDHKRRPSQTAHYILKSLEDIDMLLTSGSAEGSLQKAEKV
SEG      .....
PRD      cchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhheeeccccchhhhhhhhh

SEQ      LKKVLEWNKEEVPNKDELVGNLYSCIGNAQIELGQMEALQSHRKDLEIAKEYDLPDAKS
SEG      .....
PRD      hhhhhhhhhccccccccceeeccccccchhhhhhhhhhhhhhhhhhhhhhhccccchh

SEQ      RALDNIGRVFARVGKFQQAIDTWEEKIPLAKTTLEKTWLFHEIGRCYLELDQAWQAQNYG
SEG      .....
PRD      hhhccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhh

SEQ      EKSQQCAEEEGDIEWQLNASVLVAQAQVKLRDFESAVNNFEKALERAKLVHNNEAQQAII
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhh

SEQ      SALDDANKGIIRELRKTNYVENLKEKSEGEASLYEDRIITREKDMRRVRDEPEKVVKQWD
SEG      .....
PRD      hhhhccchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhccccceec

SEQ      HSEDEKETDEDEAFGEALQSPASGKQSVEAGKARSDLGAVAKGLSGELGTRSGETGRKL
SEG      .....XXXXXXXXXXXXXXXXXXXXX.....
PRD      cccccccccccchhhhhhhccccccccchhhhhccccccccceeeccccccccccccccchhh

SEQ      LEAGRRESREIYRRPSGELEQRLSGEFSRQEPEELKKLSEVGRREPEELGKTQFGEIGET
SEG      .....
PRD      hhhccccccccceeeccccchhhhhccccccchhhhhhhhhhhcccccccccccccccccccc

SEQ      KKTGNEMEKEYE
SEG      .....
PRD      cccccccccccc

```

Prosites for DKFZphtes3_15h1.3

PS00001	128->132	ASN_GLYCOSYLATION	PDOC00001
PS00001	438->442	ASN_GLYCOSYLATION	PDOC00001
PS00004	265->269	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	605->609	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	613->617	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	636->640	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	8->11	PKC_PHOSPHO_SITE	PDOC00005
PS00005	66->69	PKC_PHOSPHO_SITE	PDOC00005
PS00005	136->139	PKC_PHOSPHO_SITE	PDOC00005
PS00005	180->183	PKC_PHOSPHO_SITE	PDOC00005
PS00005	183->186	PKC_PHOSPHO_SITE	PDOC00005
PS00005	186->189	PKC_PHOSPHO_SITE	PDOC00005
PS00005	214->217	PKC_PHOSPHO_SITE	PDOC00005
PS00005	342->345	PKC_PHOSPHO_SITE	PDOC00005
PS00005	564->567	PKC_PHOSPHO_SITE	PDOC00005
PS00005	596->599	PKC_PHOSPHO_SITE	PDOC00005
PS00005	660->663	PKC_PHOSPHO_SITE	PDOC00005
PS00006	2->6	CK2_PHOSPHO_SITE	PDOC00006
PS00006	66->70	CK2_PHOSPHO_SITE	PDOC00006
PS00006	93->97	CK2_PHOSPHO_SITE	PDOC00006
PS00006	171->175	CK2_PHOSPHO_SITE	PDOC00006
PS00006	220->224	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	382->386	CK2_PHOSPHO_SITE	PDOC00006
PS00006	392->396	CK2_PHOSPHO_SITE	PDOC00006
PS00006	481->485	CK2_PHOSPHO_SITE	PDOC00006
PS00006	507->511	CK2_PHOSPHO_SITE	PDOC00006
PS00006	512->516	CK2_PHOSPHO_SITE	PDOC00006
PS00006	542->546	CK2_PHOSPHO_SITE	PDOC00006
PS00006	548->552	CK2_PHOSPHO_SITE	PDOC00006
PS00006	628->632	CK2_PHOSPHO_SITE	PDOC00006
PS00006	663->667	CK2_PHOSPHO_SITE	PDOC00006
PS00007	506->515	TYR_PHOSPHO_SITE	PDOC00007
PS00008	119->125	MYRISTYL	PDOC00008
PS00008	132->138	MYRISTYL	PDOC00008
PS00008	213->219	MYRISTYL	PDOC00008

PS00008	288->294	MYRISTYL	PDOC00008
PS00008	320->326	MYRISTYL	PDOC00008
PS00008	334->340	MYRISTYL	PDOC00008
PS00008	590->596	MYRISTYL	PDOC00008
PS00009	596->600	AMIDATION	PDOC00009
PS00009	603->607	AMIDATION	PDOC00009
PS00009	641->645	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_15h1.3)

DKFZphtes3_15i5

group: cell structure and motility

DKFZphtes3_15i5 encodes a novel 717 amino acid protein with similarity to radial spokehead proteins.

The novel protein is similar to the *Chlamydomonas reinhardtii* radial spokehead protein of flagella or axoneme and to the *Strongylocentrotus purpuratus* sea urchin spermatozoa protein p63. This protein is important for the maintenance of a planar form of sperm flagellar beating. In addition, the novel protein contains a transferrin signature 1 for iron-binding. The new protein seems to be a part of the human radial spoke heads in spermatozoa.

BLAST results: No predictive prosite, pfam or SCOP motif.

The new protein can find application in modulating the structure of the human spermatozoa radial spoke head and modulation of sperm motility in men.

strong similarity to "radial spokehead" proteins

complete cDNA, complete cds, 1 EST hit (from a testis library)
"radial spokehead" part of flagella in *Chlamydomonas*, this protein seems to be part of the sperm motor or tail

Sequenced by GBF

Locus: unknown

Insert length: 2478 bp

Poly A stretch at pos. 2452, polyadenylation signal at pos. 2433

```
1 CACCCCTGGCC CGCTCCCCGC GCCCTCCACG GGTAACGGCC CCCTCTCTCG
51 GTGCTCAGAA ACCGGCGGTG TCGACAGGTG GCTCTCGCTT GGCCTCCTTG
101 TCTGCAAGCC TTTCTCCTAG AGATCTGTGC CTCCTGGCGA ACCATGGGAG
151 ACCTGCGGCC CTACCCTGAG CGCCCTGCCC AGCAGCCTCC GGGCCGGAGG
201 ACTTCTCAGG CCTCCCAGAG GCGGCACAGT CCGGACCAAG CTCAGGCCCT
251 GGCAGCGGAC CCCGAGGAGA GGCAGCAGAT ACCTCCAGAC GCCCAGCGAA
301 ACGCCCCCTGG TTGGTCACAG AGGGGCAGCC TGTCCCAACA GGAGAACTTG
351 CTGATGCCCC AGGTCTTCCA GGCTGAGGAA GCCCGGCTGG GTGGCATGGA
401 GTACCCATCT GTGAACACGG GCTTTCCTC AGAGTTCCAG CCTCAGCCTT
451 ACTCTGATGA AAGCAGGATG CAGGTCGCCG AGCTCACCAC CAGCCTAATG
501 CTGCAGCGGC TCCAGCAGGG CCAAAGCAGC CTGTTCCAGC AACTGGACCC
551 CACCTTCCAG GAGCCCCCAG TCAACCCCTT GGGCCAGTTC AACCTTACC
601 AGACAGACCA GTTCTCTGAA GGTGCCAGC ACGGGCCTTA CATAAGGGAT
651 GACCCTGCCC TTGAGTTCTT GCCCTCTGAG CTGGGCTTCC CACACTACAG
701 TGCCCAAGTG CCTGAGCCCG AGCCTCTGGA GCTGGCCGTG CAGAACGCCA
751 AGGCCCTACCT GCTGCAGACC AGCATCAATT GCGACCTCAG CCTGTACGAG
801 CACCTGGTAA ATCTGCTGAC CAAGATCCTG AACCAGCGGC CTGAGGACCC
851 CTGTCTGTGC CTGGAGTCTC TGAACCGCAC CACGCAGTGG GAGTGGTTCC
901 ACCCCAAGCT GGACACGCTG CGGGACGACC CCGAGATGCA GCCCACCTAC
951 AAGATGGCGG AGAAACAGAA GCGGCTGTTT ACCCGGAGTG GAGGCGGCAC
1001 TGAAGCGCAA CAGGAGATGG AGGAGGAGGT GGGGGAGACA CCAAGTCCCCA
1051 ACATCATGGA GACTGCCTTC TACTTCGAGC AGGCCGCGT CGGCCTGAGC
1101 TCGGACGAGA GCTTCCGCAT TTTCTGGGCC ATGAAACAGC TGGTGGAGCA
1151 GCAGCCCATC CACACCTGTC GCTTCTGGGG CAAGATCCTG GGAATCAAAC
1201 GCAGCTACCT GGTGGCCGAG GTGGAATTCC GGGAGGGCGA GGAGGAGGCA
1251 GAGGAGGAGG AGGTGGAGGA GATGACGGAA GGTGGCGAGG TCATGGAGGC
1301 GCAGCGCGAG GAGGAGGGCG AGGAGGACGA GGAGAAGGCC GTGGACATCG
1351 TCCCTAAGTC CGTATGGAAG CCGCCGCCCG TGATCCCCAA GGAGGAGAGC
1401 CGCTCAGGCG CCAACAAGTA CCTGTACTTT GTGTGCAACG AGCCGGGCCCT
1451 GCCATGGACG CCGCTGCCCC ACCTCACTCC AGCCCAGATC GTGAACGCCC
1501 GAAAGATCAA GAAGTTCTTC ACAGGCTACC TGGACACGCC AGTCGTGAGC
1551 TACCCACCCT TCCCGGGCAA CGAGGCCAAC TACCTGCGGG CCCAGATAGC
1601 CCGCATCTCG GCCGCCACGC AGGTGAGCCC GCTGGGCTTC TACCAGTTTA
1651 GTGAGGAGAG GGGCGACGAG GAGGAGGAAG GTGGTGTCTG GCGCGACTCC
1701 TACGAGGAGA ACCCGGACTT CGAGGGCATC CCCGTGCTGG AGCTGGTCTGA
1751 CTCATGGGCC AACTGGGTGC ATCACACACA GCACATCCTG CCGCAGGGCC
1801 GCTGCACCTT GTGAACCCCT TTGCAGAAGA CAGAGGAGGA GGAGGACCTG
1851 GGGGAGGAGG AAGAGAAGGC AGATGAGGGG CCAGAGGAGG TGGAGCAGGA
1901 GGTGAGGCCC CCACTGCTAA CGCCACTTTC AGAAGATGCA GAAATCATGC
1951 ACCTGGCACC CTGGAACACC CGCCTGTCTT GCAGCCTCTG CCCGAGTAC
2001 TCAGTGGCCG TTGTGCGCTC CAACCTCTGG CCCGGGCCCT ATGCCTATGC
2051 CAGTGGGAAA AAGTTTGAGA ACATCTACAT CGGCTGGGGT CACAAGTACA
2101 GCCCGAGAG CTTCACCCCG GCCCTGCCAG CCCCATTCA ACAAGAGTAC
2151 CCCAGTGGCC CAGAGATCAT GGAGATGAGT GACCCACAG TGGAGAGGGA
2201 GCAGGCTCTG AAAGCAGCCC AGGAACAAGC CCTGGGAGCC ACAGAGGAGG
2251 AGGAGGAGG CGAGGAGGAG GAGGAGGGCG AGGAGACAGA TGAAGGAGG
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2301 CCACCCTCTA GCCACTTTCC CCAAGCAGGT AGATAGCAA TTTCCCCTTA
 2351 GAGGTAGTTA GCATGGATTA TATTTTCACT ATGTGCTTCC TGTCCTCAGA
 2401 GGGCAGGGAT AGAAAAGGAA GGCAACTGCT TCAAATAAAA TTCCTCCACG
 2451 GCATTAAAAA AAAAAAAAAA AAAAAAAG

BLAST Results

No BLAST result

Medline entries

86251010:

Molecular cloning and expression of flagellar radial spoke and dynein genes of *Chlamydomona*

81142496:

Radial spokes of *Chlamydomonas* flagella: polypeptide composition and phosphorylation of stalk components.

9450971:

Molecular cloning and characterization of a radial spoke head protein of sea urchin sperm axonemes: involvement of the protein in the regulation of sperm motility.

Peptide information for frame 3

ORF from 144 bp to 2294 bp; peptide length: 717
 Category: strong similarity to known protein

1 MGDLPYPYPER PAQQPPGRRT SQASQRRHSR DQAQALAADP EERQQIPPPDA
 51 QRNAPGWSQR GSLSQQENLL MPQVFQAEAA RLGGMEYPSV NTGFPSEFQP
 101 QPYSDESRMQ VAELTTSMLL QRLQQQSSL FQLDPTFOE PPVNPPLGQFN
 151 LYQTDQFSEG AQHGPYIRDD PALQFLPSEL GFPHYSAQVP EPEPLELAVQ
 201 NAKAYLLQTS INCDSLSEYH LVNLLTKILN QRPEDPLSVL ESLNRTTQWE
 251 WFHPKLDTLR DDPEMQPTYK MAEKQKALFT RSGGGTEGEQ EMEEVGETP
 301 VPNIMETAFY FEQAGVGLSS DESFRIFLAM KQLVEQQPIH TCRFWGKILG
 351 IKRSYLVAEV EFREGEEAE EEEVEEMTEG GEVMEAHGEE EGEEDEEKAV
 401 DIVPKSVWKP PPVIPKEESR SGANKYLYFV CNEPGLPWTR LPHVTPAQIV
 451 NARKIKKFFT GYLDTPVVSY PFPFGNEANY LRAQIARISA ATQVSPLGFY
 501 QFSEEEGDEE EEEGAGRDSY EENPDFEGIP VLELVDSMAN WVHHTQHILP
 551 QGRCTWVNPL QKTEEEEDLG EEEKADGEP EEVEQEVGPP LLTPLSEDAE
 601 IMHLAPWTTR LSCSLCPQYS VAVVRSNLWP GAYAYASGKK FENIYIGWGH
 651 KYSPESFNPA LPAPIQQEYP SGPEIMEMSD PTVEEQALK AAQEALGAT
 701 EEEEEEEEE EGEETDD

BLASTP hits

Entry U73123_1 from database TREMBL:

product: "radial spokehead"; *Strongylocentrotus purpuratus* radial spokehead mRNA, complete cds.

Score = 1604, P = 7.4e-165, identities = 303/523, positives = 395/523

Entry B44498 from database PIR:

radial spoke protein 6 - *Chlamydomonas reinhardtii*

Score = 386, P = 3.4e-45, identities = 105/264, positives = 138/264

Alert BLASTP hits for DKFZphtes3_15i5, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_15i5, frame 3

Report for DKFZphtes3_15i5.3

[LENGTH] 717
 [MW] 80913.61
 [pI] 4.36

[HOMOL] TREMBL:U73123_1 product: "radial spokehead"; Strongylocentrotus purpuratus
radial spokehead mRNA, complete cds. 1e-130
[PROSITE] TRANSFERRIN_1 1
[PROSITE] MYRISTYL 5
[PROSITE] AMIDATION 2
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] CK2_PHOSPHO_SITE 14
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] GLYCOSAMINOGLYCAN 1
[PROSITE] PKC_PHOSPHO_SITE 8
[PROSITE] ASN_GLYCOSYLATION 1
[KW] All_Alpha
[KW] LOW_COMPLEXITY 21.48 %

```

SEQ  MGDLPYPYPERPAQPPGRRTSQASQRRHSRDQAQALAADPEERQQIPPDAGRNPAGWSQR
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  GSLSQQENLLMPQVFQAEEARLGGMEYPSVNTGFPSEFQPPYSDESRMQVAELTTSMLM
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  QRLQQGQSSLFQQLDPTFQEPVNPPLGQFNLYQTDQFSEGAQHGPYIRDDPALQFLPSEL
SEG  xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  hhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  GFPHYSAQVPEPEPELEAVQNAKAYLLQTSINCDLSLYEHLVNLTKILNQRPEDPLSVL
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  ESLNRTTQWEWFHPKLDLTDPEMQPTYKMAEKQKALFTRSGGGTEGEQEMEEVEGETP
SEG  .....
PRD  hhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  VPMIMETAFYFEQAGVGLSSDESFRIFLAMKQLEQPIHTCRFWGKILGIKRSYLVAEV
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  EFREGEERAEVEEEMTEGGEVMEAHGEEGEEDEEKAVDIVPKSVWKPVPVPIKEESR
SEG  xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  hhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccc

SEQ  SGANKYLYFVCNEPGLPWTRLPHVTPAQIVNARKIKKFFTGYLDTFVVSYPFPGNEANY
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  LRAQIARISAAQTQVPLGFYQFSEEGDEEEEGGAGRDSYEENPDFEGI PVLELVDSMAN
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccc

SEQ  WVVHTQHILPQGRCTWVNPLQKTEEEEDLGEEEKKADEGPVEVEQEVGPPLLTPLSEDAE
SEG  .....
PRD  hhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  IMHLAPWTRLSCSLCPQYSVAVVRNWLPGAYAYASGKKFENIYIGWGHKYSPEFNPFA
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  LPAPIQOEYPSGPEIMEMSOPTEVEEQALKAQEQALGATEEEEEEEEEEEGETDD
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

Prosites for DKFzphes3_15i5.3

PS00001	244->248	ASN_GLYCOSYLATION	PDOC00001
PS00002	282->286	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	18->22	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	26->30	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	24->27	PKC_PHOSPHO_SITE	PDOC00005
PS00005	58->61	PKC_PHOSPHO_SITE	PDOC00005
PS00005	258->261	PKC_PHOSPHO_SITE	PDOC00005
PS00005	268->271	PKC_PHOSPHO_SITE	PDOC00005
PS00005	323->326	PKC_PHOSPHO_SITE	PDOC00005
PS00005	341->344	PKC_PHOSPHO_SITE	PDOC00005
PS00005	608->611	PKC_PHOSPHO_SITE	PDOC00005
PS00005	637->640	PKC_PHOSPHO_SITE	PDOC00005
PS00006	64->68	CK2_PHOSPHO_SITE	PDOC00006
PS00006	137->141	CK2_PHOSPHO_SITE	PDOC00006

PS00006	216->220	CK2_PHOSPHO_SITE	PDOC00006
PS00006	238->242	CK2_PHOSPHO_SITE	PDOC00006
PS00006	247->251	CK2_PHOSPHO_SITE	PDOC00006
PS00006	258->262	CK2_PHOSPHO_SITE	PDOC00006
PS00006	286->290	CK2_PHOSPHO_SITE	PDOC00006
PS00006	319->323	CK2_PHOSPHO_SITE	PDOC00006
PS00006	503->507	CK2_PHOSPHO_SITE	PDOC00006
PS00006	519->523	CK2_PHOSPHO_SITE	PDOC00006
PS00006	563->567	CK2_PHOSPHO_SITE	PDOC00006
PS00006	671->675	CK2_PHOSPHO_SITE	PDOC00006
PS00006	682->686	CK2_PHOSPHO_SITE	PDOC00006
PS00006	700->704	CK2_PHOSPHO_SITE	PDOC00006
PS00007	639->646	TYR_PHOSPHO_SITE	PDOC00007
PS00008	284->290	MYRISTYL	PDOC00008
PS00008	315->321	MYRISTYL	PDOC00008
PS00008	350->356	MYRISTYL	PDOC00008
PS00008	435->441	MYRISTYL	PDOC00008
PS00008	475->481	MYRISTYL	PDOC00008
PS00009	16->20	AMIDATION	PDOC00009
PS00009	637->641	AMIDATION	PDOC00009
PS00205	619->628	TRANSFERRIN_1	PDOC00182

(No Pfam data available for DKF2phtes3_15i5.3)

DKFZphtes3_15j18

group: testes derived

DKFZphtes3_15j18 encodes a novel 148 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, few EST hits

Sequenced by GBF

Locus: unknown

Insert length: 905 bp

Poly A stretch at pos. 839, polyadenylation signal at pos. 815

```
1 GTGATTCATA TGCTTCCATA GCAGGTGTCT GCTTCTGAGC CAAGCTCCCA
51 GGGCAGCGGA GCAGGCACCA ACCAGCATCC CAGGGGAGGG CACAGCTTGT
101 CCAGCTGGGA TGTITGGGTG CCCTGTGAGA TGCCCCAAGC CACCAACCCA
151 GCTTATCTCA GGAGAAGCCT CGGCGGCCCG TCTGCCGCCG TGGAGAGATG
201 TGCTACAGCA GCCGGGGGTG GGGGGAGAGG GTGGGCTTAG AATCTCTTGG
251 CAGGGAGCCC CCAAGAGCAG GGTGAGACCT GCCTTCATTT CACCTGTCCC
301 CTTACAGATT CTGCAAAGCC AGCATTATCA TCCCTTTTCA GAAGGAGTGG
351 GCACTCAGGT GGAATGCCTC ACCCCAGTCC TGCGGCTGGA AAGCGATATG
401 GCCAGGACTG CACCCACCCC CTCATCCCTG CACCCCTTCC CTGCCTGGGA
451 TTCCTCCAGC CCTGTGCACT GTGGAGCGCC TCTGCCTTCC GCTCATGGAG
501 GTTCCCAAG GGCACGCGCT GAGGGCAGCT GGTCTCAGCC TGGGGCCGGG
551 TCCTAGTAAC TGTCTCTCTT TGCTTCCAG CCAGTGTTTT GGGGTTTGAA
601 GTTGGAATCT TCAGCTACTG TCAAGAACAG CCACAAAAAT GTGTCACGAT
651 CAAGATCTTT GAGAGTCCAC CAATCAGGAG GCGTCTGTGA CAGTCGCTGT
701 CTTCTCAGAA CAGAATCCAC ACCCAGGATT CAACCCAAAT GATTTCTCAT
751 CAGGTGATTC TTGGTTGTAG CAAAGTTCAT GTGAATGTGG GTGAGTTTCT
801 GTTATGAATG TGGTCAATAA ATGTTATTTG TGAAACTCTA AAAAAAAAAA
851 AAAAAAAAG GGCGCCGCT CTAGAGGATC CAAGCTTACG TACGCGAAAA
901 AAAAG
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 110 bp to 553 bp; peptide length: 148
Category: putative protein

```
1 MFGCPVRCFK PPTQLISGEA SAARLPWARD VLOQPGVGGE GGLRISWQGA
51 PKSRVRPAFI SPVPFTVLQS QHYHFFSEGV GTQVECLTPV LRLESDMART
101 APHPSSLHFF PAWDSSSPVH CGAPLPSAHG GFPRARAEGS WSQPAGGS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_15j18, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3_15j18, frame 2

Report for DKFZphtes3_15j18.2

[LENGTH] 148
[MW] 15665.78
[pI] 8.91
[PROSITE] MYRISTYL 3
[PROSITE] CK2_PHOSPHO_SITE 1
[KW] Irregular

SEQ MFGCPVRCPKPPTQLISGEASAARLPAWRDVLQQPGVGEGGLRISWQGAPKSRVRPAFI
PRD cccccccccccccccccccccchhhhhhcccccccccccccccccccccccccccc

SEQ SPVPFTVLQSQHYHPFSEGVGTQVECLTPVLRLESDMARTAPHPSSLHPFPDSSSPVH
PRD cccccccccccccccccccccchhhhhhcccccccccccccccccccccccccccc

SEQ CGAPLP SAHGGFPRARAEGSWSQPGAGS
PRD ccccccccccccccccccccccccccccccccc

Prosites for DKFZphtes3_15j18.2

PS00006	82->86	CK2_PHOSPHO_SITE	PDOC00006
PS00008	38->44	MYRISTYL	PDOC00008
PS00008	42->48	MYRISTYL	PDOC00008
PS00008	49->55	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_15j18.2)

DKFZphtes3_15j3

group: nucleic acid management

DKFZphtes3_15j3 encodes a novel 743 amino acid protein with similarity to proteins with unknown function.

The novel protein contains a RNA recognition motif, predicted by Pfam and therefore binds to RNA. The protein is similar to YGR276c, a ribonuclease H of *S. cerevisiae*. Thus, the protein seems to be a new RNA-modifying protein.

The new protein can find application in modulating the RNA metabolism in human cells and as a tool for biotechnologic manipulations.

"44M2.3"; product, differences to genmodel, similarity to ribonuclease H

complete cDNA, complete cds, EST hits
YGR276c = ribonuclease H
differences to genmodel of 44M2.3

Sequenced by GBF

Locus: /map="16p11.2"

Insert length: 2695 bp

Poly A stretch at pos. 2601, polyadenylation signal at pos. 2579

```
1 GCGGTTGTTG TTGGCAGCTG TGGCTAAGGA GGGGAGAACC TCTGCTCCCC
51 GCCCGTCTTC TCTTCTGCGT TTCCCGGGCT AGGGGGCGTG GGGAGTGGTT
101 TTAGGCGGCG AAGCCGCTCG GCAGCACCTT CCTTCTTTCG CAGGCAGACG
151 CCCGTGTAG CCGTTGGGGA ACCGTTGAGA ATCCGCCATG GAGCCAGAGA
201 GGGAAAGGGAC CGAGAGACAC CCCAGGAAGG TCAGGGAAG CAGGCAGGCC
251 CCAAATAAGC TGGTCGGGGC AGCTGAGGCG ATGAAAGCCG GTTGGGATCT
301 CGAGGAGAGT CAGCCCGAGG CCAAGAAAGC CCGCTTATCT ACCATTTTAT
351 TTAAGTACAA CTGTGAAGTA ACCCATGACC AGCTGTGTGA ATTGCTGAAG
401 TATGCAGTTC TGGGCAAATC CAATGTTCCA AAACCCAGCT GGTGCCAGCT
451 TTTTCATCAA AACACCTAA ACAACGTAGT GGTTTTGTG CTGCAGGGAA
501 TGAGTCAGCT ACACCTTTAC AGGTTCTATT TGGAGTTTGG ATGTCTTCGA
551 AAAGCATTC AACAATAATT CCGCTTGCCT CCACCATCAT CTGATTTTCT
601 AGCTGATGTT GTTGGGCTAC AAAGTGAACA AAGAGCTGGA GATCTGCCCC
651 AGAAGTGAAG AGGGCCTTTA CCTTCTAATG CAAAAGCCCG CATCAACCTT
701 CAGGATGATC CCATCATTC AAGATATGGC TCTAAGAAAG TGGGCTTGAC
751 CAGATGCCTT CTGACAAAGG AGGAAATGAG AACGTTTCAC TTTCCATTAC
801 AAGGTTTTC CTGATGTGAA AACTTTTAC TTACCAATG TAATGGTTCT
851 ATAGCAGACA ATAGTCTCT CTTTGGACTT GACTGTGAAA TGTGCCTCAC
901 ATCCAAGGGG AGAGAGCTAA CACGCATCTC ACTGGTTGCT GAAGGAGGCT
951 GCTGTGTTAT GGATGAACCT GTCAAAACCTG AAAACAAGAT TCTGGACTAC
1001 CTCACAGCTT TTTCGGGAAT CACGAAGAAG ATTCTTAACC CAGTGACGAC
1051 CAAACTCAA AATGTACAGA GGCAGTTAAA AGCACTGCTT CCTCTGATG
1101 CTGTGTTAGT GGGCCACTCC TTAGATTGAG ATCTCAGAGC ACTGAAAATG
1151 ATACATCCAT ATGTTATTGA TACATCGTTG CTTTATGTCA GAGAGCAGGG
1201 CAGAAGATT AAGCTCAAGT TCTTAGCCAA AGTTATTTTG GGAAGGATA
1251 TACAGTGTC ACACAGACTT GGTCATGATG CCACAGAAGA TGCTAGAACA
1301 ATCCTTGAAT TGGCTCGGTA TTTCCTTAAG CATGGCCCAA AAAAGATTGC
1351 AGAACTAAAT CTAGAAGCAC TAGCTAATCA CCAAGAAATA CAAGCAGCAG
1401 GCCAAGAGCC TAAAAACACA GCAGAAGTAC TTCAGCACCC AAACACAAGT
1451 GTTTTAGAAT GCTTGGATTG AGTGGGTGAG AAGCTTCTTT TTTTGACCCG
1501 GGAGACAGAT GCTGGTGAAC TTCCATCTTC CAGAAATTGT CAACTATTA
1551 AGTGTCTTTC AAATAAAGAG GTTCTTGAGC AGGCCAGAGT GGAATCCCC
1601 CTGTTTCCCT TCAGCATGTT TCAGTTCTCT TTTAAGGCCCT TTTCACCTGT
1651 CCTCACTGAG GAGATGAACA AAAGGATGAG GATCAAGTGG ACAGAGATAT
1701 CAACTGTCTA TGCTGGGCCA TTTAGCAAAA ATTGCAATCT CAGGGCTCTG
1751 AAGAGGCTGT TTAAGAGCTT TGGCCAGTGC CAGTCAATGA CTTTGTGTTCT
1801 TGAACCCCGT AGCGTGAGA GGCCTGTGAC AGAGCTCACG CTTGATTGTG
1851 ACACCCTCGT GAATGAGCTG GAAGGAGATT CTGAAAACCA AGGCTCTATA
1901 TATCTGTCTG GAGTGAGTGA AACCTTCAAA GAACAGCTAT TGCAGGAGCC
1951 CCGCCTCTTT CTGGCCTGG AAGCTGTGAT CTTGCCTAAA GATCTTAAAA
2001 GTGGAAGACA GAAAAATAC TGTTCCTGTA AATTCAAAAG TTTTGGCAGT
2051 GCCCAGCAGG CCTCAACAT TCTCACAGGC AAGGACTGGA AGCTGAAAGG
2101 CAGCATGGCC CTAAACCCCA GGCACCTCCA TGCTTGGCTC AGAGGCTTAC
2151 CACCTGAATC AACAAGGCTC CCAGGGCTTC GTGTTGTACC TCCCCCTTT
2201 GAACAGGAGG CCTTGACAGC TGTGAACTG GACCACCCGA AGATAGCAGC
2251 CTGGCGCTGG AGCCGGAAGA TTGGAAGCT CTACAACAGC TGTGCCCCG
2301 GCACTCTCTG CCTCATCTG CTGCCAGGAA CCAAGAGCAC TCATGGTTCA
2351 CTCTCTGGTC TAGGACTGAT GGAATAAAA GAGGAAGAAG AAAGCGCTGG
2401 CCCAGGCTG TGTTCGTGAG TCGGCCTGCC ATGTTTCCAT GTGCCATTTT
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2451 TTACCCTTG TAGGCAATGG CAAAGAATGT GGTGAGGCTG TAGCCTCCCC
2501 AACCAGCAGA CAGTTTTATG GAACTTGGT ATAGCAGCTA AAAGAGTTTA
2551 GTTTGTTTAT ATGGCATGTA TAAGTTTCA ATAAATGCCT AAAGTTCAAG
2601 CATAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2651 AGGCGGCGCG CTCTAAAGGA TCCAAGCTTA CGTACGCGAA AAAAG

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 188 bp to 2416 bp; peptide length: 743
 Category: similarity to known protein

```

1 MEPEREGTER HPRKVRESRQ APNKLVGAAE AMKAGWDL EE SQPEAKKARL
51 STILFTDNCE VTHDQLCELL KYAVLGKSNV PKPSWCQLFH QNHLNNVVVF
101 VLQGMSQLHF YRFYLEFGCL RKAFRHKFRL PPPSSDFLAD VVGLQTEQRA
151 GDLPKTMEGP LPSNAKAAN LQDDPIIQKY GSKKVGLTRC LLTKEEMRTF
201 HFPLQGFPDC ENFLLTKCNG SIADNSPLFG LDCEMCLTSK GRELTRISLV
251 AEGGCCVMDE LVKPENKILD YLTSFSGITK KILNPVTTKL KDVQRQLKAL
301 LPPDAVLVGH SLDLDRALK MIHPYVIDTS LLYVREQGRR FKLKFLAKVI
351 LGKDIQCPDR LGHDATEDAR TILELARYFL KHGPKKIAEL NLEALANHQE
401 IQAAGQEPKN TAEVLQHPNT SVLECLDSVG OKLLFLTRET DAGELPSSRN
451 CQTIKCLSNK EVLEQARVEI PLFPFSIVQF SFKAFSPVLT EEMNKRMRK
501 WTEISTVYAG PFSKNCNLRA LKRLFKSFGP VQSMTFVLET RQVQRPVTEL
551 TLQCDTLVNE LEGDSENQGS IYLSGVSETF KEQLLQEPRL FLGLEAVILP
601 KDLKSGKQKK YCFLKFKSFG SAQQALNILT GKDWKLKGRH ALTPRHLHAW
651 LRGLPPESTR LPGLRVVPPP FEQALQTLK LDHPKIAAWR WSRKIGKLYN
701 SLCPGTLC LI LLPGTKSTHG SLSGLGLMGI KEEESAGPG LCS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_15j3, frame 2

TREMBL:AC004381_4 gene: "44M2.3"; product: "Unknown gene product";
 Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.,
 N = 2, Score = 1827, P = 2.1e-284

TREMBL:AF016430_4 gene: "C05C8.5"; Caenorhabditis elegans cosmid
 C05C8., N = 2, Score = 370, P = 1.7e-34

PIR:S64609 hypothetical protein YGR276c - yeast (Saccharomyces
 cerevisiae), N = 2, Score = 334, P = 1.8e-27

TREMBLNEW:SPAC637_9 gene: "SPAC637.09"; product: "putative
 exonuclease"; S.pombe chromosome I cosmid c637., N = 3, Score = 326, P
 = 2.8e-27

>TREMBL:AC004381_4 gene: "44M2.3"; product: "Unknown gene product"; Homo
 sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.
 Length = 547

HSPs:

Score = 1827 (274.1 bits), Expect = 2.1e-284, Sum P(2) = 2.1e-284
 Identities = 358/373 (95%), Positives = 358/373 (95%)

```

Query: 105 MSQLHFYRFYLEFGCLRKAFRHKFRLPPPSSDFLADVGLQTEQQRAGDLPKTMEGPLPSN 164
      MSQLHFYRFYLEFGCLRKAFRHKFRLPPPSSDFLADVGLQTEQQRAGDLPKTMEGPLPSN
Sbjct: 1 MSQLHFYRFYLEFGCLRKAFRHKFRLPPPSSDFLADVGLQTEQQRAGDLPKTMEGPLPSN 60

Query: 165 AKAANLQDDPIIQKYGSKKVGLTRCLLTKEEMRTFHFPLOQFPDCENFLLTKCNGSIAD 224
      AKAANLQDDPIIQKYGSKKVGLTRCLLTKEEMRTFHFPLOQFPDCENFLLTKCNGSIAD
Sbjct: 61 AKAANLQDDPIIQKYGSKKVGLTRCLLTKEEMRTFHFPLOQFPDCENFLLTKCNGSIAD 120

```

Query: 225 NSPLFGLDCM-----CLTSKGRELTRISLVAEGGCCVMDLVKPKENKIL 269
 NSPLFGLDCM CLTSKGRELTRISLVAEGGCCVMDLVKPKENKIL
 Sbjct: 121 NSPLFGLDCMARTTFNF SIGVLQAECCLTSKGRELTRISLVAEGGCCVMDLVKPKENKIL 180

Query: 270 DYLTFSFGITKKILNPVTTKLKDVQRQLKALLPPDAVLVGHSLDLDLRALKMIHPYVIDT 329
 DYLTFSFGITKKILNPVTTKLKDVQRQLKALLPPDAVLVGHSLDLDLRALKMIHPYVIDT
 Sbjct: 181 DYLTFSFGITKKILNPVTTKLKDVQRQLKALLPPDAVLVGHSLDLDLRALKMIHPYVIDT 240

Query: 330 SLLYVREQRRFKLFLAKVILGKDIQCPDRLGHDATEDARTILELARYFLKHGPKKIAE 389
 SLLYVREQRRFKLFLAKVILGKDIQCPDRLGHDATEDARTILELARYFLKHGPKKIAE
 Sbjct: 241 SLLYVREQRRFKLFLAKVILGKDIQCPDRLGHDATEDARTILELARYFLKHGPKKIAE 300

Query: 390 LNLEALANHQEIQAAGQEPKNTAEVLQHPNTSVLECLDSVGQKLLFLTRET DAGELPSSR 449
 LNLEALANHQEIQAAGQEPKNTAEVLQHPNTSVLECLDSVGQKLLFLTRET DAGELPSSR
 Sbjct: 301 LNLEALANHQEIQAAGQEPKNTAEVLQHPNTSVLECLDSVGQKLLFLTRET DAGELPSSR 360

Query: 450 NCQTIKCLSNKEV 462
 NCQTIKCLSNKEV
 Sbjct: 361 NCQTIKCLSNKEV 373

Score = 929 (139.4 bits), Expect = 2.1e-284, Sum P(2) = 2.1e-284
 Identities = 175/179 (97%), Positives = 177/179 (98%)

Query: 538 LETRQVQRPVTELTLDCTLVNELEGDSNQSGSIYLSGVSETFKEQLLQEPRLFGLLEAV 597
 L ++VQRPVTELTLDCTLVNELEGDSNQSGSIYLSGVSETFKEQLLQEPRLFGLLEAV
 Sbjct: 368 LSNKEVQRPVTELTLDCTLVNELEGDSNQSGSIYLSGVSETFKEQLLQEPRLFGLLEAV 427

Query: 598 ILPKDLKSGKQKCYCFLKFKSFGSAQALNLTGKDWKLGKRHALTPRHLHAWLRGLPPE 657
 ILPKDLKSGKQKCYCFLKFKSFGSAQALNLTGKDWKLGKRHALTPRHLHAWLRGLPPE
 Sbjct: 428 ILPKDLKSGKQKCYCFLKFKSFGSAQALNLTGKDWKLGKRHALTPRHLHAWLRGLPPE 487

Query: 658 STRLPGLRVVPPPFQEALQTLKLDHPKIAAWRWSRKIGKLYNSLCPGTLCLILLPGTK 716
 STRLPGLRVVPPPFQEALQTLKLDHPKIAAWRWSRKIGKLYNSLCPGTLCLILLPGTK
 Sbjct: 488 STRLPGLRVVPPPFQEALQTLKLDHPKIAAWRWSRKIGKLYNSLCPGTLCLILLPGTK 546

Pedant information for DKFZphtes3_15j3, frame 2

Report for DKFZphtes3_15j3.2

[LENGTH] 743
 [MW] 83536.58
 [pI] 8.87
 [HOMOL] TREMBL:AC004381_4 gene: "44M2.3"; product: "Unknown gene product"; Homo sapiens
 Chromosome 16 BAC clone CIT987SK-44M2, complete sequence. 0.0
 [FUNCAT] 01.03.16 polynucleotide degradation [S. cerevisiae, YGR276c] 4e-30
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR107w] 3e-13
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YGL094c] 1e-10
 [FUNCAT] 04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S. cerevisiae, YGL094c] 1e-10
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YOL080c] 2e-10
 [PROSITE] MYRISTYL 5
 [PROSITE] AMIDATION 1
 [PROSITE] CK2_PHOSPHO_SITE 8
 [PROSITE] TYR_PHOSPHO_SITE 1
 [PROSITE] GLYCOSAMINOGLYCAN 1
 [PROSITE] PKC_PHOSPHO_SITE 16
 [PROSITE] ASN_GLYCOSYLATION 2
 [PFAM] RNA_recognition_motif. (aka RRM, RBD, or RNP domain)
 [KW] Alpha_Beta

SEQ MEPEREGTERHPRKVRRESQAPNKLVGAAEAMKAGWDLEESQPEAKKARLSTILFTDNCE
 PRD cccchhhhhccccchhhhhhhcchhhhhhhhhccccccccccccchhhhhcccccccccc

SEQ VTHDQCELLKYAVLGKSNVPKPSWCQLFHQNLNNVVVFVLQMSQLHFYRFYLEFGCL
 PRD eehhhhhhhhhhhhhccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhh

SEQ RKAFRHKFRLPPSSDFLADVGLQTEQRAGDLPKTMEGPLPSNAKAAINLQDDPIIQKY
 PRD hhhhhhhhhccccccccchhhhhhhhhhhhhccccccccccccccccchhhhhhhhhcccccc

SEQ GSKKVLTRCLLTKEEMRTFHFPLQGFDCENFLLTKCNGSIADNSPLFGLDCMCLTSK
 PRD cccccchhhhhhhhhhhhhcc

SEQ GRELTRISLVAEGGCCVMDLVKPKENKILDYLTFSFGITKKILNPVTTKLKDVQRQLKAL
 PRD cchhhhhheeeccchhhhhhhhhhh

```

SEQ      LPPDAVLVGHSLDLDRALKMIHPYVIDTSLLYVREQRRFKLFLAKVILGKDIQCPDR
PRD      hccccccccchhhhhhhhhhhccccccccccccchhhhhhhhhhhhhhhcccccc

SEQ      LGHDATEDARTILELARYFLKHGPKKIAELNLEALANHQEIQAAGQEPKNTAEVLQHPNT
PRD      cccccchhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccc

SEQ      SVLECLDSVGQKLLFLTRETDAHELPSRRNCQTIKCLSNKEVLEQARVEIPLFPFSIVQF
PRD      cccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhcccccccccccc

SEQ      SFKAFSPVLTEEMNKRMRKIKWTEISTVYAGPFSKNCNLRALKRLFKSFGPVQSMFTVLET
PRD      eeeeeeeehhhhhhhhhhhhhhhheeeeeccccccccchhhhhhhhhhhhhcccccccccccccccc

SEQ      RQVQRVPVTELTLDCTLVNELEGDSSENGSIYLSGVSETFKEQLLQEPRLFLGLEAVILP
PRD      cccccccccccccchhhhhhhccccccccccccccccccccccccchhhhhhhhhhhhhcccccccccccc

SEQ      KDLKSGKQKKYCFLKFSFGSAQQALNLTGDKDWLKGRRHALTPRHLHAWLRGLPPESTR
PRD      cccccccccccccccccccccccccchhhhhhhhhhhcccccccccccccccccccccccccccccccc

SEQ      LPGLRVVPPPFQEALQTLKLDHPKIAAWRWSRKIGKLYNSLCPGTLCLILLPGTKSTHG
PRD      cccccccccchhhhhhhhhhhccccchhhhhhhhhhhhhhhhhheeeeecccccccccccccccccccc

SEQ      SLSGLGLMGIKEEESAGPGLCS
PRD      cccccccccchhhhhhhcccccccccc

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Prosites for DKFZphtes3_15j3.2

PS000001	219->223	ASN_GLYCOSYLATION	PDOC000001
PS000001	419->423	ASN_GLYCOSYLATION	PDOC000001
PS000002	723->727	GLYCOSAMINOGLYCAN	PDOC000002
PS000005	8->11	PKC_PHOSPHO_SITE	PDOC000005
PS000005	182->185	PKC_PHOSPHO_SITE	PDOC000005
PS000005	238->241	PKC_PHOSPHO_SITE	PDOC000005
PS000005	279->282	PKC_PHOSPHO_SITE	PDOC000005
PS000005	287->290	PKC_PHOSPHO_SITE	PDOC000005
PS000005	447->450	PKC_PHOSPHO_SITE	PDOC000005
PS000005	453->456	PKC_PHOSPHO_SITE	PDOC000005
PS000005	458->461	PKC_PHOSPHO_SITE	PDOC000005
PS000005	481->484	PKC_PHOSPHO_SITE	PDOC000005
PS000005	579->582	PKC_PHOSPHO_SITE	PDOC000005
PS000005	605->608	PKC_PHOSPHO_SITE	PDOC000005
PS000005	630->633	PKC_PHOSPHO_SITE	PDOC000005
PS000005	643->646	PKC_PHOSPHO_SITE	PDOC000005
PS000005	658->661	PKC_PHOSPHO_SITE	PDOC000005
PS000005	678->681	PKC_PHOSPHO_SITE	PDOC000005
PS000005	692->695	PKC_PHOSPHO_SITE	PDOC000005
PS000006	41->45	CK2_PHOSPHO_SITE	PDOC000006
PS000006	193->197	CK2_PHOSPHO_SITE	PDOC000006
PS000006	221->225	CK2_PHOSPHO_SITE	PDOC000006
PS000006	371->375	CK2_PHOSPHO_SITE	PDOC000006
PS000006	421->425	CK2_PHOSPHO_SITE	PDOC000006
PS000006	458->462	CK2_PHOSPHO_SITE	PDOC000006
PS000006	579->583	CK2_PHOSPHO_SITE	PDOC000006
PS000006	630->634	CK2_PHOSPHO_SITE	PDOC000006
PS000007	370->379	TYR_PHOSPHO_SITE	PDOC000007
PS000008	27->33	MYRISTYL	PDOC000008
PS000008	186->192	MYRISTYL	PDOC000008
PS000008	575->581	MYRISTYL	PDOC000008
PS000008	714->720	MYRISTYL	PDOC000008
PS000008	720->726	MYRISTYL	PDOC000008
PS000009	337->341	AMIDATION	PDOC000009

Pfam for DKFZphtes3 15j3.2

HMM_NAME	RNA recognition motif. (aka RRM, RBD, or RNP domain)		
HMM	*IYVGNLPWDtTEEDLrDlFsQFGpIvsIrMMrDreTGRSRGFAFVEFED		
		IY+ + + + T +E+L + + F + + + + +D G+ + +F +F++	
Query	571	IYLSGVS-ETFKEQLLQEPRLFLGLEAVILPKDLKSGKKYKCYFLKFKS	618
HMM	EEDAekAIdemNG..meFmGRrIRV*		
		+A+ A+ + G ++ GR +	
Query	619	FGSAQQALNILTGGDKWLKGRHALT	643

DKFZphtes3_15k11

group: signal transduction

DKFZphtes3_15k11 encodes a novel 958 amino acid protein C-terminal identical with human KIAA0781 protein and high similarity to protein kinases.

The novel protein contains a protein kinase ATP-binding region signature and a serine/threonine protein kinase active-site signature. The related murine kinase was cloned from the myocardium of the developing heart.

The new protein can find application in modulation of intracellular signal pathways dependent on this kinase.

KIAA0781, 5' extension

complete cDNA, complete cds, potential start at Bp 97, EST hits

Sequenced by GBF

Locus: /map="11"

Insert length: 4868 bp

Poly A stretch at pos. 4798, polyadenylation signal at pos. 4776

```

1 GAGCAAGCGG AGCGGCCGTC GCCCAAGCCA AGCCGCGCTG CCAACCCTCC
51 CGCCCCGCCG CGCTCCTGTC CGCCGTGTCT AGCAGCGGGG CCCAGCATGG
101 TCATGGCGGA TGGCCCGAGG CACTTGCAGC GCGGGCCGGT CCGGGTGGGG
151 TTCTACGACA TCGAGGGCAC GCTGGGCAAG GGCAACTTCG CTGTGGTGAA
201 GCTGGGGCGG CACCGGATCA CCAAGACGGA GGTGGCAATA AAAATAATCG
251 ATAAGTCTCA GCTGGATGCA GTGAACCTTG AGAAAATCTA CCGAGAAGTA
301 CAAATAATGA AAATGTTAGA CCACCTCAC ATAATCAAAC TTTATCAGGT
351 AATGGAGACG AAAAGTATGT TGTACCTTGT GACAGAATAT GCCAAAAATG
401 GAGAAATTTT TGACTATCTT GCTAATCATG GCCGGTTAAA TGAGTCTGAA
451 GCCAGGCGAA AATTCTGGCA AATCCTGTCT GCTGTTGATT ATGTGTCATGG
501 TCGGAAGATT GTGCACCGTG ACCTCAAAGC TGAAAATCTC CTGCTGGATA
551 ACAACATGAA TATCAAATA GCAGATTTCT GTTTTGGAAA TTTCTTTAAA
601 AGTGGTGAAC TGCTGGCAAC ATGGTGTGGC AGCCCCCTTT ATGCAGCCCC
651 AGAAGTCTTT GAAGGCGAGC AGTATGAAGG ACCACAGCTG GACATCTGGA
701 GTATGGGAGT TGTTCTTTAT GTCCTTGTCT GTGGAGCTCT GCCCTTTGAT
751 GGACCGACTC TTCCAATTTT GAGGCAGAGG GTTCTGGAAG GAAGATTCCG
801 GATTCCGTAT TTCATGTCAG AAGATTGCGA GCACCTTATC CGAAGGATGT
851 TGGTCCTAGA CCCATCCAAA CGGCTAACCA TAGCCCAAAT CAAGGAGCAT
901 AAATGGATGC TCATAGAAAT TCCTGTCCAG AGACCTGTTC TCTATCCACA
951 AGAGCAAGAA AATGAGCCAT CCATCGGGGA GTTTAATGAG CAGGTTCTGC
1001 GACTGATGCA CAGCCTTGGA ATAGATCAGC AGAAAACCAT TGAGTCTTTG
1051 CAGAACAAAG GCTATAACCA CTTTGCTGCC ATTTATTCTT TGTTGGTGGA
1101 GCGCCTGAAA TCACATCGGA GCAGTTTCCC AGTGGAGCAG AGACTTGATG
1151 GCCGCCAGCG TCGGCTAGC ACCATTGCTG AGCAAACAGT TGCCAAGGCA
1201 CAGACTGTGG GGCTCCAGT GACCATGCAT TCACCGAACA TGAGGCTGCT
1251 GCGATCTGCC CTCTCCCCC AGGCATCCAA CGTGGAGGCC TTTTCATTTC
1301 CAGCATCTGG CTGTCAGGCG GAAGTCGAT TCATGGAAGA AGAGTGTGTG
1351 GACACTCCAA AGGTCAATGG CTGTCTGCTT GACCCTGTGC CTCCTGTCTT
1401 GGTGCGGAAG GGATGCCAGT CACTGCCCAG CAACATGATG GAGACCTCCA
1451 TTGACGAAGG GCTGGAGACA GAAGGAGAGG CCGAGGAAGA CCCCCTCAT
1501 GCCTTTGAGG CATTTCAGTC CACACGCAGC GGGCAGAGAC GGCACACTCT
1551 GTCAGAAAGT ACCAATCAAC TGGTCGTGAT GCCTGGGGCA GGGAAAATTT
1601 TCTCCATGAA TGACAGCCCC TCCCTGCACA GTGTGGACTC TGAGTATGAT
1651 ATGGGGTCTG TTCAGAGGGA CCTGAACTTT CTGGAAGACA ACCCTTCCCT
1701 TAAGGACATC ATGTTAGCCA ATCAGCCTTC ACCCCGCATG ACATCTCCCT
1751 TCATAAGCCT GAGACCTACC AACCAGCCA TGCAGGCTCT GAGCTCCCAG
1801 AAACGAGAGG TCCACAACAG GTCTCCAGTG AGCTTCAGAG AGGGCCGCG
1851 AGCATCAGAT ACCTCCCTCA CCCAGGGAAT TGTAGCATTT AGACAACATC
1901 TTCAGAATCT GGCTAGAAC AAAGGAATTC TAGAGTTGAA CAAAGTGCAG
1951 TTGTTGTATG AACAATAGG ACCGGAGGCA GACCCTAACC TGGCGCCGGC
2001 GGCTCCTCAG CTCACGAGC TTGCTAGCAG CTGCCCTCAG GAAGAAGTTT
2051 CTCAGCAGCA GGAAAGCGTC TCCACTCTCC CTGCCAGCGT GCATCCCCAG
2101 CTGTCCCCAC GGCAGAGCCT GGAGACCCAG TACCTGCAGC ACAGACTCCA
2151 GAAGCCGAGC CTTTGTCAA AGGCCAGAA CACCTGTGAG CTTATTGCA
2201 AAGAACCACC GCGGAGCCTT GAGCAGCAGC TGCAGGAACA TAGGCTCCAG
2251 CAGAAGCGAC TCTTTCTTCA GAAGCAGTCT CAACTGCAGG CCTATTTTAA
2301 TCAGATGACA ATAGCAGAGA GCTCCTACCC ACAGCCAAGT CAGCAGCTGC
2351 CCCTTCCCCG CCAGGAGACT CCACCGCCTT CTCAGCAGGC CCCACCGTTC
2401 AGCCTGACCC AGCCCTGAG CCCCCTCCTG GAGCCTTCCT CCGAGCAGAT
2451 GCAATACAGC CCTTTCTTCA GCCAGTACCA AGAGATGCAG CTTACGCCCC
2501 TGCCCTCCAC TTCCGGTCCC CGGGCTGCTC CTCCTCTGCC CACGCAGCTA
2551 CAGCAGCAGC AGCCGCCACC GCCACCACCC CCTCCACCAC CACGACAGCC
2601 AGGAGCTGCC CCAGCCCCCT TACAGTTCTC CTATCAGACT TGTGAGCTGC

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2651 CAAGCGCTGC TTCCCCTGCG CCAGACTATC CCACTCCCTG TCAGTATCCT
2701 GTGGATGGAG CCCAGCAGAG CGACCTAACG GGGCCAGACT GTCCCAGAAG
2751 CCCAGGACTG CAAGAGGCCC CCTCCAGCTA CGACCCACTA GCCCTCTCTG
2801 AGCTACCTGG ACTCTTTGAT TGTGAAATGC TAGACGCTGT GGATCCACAA
2851 CACAACGGGT ATGTCCTGGT GAATTAGTCT CAGCACAGGA ATTGAGGTGG
2901 GTCAGGTGAA GGAAGAGTGT ATGTTCTTAT TTTTATTCCA GCCTTTTAAA
2951 TTTAAAGCTT ATTTTCTTGC CCTCTCCCTA ACGGGGAGAA ATCGAGCCAC
3001 CCAACTGGAA TCAGAGGGTC TGGCTGGGGT GGATGTTGCT TCCTCCTGGT
3051 TCTGCCCCAC CACAAAAGTTT TCTGTGGCAA GTGCTGGAAC ATAGTTGTAG
3101 GCTGAGGCTC CTGCCCTTCG GTCGAGTGGA GCAAGCTCTC GAGGGCAGCA
3151 CTGACAAATG TGTTCCTAAG AAGACATTCA GACCCAGGTC TTATGCAGGA
3201 TTACATCCGT TTATTATCAA GGGCAACCTT GGTGAAAGCA GAAAGGGTGT
3251 GTGCTATTGC ATATATATGG GGGAAAAGGC AATATATTTT TCACTGAAGC
3301 TGAGCAACCA CATATTGCTA CAAGGCAAT CAAGAAGACA TCAGGAAATC
3351 AGATGGACAG GAAATAAAGG AAAGCTGTGC TTTGTCTATT AATCCTAAGT
3401 TCTTAGCTGC TGATGCAAGT TGTCCCCCAA GGCCATCACA AAGCAGTGGG
3451 GCATGAGCTG TGTTCAGGG GCCACTAAAT AACAGCTGGT ACTGACCCCA
3501 GAAACCGCTC TCATCTCCAT TCGGAAGCAG GTGACACACC CCTTCAGAAG
3551 GTGCCCTGGG TTGCCGAGTG TCAGAAATATA CTCAGGACTC CAGAGGTGTC
3601 ACACGTGGAA CTGACAGGAG ACCCGCCACC GTGGAGGCAG GGGGCAAGAA
3651 ACTCAAGAAC GCATCAAGAG CACCAGCCCT GGGCCAGGGA AGACAGGCTC
3701 TTCCTGCAGT TTCTCGTGGA CACTGCTGGC TTGCGGGCAG TCGGTCTCCA
3751 GGGTACCTGT TGTCTCTTTT CCGATGTAAT AACTACTTTG ACCTTACACT
3801 ATATGTTGCT AGTAGTTTAT TGAGCTTTGT ATATTTGGAC AGTTTCATAT
3851 AGGGCTTAGA GATTTTAAAG ACATGATAAA TGAACTTTTC TGTCCCATGT
3901 GAAGTGGTAG TGCGGTGCCT TTCCCCCAGA TCATGCTTTA ATTCTTTCTT
3951 TTCTGTAGAA ACCAACAGTT TCCATTTATG TCAATGCTAA ATCCAAAGTC
4001 ACTTCAGAGT TGTTTTCCA CCATGTGGGA ATCAGCATTC TTAATTTCTG
4051 TAAAGTTTGT ACTTGTAAATG AAATGTTCAA GTATTACAGC AATATTCAA
4101 GAAAGAACCA CAGATGTGTT AACCATTAA GCAGATCATC TGCCAAACAT
4151 TATATTACTA ATAAAACTTA ACCAACACTT ACAATTCACT CATCAAAGTA
4201 AGTAAAAATT ACATGCTACA GCTAGCTAAC TGTATCCCTA GAAATGATGA
4251 ATAATTGCCC ATTTGGACAG TTAACATCCA GGTGTTACAA AGTCAGTGT
4301 AATTCTAAAG ATGATCATTT CTGCCCTTTA GAATGGCTTG TCCCATCAGC
4351 AGATGAATGT GTTAAGCACA AAGCATCTTC CTTAAAGCAC AAAGAGAGGG
4401 ACTAACTGAT GCTGCATCTA GAAAACACCT TTAAGTTGCC TTTCTCTTT
4451 GTAGTTAGCG TTCAGGCAGG TGACGTGTGG AAAGTCTAGG GGGTTCCATT
4501 CTGGCCATGC GAGCCAGCT CCTACCAACG TCGGTAACCT GAGCAGTCCC
4551 TGTTGCTGGC CAGAGACTGC CTGGTCGCCA GCGCTCACC TGGGTGCCAG
4601 GATGCTTCGC AGAGGCACTG TGCTCACGGT TGGACTTGGT GTCAGTGGGA
4651 AAGGGCAGTG TGGGGACTGT CATTTTGTG ATTTAATAAC ACACAGTGAA
4701 AATCCAGGAA GAATGAATTA AGCTTCTTCT GGGAGTTGTT TATTCCTGCT
4751 CGTGCTTAAG ATTGATGATT TCGTGAAATA AAGAACATCA TTTCATTTAA
4801 AAAAAAAGG AAAAAAGGG CGGCCGTCT AGAGGATCCA AGCTTACGTA
4851 CGCGTGAAGA AAAAAAG

```

BLAST Results

Entry HSG4921 from database EMBL:
human STS SHGC-37164.
Score = 1605, P = 1.9e-66, identities = 349/369

Entry AB018324 from database EMBL:
Homo sapiens mRNA for KIAA0781 protein, partial cds.
Score = 10725, P = 0.0e+00, identities = 2145/2145

Medline entries

No Medline entry

Peptide information for frame 1

ORF from the beginning to 2874 bp; peptide length: 959
Category: known protein

```

1 EQAERPSPKP SRAANPPARP RSCPPCLAAG PSMVMADGPR HLQRPVVRVG
51 FYDIEGTLGK GNFAVVKLGR HRITKTEVAI KIIDKSQALD VNLEKIYREV
101 QIMKMLDHPH IIKLYQVMET KSMPLYLVTEY AKNGEIFDYI ANHGRLENESE
151 ARRKFWQILS AVDYCHGRKI VHRDLKAENL LLDNNMNIKI ADFGFGNFEK
201 SGELLATWCG SPPYAAPEVF EGQOYEGPOL DIWSMGVVLY VLVCGALPFD
251 GPTLPILRQR VLEGRFRIPY FMSEDCEHLI RRMLVLDPK RLTIQAIKEH

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301 KWMLEIVPVQ RPYLYPQEQE NEPSIGEFNE QVLRMLHSLG IDQQKTIESL
351 QNKSYNHFAA IYFLLVERLK SHRSSFPVEQ RLDGRQRRPS TIAEQTVAKA
401 QTVGLPVTMH SPNMRLLRSA LLPOASNVEA FSFPASGCCA EAAFMEEECV
451 DTPKVNGCLL DPVPPVLVRK GCQSLPSNMM ETSIDEGLET EGAEEDPAH
501 AFEAFQSTRS QRRHTLSEV TNQLVVMPGA GKIFSMNDSP SLDSVDSEYD
551 MGSVQRDLNF LEDNPSLKDI MLANQPSPRM TSPFISLRPT NPAMQALSSQ
601 KREVHNRSPV SFREGRRASD TSLTQGI VAF RQHLQNLART KGILELNKVQ
651 LLYEQIGPEA DPNLAPAAPQ LQDLASSCPQ EEVSQQQESV STLPAVHPQ
701 LSPRQSLETO YLQHLRLQKPS LLSKAQNTCQ LYCKEPPRSL EQQLOEHLRQ
751 QKRFLQKQS QLQAYFNQM Q IAESSYPQPS QQLPLPRQET PPPSQQAPPF
801 SLTQPLSPVL EPSSEMQYS PFLSQYQEMQ LQPLPSTSGP RAAPPLPTQL
851 QQQQPPPPPP PPPPRQPGAA PAPLOFSYQT CELPSAASPA PDYPTPCQYP
901 VDMAQQSDLT GPDCPRSPGL QEAPSSYDPL ALSELPLGLFD CEMLDAVDPQ
951 HNGYVLVN

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_15k11, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_15k11, frame 1

Report for DKFZphtes3_15k11.1

```

[LENGTH]      926
[MW]           103915.77
[PI]           5.70
[HOMOL]        TREMBL:AB018324_1 gene: "KIAA0781"; product: "KIAA0781 protein"; Homo sapiens
mRNA for KIAA0781 protein, partial cds. 0.0
[FUNCAT]       01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDR477w]
8e-76
[FUNCAT]       11.01 stress response [S. cerevisiae, YDR477w] 8e-76
[FUNCAT]       30.03 organization of cytoplasm [S. cerevisiae, YDR477w] 8e-76
[FUNCAT]       98 classification not yet clear-cut [S. cerevisiae, YCL024w] 4e-58
[FUNCAT]       03.25 cytokinesis [S. cerevisiae, YDR507c] 3e-56
[FUNCAT]       03.04 budding, cell polarity and filament formation [S. cerevisiae, YDR507c]
3e-56
[FUNCAT]       30.02 organization of plasma membrane [S. cerevisiae, YDR122w] 1e-53
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YKL101w] 3e-53
[FUNCAT]       30.10 nuclear organization [S. cerevisiae, YKL101w] 3e-53
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YPL141c] 5e-51
[FUNCAT]       03.19 recombination and dna repair [S. cerevisiae, YPL153c] 3e-42
[FUNCAT]       03.22.01 cell cycle check point proteins [S. cerevisiae, YPL153c] 3e-42
[FUNCAT]       10.99 other signal-transduction activities [S. cerevisiae, YPL153c] 3e-42
[FUNCAT]       11.04 dna repair (direct repair, base excision repair and nucleotide excision
repair) [S. cerevisiae, YPL153c] 3e-42
[FUNCAT]       03.01 cell growth [S. cerevisiae, YFR014c] 5e-42
[FUNCAT]       03.16 dna synthesis and replication [S. cerevisiae, YMR001c] 2e-34
[FUNCAT]       03.10 sporulation and germination [S. cerevisiae, YGL180w] 1e-27
[FUNCAT]       08.13 vacuolar transport [S. cerevisiae, YGL180w] 1e-27
[FUNCAT]       06.13.04 lysosomal and vacuolar degradation [S. cerevisiae, YGL180w] 1e-27
[FUNCAT]       10.02.11 key kinases [S. cerevisiae, YBL105c] 3e-26
[FUNCAT]       04.99 other transcription activities [S. cerevisiae, YER129w] 3e-26
[FUNCAT]       02.19 metabolism of energy reserves (glycogen, trehalose) [S. cerevisiae,
YPL031c] 1e-23
[FUNCAT]       01.04.04 regulation of phosphate utilization [S. cerevisiae, YPL031c]
1e-23
[FUNCAT]       04.05.01.04 transcriptional control [S. cerevisiae, YPL031c] 1e-23
[FUNCAT]       03.13 meiosis [S. cerevisiae, YOR351c] 2e-23
[FUNCAT]       10.05.11 key kinases [S. cerevisiae, YHL007c] 8e-21
[FUNCAT]       03.07 pheromone response, mating-type determination, sex-specific proteins
[S. cerevisiae, YHL007c] 8e-21
[FUNCAT]       09.01 biogenesis of cell wall [S. cerevisiae, YPL140c] 2e-20
[FUNCAT]       10.03.11 key kinases [S. cerevisiae, YLR113w] 7e-20
[FUNCAT]       04.05.01.01 general transcription activities [S. cerevisiae, YDL108w]
3e-19
[FUNCAT]       10.05.09 regulation of g-protein activity [S. cerevisiae, YBL016w] 2e-18
[FUNCAT]       10.04.11 key kinases [S. cerevisiae, YLR362w] 3e-18
[FUNCAT]       04.03.99 other trna-transcription activities [S. cerevisiae, YOR061w]
4e-18
[FUNCAT]       06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YFL033c] 4e-17
[FUNCAT]       05.07 translational control [S. cerevisiae, YDR283c] 2e-16
[FUNCAT]       01.02.04 regulation of nitrogen and sulphur utilization [S. cerevisiae,
YNL183c] 2e-14

```

[FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL183c] 2e-14

[FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae, YNL020c] 5e-14

[FUNCAT] c energy conversion [M. genitalium, MG109] 2e-12

[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YBR097w] 1e-10

[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YBR097w] 1e-10

[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YBR097w] 1e-10

[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YBR097w] 1e-10

[FUNCAT] 10.04.99 other nutritional-response activities [S. cerevisiae, YJR059w] 4e-09

[FUNCAT] 01.06.10 regulation of lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YHR079c] 1e-07

[FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YHR079c] 1e-07

[FUNCAT] 08.19 cellular import [S. cerevisiae, YNL154c] 2e-04

[BLOCKS] BL00415A Synapsins proteins

[BLOCKS] BL00239B Receptor tyrosine kinase class II proteins

[BLOCKS] BL00107A Protein kinases ATP-binding region proteins

[SCOP] dlgol_ 5.1.1.1.9 MAP kinase Erk2 [rat Rattus norvegicus] 3e-78

[SCOP] dlwfc_ 5.1.1.1.8 MAP kinase p38 [human (Homo sapiens)] 1e-81

[SCOP] dlkoa_ 5.1.1.1.7 (1-350) Twitchin, kinase domain [Caenorhabditis] 5e-89

[SCOP] dlkoba_ 5.1.1.1.6 Twitchin, kinase domain [california sea har] 5e-86

[SCOP] dlphk_ 5.1.1.1.5 gamma-subunit of glycogen phosphorylase kinase 3e-80

[SCOP] dlirk_ 5.1.1.2.4 insulin receptor [Human (Homo sapiens)] 6e-70

[SCOP] dlapme_ 5.1.1.1.4 cAMP-dependent PK, catalytic subunit [mouse (Mu)] 1e-95

[SCOP] dlfgka_ 5.1.1.2.3 Fibroblast growth factor receptor 1 [human (Hom)] 7e-71

[SCOP] dlydse_ 5.1.1.1.3 cAMP-dependent PK, catalytic subunit [bovine (Bo)] 2e-96

[SCOP] dlfmk_ 5.1.1.2.2 (168-437) c-src tyrosine kinase [human (Hom)] 2e-72

[SCOP] dlcdka_ 5.1.1.1.2 cAMP-dependent PK, catalytic subunit [pig (Su)] 5e-97

[SCOP] d2hckb3_ 5.1.1.2.1 (167-437) Haemopoietic cell kinase Hck [huma] 2e-68

[SCOP] dlcsn_ 5.1.1.1.11 Casein kinase-1, CK1 [Schizosaccharomyces pombe] 3e-53

[SCOP] dljsua_ 5.1.1.1.1 Cyclin-dependent PK [Human (Homo sapiens)] 3e-78

[SCOP] dlckia_ 5.1.1.1.10 Casein kinase-1, CK1 [rat (Rattus norvegicus)] 1e-58

[EC] 2.7.1.117 Myosin-light-chain kinase 3e-49

[EC] 2.7.1.109 (Hydroxymethylglutaryl-CoA reductase(NADPH)) kinase 4e-78

[EC] 2.7.1.38 Phosphorylase kinase 3e-41

[EC] 2.7.1.37 Protein kinase 7e-45

[EC] 2.7.1.123 Ca2+/calmodulin-dependent protein kinase 5e-42

[EC] 2.7.1.128 [Acetyl-CoA carboxylase] kinase 4e-78

[PIRKW] phosphotransferase 3e-93

[PIRKW] nucleus 2e-74

[PIRKW] calcium 2e-40

[PIRKW] transferase 3e-33

[PIRKW] duplication 2e-32

[PIRKW] tandem repeat 7e-45

[PIRKW] phorbol ester binding 4e-33

[PIRKW] zinc 4e-33

[PIRKW] ion transport 1e-32

[PIRKW] cell cycle control 1e-45

[PIRKW] serine/threonine-specific protein kinase 2e-97

[PIRKW] oncogene 1e-34

[PIRKW] phospholipid binding 2e-32

[PIRKW] autophosphorylation 2e-74

[PIRKW] brain 6e-36

[PIRKW] heterotetramer 8e-38

[PIRKW] mitosis 1e-45

[PIRKW] polymer 5e-41

[PIRKW] magnesium 6e-80

[PIRKW] ATP 2e-97

[PIRKW] polyprotein 1e-34

[PIRKW] alternative initiators 2e-31

[PIRKW] phosphoprotein 2e-74

[PIRKW] apoptosis 8e-38

[PIRKW] cGMP binding 4e-33

[PIRKW] glycoprotein 3e-36

[PIRKW] skeletal muscle 8e-38

[PIRKW] protein kinase 2e-50

[PIRKW] testis 5e-41

[PIRKW] cAMP binding 8e-38

[PIRKW] transforming protein 4e-33

[PIRKW] purine nucleotide binding 7e-52

[PIRKW] calcium binding 7e-45

[PIRKW] alternative splicing 5e-42

[PIRKW] P-loop 7e-52

[PIRKW] lipoprotein 8e-38

[PIRKW] proto-oncogene 4e-33

[PIRKW] segmentation 1e-34

[PIRKW] core protein 1e-34

[PIRKW] muscle 8e-38
 [PIRKW] myristylation 8e-38
 [PIRKW] EF hand 7e-45
 [PIRKW] cell division 3e-49
 [PIRKW] homodimer 1e-32
 [PIRKW] calmodulin binding 5e-42
 [SUPFAM] ribosomal protein S6 kinase II 1e-34
 [SUPFAM] calcium-dependent protein kinase 7e-45
 [SUPFAM] AMP-activated protein kinase 6e-80
 [SUPFAM] protein kinase akt 3e-36
 [SUPFAM] protein kinase SPK1 7e-41
 [SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 8e-99
 [SUPFAM] Ca2+/calmodulin-dependent protein kinase 5e-42
 [SUPFAM] calmodulin repeat homology 7e-45
 [SUPFAM] cAMP receptor protein cyclic nucleotide-binding domain homology 3e-33
 [SUPFAM] protein kinase DUN1 6e-36
 [SUPFAM] protein kinase C zeta 4e-33
 [SUPFAM] Dictyostelium cAMP-dependent protein kinase catalytic chain 2e-34
 [SUPFAM] death-associated protein kinase 8e-38
 [SUPFAM] pleckstrin repeat homology 3e-36
 [SUPFAM] ankyrin repeat homology 8e-38
 [SUPFAM] protein kinase homology 8e-99
 [SUPFAM] Ca2+/calmodulin-dependent protein kinase II 6e-38
 [SUPFAM] protein kinase C zinc-binding repeat homology 4e-33
 [SUPFAM] protein kinase C delta 2e-32
 [SUPFAM] cGMP-dependent protein kinase 3e-33
 [SUPFAM] protein kinase cdrl 1e-45
 [SUPFAM] kinase-related transforming protein 2e-50
 [SUPFAM] Ca2+/calmodulin-dependent protein kinase I 8e-42
 [SUPFAM] kinase interaction domain homology 7e-41
 [SUPFAM] gag-akt polyprotein 1e-34
 [PROSITE] PROTEIN_KINASE_ATP 1
 [PROSITE] MYRISTYL 3
 [PROSITE] AMIDATION 2
 [PROSITE] CAMP_PHOSPHO_SITE 4
 [PROSITE] CK2_PHOSPHO_SITE 15
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 10
 [PROSITE] ASN_GLYCOSYLATION 2
 [PROSITE] PROTEIN_KINASE_ST 1
 [PFAM] Eukaryotic protein kinase domain
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 12.31 %

SEQ MVMADGPRHLQRGVVRVGFYDIEGLGKGNFAVVKLGRHRITKTEVAIKIIDKSQLDVN
 SEG
 1ctpEEEECTTTEEEEEETTTTEEEEEEEHHHHHHHC

SEQ LEKIYREVQIMKMLDHPHIKLYQVMETKSMYLVTEYAKNGEIFDYLANHGRNLNESEAR
 SEG
 1ctpE HHHHHHHHHHHHCCCTTTBCCEEEEEETTEEEEEECTTTTBHHHHHHHHHCCCHHHHH

SEQ RKFWQILSAVDYCHGRKIVHRDLKAENLLLDNNMNIKIADFGFGNFFKSGELLATWCGSP
 SEG
 1ctpE HHHHHHHHHHHHHHCCCECCCGGGEEETTTTCEBECCTTTTEETT-TTBC-CCCCCG

SEQ PYAAPEVFEGQQYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPIYFM
 SEG
 1ctpE GGCCHHHHHHCCBC-HHHHHHHHHHHHHHHHCCCTTTTTHHHHHHHHHHCCCCCTTTT

SEQ SEDCEHLIRRLMLVDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
 SEG
 1ctpE CHHHHHHHHHTTTTGGGTTHHHHHHCGG.....

SEQ LRLMHSGLIDQQKTIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
 SEG
 1ctpE

SEQ AEQTVAKAQTVGLPVTMHSFNMRLRSALLPQASNVEAFSPASGCQAEAAFMEEEECVDT
 SEG
 1ctpE

SEQ PKVNGCLLDPPVPVLVRKGCQSLPSNMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ
 SEGxxxxxxxxxxxxx.....
 1ctpE

SEQ RRHTLSEVTNQLVVMPPGAGKIFSMNDSPSLDSVDSEYDMGSVQRODLNFDNPSLKDIML
 SEG
 1ctpE


```

SEQ      ANQPSPRMTSPFISLRPTNPAMQALSSQKREVNHRSPVSFREGRRASDTSLTQGIVAFRQ
SEG      .....
lctpe    .....

SEQ      HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
SEG      .....XXXXXXXXXXXXXXXXXXXXXXX.....
lctpe    .....

SEQ      LPASVHPQLSPRQSLETQYLQHLRLQKPSLLSKAQNTCQLYCKEPPRSLEQQQLQEHRLQOK
SEG      .....XXXXXXXXXXXXXXXXXXXXXXX.....
lctpe    .....

SEQ      RLFLQKQSQLQAYFNQMQUIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SEG      .....XXXXXXXXXXXXXXXXXXXXXXX.....
lctpe    .....

SEQ      SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQPPPPPPPPRQPGAAPA
SEG      .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX.....
lctpe    .....

SEQ      PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDPCRSPGLQEAPSSYDPLAL
SEG      xxx.....
lctpe    .....

SEQ      SELPGLFDCEMLDAVDPQHNGYVLVN
SEG      .....
lctpe    .....

```

Prosites for DKFZphtes3_15k11.1

PS00001	115->119	ASN_GLYCOSYLATION	PDOC00001
PS00001	320->324	ASN_GLYCOSYLATION	PDOC00001
PS00004	258->262	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	355->359	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	481->485	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	584->588	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	257->260	PKC_PHOSPHO_SITE	PDOC00005
PS00005	339->342	PKC_PHOSPHO_SITE	PDOC00005
PS00005	420->423	PKC_PHOSPHO_SITE	PDOC00005
PS00005	475->478	PKC_PHOSPHO_SITE	PDOC00005
PS00005	534->537	PKC_PHOSPHO_SITE	PDOC00005
PS00005	545->548	PKC_PHOSPHO_SITE	PDOC00005
PS00005	554->557	PKC_PHOSPHO_SITE	PDOC00005
PS00005	567->570	PKC_PHOSPHO_SITE	PDOC00005
PS00005	579->582	PKC_PHOSPHO_SITE	PDOC00005
PS00005	670->673	PKC_PHOSPHO_SITE	PDOC00005
PS00006	42->46	CK2_PHOSPHO_SITE	PDOC00006
PS00006	54->58	CK2_PHOSPHO_SITE	PDOC00006
PS00006	128->132	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
PS00006	359->363	CK2_PHOSPHO_SITE	PDOC00006
PS00006	394->398	CK2_PHOSPHO_SITE	PDOC00006
PS00006	450->454	CK2_PHOSPHO_SITE	PDOC00006
PS00006	458->462	CK2_PHOSPHO_SITE	PDOC00006
PS00006	484->488	CK2_PHOSPHO_SITE	PDOC00006
PS00006	503->507	CK2_PHOSPHO_SITE	PDOC00006
PS00006	515->519	CK2_PHOSPHO_SITE	PDOC00006
PS00006	534->538	CK2_PHOSPHO_SITE	PDOC00006
PS00006	579->583	CK2_PHOSPHO_SITE	PDOC00006
PS00006	878->882	CK2_PHOSPHO_SITE	PDOC00006
PS00006	893->897	CK2_PHOSPHO_SITE	PDOC00006
PS00007	672->680	TYR_PHOSPHO_SITE	PDOC00007
PS00007	100->108	TYR_PHOSPHO_SITE	PDOC00007
PS00008	372->378	MYRISTYL	PDOC00008
PS00008	871->877	MYRISTYL	PDOC00008
PS00008	905->911	MYRISTYL	PDOC00008
PS00009	134->138	AMIDATION	PDOC00009
PS00009	582->586	AMIDATION	PDOC00009
PS00107	26->50	PROTEIN_KINASE_ATP	PDOC00100
PS00108	138->151	PROTEIN_KINASE_ST	PDOC00100

Pfam for DKFZphtes3_15k11.1

HMM_NAME Eukaryotic protein kinase domain

HMM		*YeigRiIGeGsFGtVykGiWr.TGeIVAIIKIIkrsms.....FlREI	
		Y I++++G+G+F++V++++R T +VAIKII+K++++ + RE+	
Query	20	YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQLDVAVNLEKIYREV	68
HMM		qIMRrLnHPNIIRFYDwFedddDHIYMIMEYMeGGDLFDYIrrngpMsEw	
		QIM++L+HP+II++Y ++E +++ +Y+++EY+ +G+++FDY+ ++G+++E	
Query	69	QIMKMLDHPHIKLYQVME-TKSMLYLVTEYAKNGEIFDYLANHGRLNES	117
HMM		eIrfIMyQILrGMeYLHSMgIIHRDLKPENILIdENgqIKIcDFGLARqM	
		E+R+ ++QIL++++Y+H ++I+HRDLK+EN+L+D+N++IKI+DFG+ ++	
Query	118	EARRKFWQILSAVDYCHGRKIVHRDLKAENLLDNMMNIKIADFGFGNFF	167
HMM		nnYerMttfCGTPWYMMAPEVIimg.nyYttkVOMWSFGCILWEMMTGep	
		+++E++ T CG+P+Y APEV +G +Y +++ D+WS+G++L+ +++G +	
Query	168	KSGELLATWCGSPPYA-APEV-FEGQQYEGPQLDIWSMGVLYVLVCGAL	215
HMM		PFyddnMemImrIiqrfrfpfWpnCSeElyDFMrwCWnyDPekRPTFrQI	
		PF++ ++ + + +++ R+++++ +SE++ +++R+++ +DP+KR+T+ QI	
Query	216	PFDGPTLPILRQVRLEGRFRIPYFMSCEDCEHLIRMLVLDPSKRLTIAQI	265
HMM		LnHPWF*	
		+H W+	
Query	266	KEHKWM 271	

DKFZphtes3_17f10

group: testes derived

DKFZphtes3_15j18 encodes a novel 710 amino acid protein with weak similarity to neurofilament proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to neurofilament proteins

Sequenced by GBF

Locus: unknown

Insert length: 2533 bp

Poly A stretch at pos. 2507, no polyadenylation signal found

```
1 CTTCACTTCA ACTAAAAATG GACAGATCTC AGCAGACCAG CCGTACAGGA
51 TACTGGACCA TGATGAACAT CCCCCCTGTA GAAAAAGTGG ACAAGGAACA
101 ACAGACATAC TTTAGTGAAT CAGAAATAGT GGTATTTCCT AGGCCAGATA
151 GTTCTTCTAC AAAGTCAAAG GAAGATGCCG TGAAACATAA ATCGTCGGGA
201 AAGATTTTTC CTAGTGAACA CCCTGAATTT CAACCAGCAA CAAACAGCAA
251 TGAAGAAATT GGGCAGAAAA ATATCAGCAG AACTTCATTT ACTCAGGAGA
301 CTAAAAAAGG TCCCCCAGTA CTTTATAGAAG ATGAGCTTAG GGAAGAAGTA
351 ACTGTACCTG TTGTACAAGA AGGTTCTGCT GTTAAAAAAG TGGCTTCTGC
401 TGAATATAGAG CCTCCATCAA CAGAAAAATT CCCAGCTAAA ATACAGCCTC
451 CATTAGTTGA AGAGGCCACT GCTAAAGCGG AGCCCAGACC TGCTGAAGAG
501 ACCCATGTCC AAGTACAGCC ATCAACTGAA GAGACTCCTG ATGCTGAGGC
551 AGCCACTGCA CTTCGCGAGA ATTCTGTAA AGTTCAGCCT CCACCTGCTG
601 AAGAGGCCCC TTTAGTGGAG TTCCTGCTG AAATTCAGCC TCCATCAGCT
651 GAAGAGTCTC CTTCTGTAGA GCTTCTGGCT GAAATTCCTG CTCCATCAGC
701 TGAAGAGTCC CCTTCAGAAG AGCCTCCTGC TGAAATTCCT CCTCCACCAG
751 CTGAAAAAGT TCCTTCAGTA GAGCTTCTTG GTGAAATTCG GTCTCCCTCA
801 GCACAAAAGG CTCCCATTGA AGTACAGCCT TTACCAGCTG AGGGCGCCCT
851 TGAAGAGGCC CCAGCTAAAG TAGAGCCTCC CACTGTTGAA GAGACCCTTG
901 CTGAAGTTCA GCCTCTATTA CCTGAAGAGG CTCCTAGAGA AGAGGCTCGA
951 GAACTTCAGC TTTCAACAGC TATGGAGACC CCTGCAGAAG AGGCTCCTAC
1001 TGAATTTTCAG TCTCCATTAC CTAAAGAGAC CACTGCAGAA GAGGCCTCTG
1051 CTGAAATTC A GCTTCTAGCA GCTACGGAGC CTCCTGCAGA TGAAACTCCT
1101 GCCGAAGCTC GGTCTCCACT ATCTGAGGAG ACTTCTGCAG AAGAGGCTCA
1151 TGCTGAAGTT CAATCTCCAT TAGCTGAAGA GACCACTGCA GAAGAGGCCT
1201 CTGCTGAAAT TCAGCTTCTA GCAGCTATAG AGGCTCCTGC AGATGAACT
1251 CCTGCTGAAG CTCAGTCTCC ACTATCTGAG GAGACTTCTG CAGAAGAGGC
1301 TCCCTGCTGA GTTCAGTCTC CATCAGCTAA GGGAGTTTCT ATAGAAGAGG
1351 CCCCTCTTGA GCTTCAGCCT CCATCAGGTG AAGAGACCAG TGCAGAAGAG
1401 GCCTCTGCTG CAATTCAGCT TCTAGCAGCT ACAGAGGCTT CTGCAGAAGA
1451 GGCTCCTGCT GAAGTTCAGC CTCCACCAGC TGAGGAGGCC CCCGCTGAAG
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1551 GCTGAGGAGG CCCCCGCTGA AGTTCAGCCT CCACCAGCTG AGGAGGCCCC
1601 CGCTGAAGTT CAGCCTCCAC CAGCTGAGGA GGCCCCCGCT GAAGTTCAGC
1651 CTCCACCAGC TGAGGAGGCC CCTCTGAAG TTCAGCCTCC ACCAGCTGAG
1701 GAGGCCCTG CTGAAGTTCA GTCTCTACCA GCTGAGGAGA CTCTATAGA
1751 AGAGACCCTT GCTGCAGTAC ACTCTCCCCC AGCTGATGAT GTCCCTGCAG
1801 AAGAGGCCTC CGTTGACAAA CATTCCCCAC CAGCTGATTT GCTTCTGACT
1851 GAGGAGTTTC CTATAGGAGA GGCTCTGCT GAAGTTTCAC CTCCACCATC
1901 TGAACAAACC CCTGAAGATG AGGCTCTGGT AGAGAATGTG TCTACAGAA
1951 TCTCAGTCACC GCAGGTGGCA GGAATTCCAG CAGTAAATTT AGGATCGGTT
2001 GTTTTGGAAG GTGAAGCAAA ATTTGAAGAG GTTCAAAAA TCAATTCTGT
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2301 AAAGTGTAGC AGCATAAAAT TACTTGTGTT AATTTTCATC AAATTTATGG
2351 CATGAAAAAT ACCTATTTTG AAAGTAAGTT TATAATTGAA AAAAATTGCT
2401 TAAATATATC TTCTTACAGT AAACCTGTTG ACACGAGTAA AGTTTAACT
2451 GCAGCCATCT TTTCTGTGCT TTGCCTTCCC TTATAAGTA AATATAGTTT
2501 CTAGTGGAAA AAAAAAAAAA AAAAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 18 bp to 2147 bp; peptide length: 710
Category: similarity to known protein
Classification: unclassified

```
1 MDRSQOTSRT GYWTMMNIPP VEKVDKEQQT YFSESEIVVI SRPDSSSTKS
51 KEDALKHKSS GKIFASEHPE FQPATNSNEE IGQKNISRTS FTQETKKGPP
101 VLLEDELREE VTPVVOEGS AVKKVASAEI EPPSTEFKPA KIQPLVEEA
151 TAKAEPRPAE ETHVQVPST EETPDAAEAT AVAENSVKVQ PPPAEAPLV
201 EFP AEIQPPS AEESPSVELL AEILPPSAEE SPSEEP AEI LPPPAEKSPS
251 VELLGEIRSP SAQKAPIEVQ PLPAEGALEE APAKVEPPTV EETLAEVQPL
301 LPEEAPREEA RELQLSTAME TPAAEAPTEF QSPLPKETTA EEASAEIQLL
351 AATEPPADET PAEARSPLSE ETSAAEHAEE VQSPLAEETT AEEASAEIQL
401 LAAIEAPADE TPAAEQSPLS EETSAAEAPA EVQSPSAKGV SIEEAPLELQ
451 PPSGEETTAE EASAAIQLLA ATEASAEAP AEVQPPPAEE APAEVQPPPA
501 EEP AEVQPP PAEEAPAEVQ PPPAEAPAE VQPPPAEAP AEVQPPPAEE
551 APSEVQPPPA EEP AEVQSL PAETPIET LAHVSPPAD DVPAEEASVD
601 KHSPPADLLL TEEFFIGAS AEVSPPSEQ TPEDEALVEN VSTEFQSPQV
651 AGIPAVKLS VVLEGEAKFE EVSKINSVLK DLSNTNDGQA PTLEIESVFH
701 IELKQRPPEL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_17f10, frame 3

PIR:A37221 neurofilament triplet H protein - rat, N = 1, Score = 480, P
= 7.4e-43

TREMBL:RNNFLH_1 Rat heavy neurofilament subunit (NF-H) mRNA, 3' end., N
= 1, Score = 475, P = 1e-42

>PIR:A37221 neurofilament triplet H protein - rat
Length = 1,072

HSPs:

Score = 480 (72.0 bits), Expect = 7.4e-43, P = 7.4e-43
Identities = 185/622 (29%), Positives = 320/622 (51%)

```
Query: 33 SESEIVVISRPDSSSTKSKEDALKHKSSGKIFASEHPEFQPATNSNEEIGQKNISRTSFT 92
SE +I V+ + + + +E + + + + + E E Q E G + + TS
Sbjct: 436 SEEKIKVVEKSEKETVIVVEEQTEEIQTVEETEEEDKEAQGEEEEAAEGGEEAATTSP 495

Query: 93 QETKKGPPVLLEDELREEVTPVVOEGSAVKKVASAEIEPPSTEFKPAKIQPLVEEATA 152
E P + ++EE P + A K + AE + P+ K PA+++ P ++ A
Sbjct: 496 AEEAASPEKETKSPVKEEAKSPA EAKSPA EAKSPA EAKSPA EAKSPA EAKSPA 554

Query: 153 KAEPRAEETHVQVPSTEETPDAAEATAVAENSVKVQPPPAEEAP-LVEFP AEIQPPSA 211
+A+ PAE V+ P+T ++P + A A++ +V+ P ++P + PAE + P+
Sbjct: 555 EAKS-PAE---VK-SPATVKSPA EAKSPA EAKSPA EAKSPA EAKSPA EAKSPA 609

Query: 212 EESP-SVELLAEILPPSAEESPS-EPPAEILPPPAEKSPS-VELLGEIRSPSAQKAPIE 268
+SP + AE P++ +SP E + PAE P KSP+ V+ E +SP+ K+P+
Sbjct: 610 VKSPVEAKSPA EAKSPASVKSPGEAKSPA EAKSPA EAKSPA EAKSPA EAKSPA 669

Query: 269 VQPLPAEGALEEAPAKVEPPTVEETLAEVQPLPEEAPREEARELQLSTAMETPAE-EAP 327
V+ PAE ++P +V+ P ++ +E + ++P E A+ ++PAE ++P
Sbjct: 670 VKS-PAEA---KSPVEVKSPASVKSPGEAKSPA EAKSPA EAKSPA EAKSPA 721

Query: 328 TEFQSPLPKETTAEEASAEIQLLAATEPPAD-ETPAEARSPLSEETSAAEHAEEVQS--- 383
E + P ++ AE S A + PA+ ++PAEA+SP+ E S E+A + V+
Sbjct: 722 AEAKPPAEAKSPA EAKSP-----AEAKSPA EAKSPA EAKSPA EAKSPA 775

Query: 384 PLAEETTAEEASAEIQLLAIEAPAD-ETPAEARSPLSEET-SAE EAPA-EVQSPSAKGV 440
```

LAE + E+A + ++ I+ PA+ ++P +A+SP+ EE S E+A +V+SP AK
 Sbjct: 776 SLAEAKSPEKAKSPVK--EEIKPPAEVKSPEKAKSPMKEEAKSPEKAKTLDVKSPEAKTP 833
 Query: 441 SIEEA--PLELQPPSGEETTA--EASAAIQLLAATEASA---EEAPAEVQPPPAEEAPAE 494
 + EEA P +++ P ++ A EEA + + TE A EE + V+ A+E P +
 Sbjct: 834 AKEEAKRPADIRSPEQVKSPEKAKSPEKEETRTEKVAPKKEEVKSPVEEVKAKEPPKK 893
 Query: 495 VQPPPAEEAP-AEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAEEAPS 553
 V+ P EV+ +EAP E Q P AEE + P +++P E + EEA
 Sbjct: 894 VEEKTPATPKTEVKESKKDEAPKEAQKPKAEEKEPLTEKP--KDSPEGAKK---EEAKE 948
 Query: 554 EVQPPPAEEAPAEV---QSLP---AEETPIEETL--AAVHSPPADDVPAEEASVD-KHS 603
 + P EE PA++ ++ P AE+ +E + P ++VPA D K
 Sbjct: 949 KKAAPPEETPAKLGVKKEAKPKAEADAKAKEPSKPSKEKPKKEEVPAAPEKDKTKEE 1008
 Query: 604 PPADLLLTTEFFIGEASAEVSPP--PSEQT-PEDEALVENVSTEFQSPQ 649
 + EE P +A A+ P E + P+ E ++ ST+ + Q
 Sbjct: 1009 KTTESKKPEEKPMQAKAKEEDKGLPQEPSKPKTEKAEKSSSTDQKDSQ 1057

Score = 473 (71.0 bits), Expect = 4.8e-42, P = 4.8e-42
 Identities = 184/628 (29%), Positives = 310/628 (49%)

Query: 18 IPPVEKVDKEQQTTFSESEIVVISRP---DSSSTKSKEDALKHKSSGKIFASEHPEFQPA 74
 I VEK +KE ++E + ++ + E+ + + G+ A+ P + A
 Sbjct: 440 IKVVEKSEKETVIVVEEQTEEQVTEEVTEEDKEAQEEEEAEEGGEEAATTSPPAEEA 499
 Query: 75 TNSNEEIGQKNISRTSFTQETKKGPPVLLEDELREEVTVPVVQEGSAVKKVASAEIEPPS 134
 + +E + + + + K P E + E P + A K + AE + P+
 Sbjct: 500 ASPEKET-KSPVKEEAKSPAESKPA---EAKSPAEEKSPAENVKSPAENVK-SPAESKPA 554
 Query: 135 TEKFPKIQPPLVEEATAKAEPRAETHVQVQ-PSTEETPDAAEATAVAENSVKVPQPP 193
 K PA+++ P ++ A+A+ ++ +V+ P+T ++P + A A++ +V+ P
 Sbjct: 555 EAKSPAENVKSPATVKSPAEEKSPAEEKSPAENVKSPATVKSPGEAKSPAEEKSPAENVKSPV 614
 Query: 194 AEEAPL-VEFPKAEIQPPSAEESPS-VELLAEILPPSAEESPS-EPPAEILPPPAEKSPS 250
 ++P + PA ++ P +SP+ + AE+ P+ +SP E + PAE+ P KSP+
 Sbjct: 615 EAKSPAEEKSPASVKSPEAKSPAEEKSPAENVKSPATVKSPVEAKSPAENVKSPVTVKSPA 674
 Query: 251 -VELLGEIRSPSAQKAPIEVQ-PLPAEGALE-EAPAKVEPPTVEETLAEVQPLLPPEEAPR 307
 + E++SP++ K+P E + P A+ E ++P + P ++ AE +P ++P
 Sbjct: 675 EAKSPVEVKSPASVKSPEAKSPAGAKSPAEEKSPVVAKSPAEEKSPAEEKSPAEEKSPA 734
 Query: 308 EEARELQSLSTAME--TPAE-EAPTEFQSP---LP-KE---TTAEASAEIQLLAATE-- 354
 E + + E +PAE ++P E +SP P KE + AE S E E
 Sbjct: 735 EAKSPAEEKSPAEEKSPAEEKSPVEVKSPAEEKSPVKEGAKSLAEAKSPEKAKSPVKEEI 794
 Query: 355 -PPAD-ETPAEARSPLSEET-SAEAAHA-EVQSPLAEEETAEAS--AEIQLLAIEAPA 408
 PPA+ ++P +A+SP+ EE S E+A +V+SP A+ EEA A+I+ +++PA
 Sbjct: 795 KPPAEVKSPEKAKSPMKEEAKSPEKAKTLDVKSPEAKTPAKEEAKRPADIRSPEQVKS 854
 Query: 409 DETPAEAQSPLEETSAAE-APA--EVQSPSAKGVSEIAPLELQPPSGEETTAEEASAA 465
 E EA+SP EET E+ AP EV+SP +EE + +PP E EE + A
 Sbjct: 855 KE---EAKSPEKEETRTEKVAPKKEEVKSP-----VEEVKAK-EPPKKVE---EEKTPA 901
 Query: 466 IQLLAATEASAEAPAEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAE 525
 E+ +EAP E Q P AEE + P +++P E + A+E A P E
 Sbjct: 902 TPKTEVKESKKDEAPKEAQKPKAEEKEPLTEKP--KDSPEAKKEEAKKAAA---PEE 956
 Query: 526 EAPAEV---QPPPAEEAPAEVQPPPAEEAPSEVQPPPAEEAPAEVQSLPAEETPIEETL 581
 E PA++ + P E+A P++ PSE + P EE PA + +E E+
 Sbjct: 957 ETPAKLGVKKEAKPKAEADAKAKEPSK--PSEKEKPKKEEVPAAPEKDKTKEEKTESK 1014
 Query: 582 AAVHSPPADDVPAEEASVDKHSPPADLL-LTEFFIGEASAEVSPPSEQTPEDEA 636
 P EE DK P TE+ ++ + PSE+ PED+A
 Sbjct: 1015 KPEEKPKMQAKAKEE---DKGLPQEPSKPKTEKAEKSSSTDQKDSQPSEKAPEDKA 1067

Score = 421 (63.2 bits), Expect = 3.7e-36, P = 3.7e-36
 Identities = 162/540 (30%), Positives = 275/540 (50%)

Query: 135 TEKFPKIQPPLVEEATAKAEPR-----PAETHVQVQPPSTEETPDAAEATAVAENSVKV 189
 TE P KI P + K+E + +E+ V V+ TEE E T E +
 Sbjct: 419 TEGLP-KI-PSMSTHIKVKSEKIKVVEKSEKETVIVVEEQTEEQVTEEVTE--EEDKEA 474
 Query: 190 QPPPAEEAPLVEFPKAEIQPPSAEESPSVELLAEILPPSAEE--SPSE-EPPAEILPPPAE 246
 Q EEA A P AEE+ S E E P EE SP+E + PAE P
 Sbjct: 475 QGEEEEAAEEGGEEAATTSPPAEEAASPE--KETKSPVKEEAKSPAEEKSPAEEKSPA 532
 Query: 247 KSPVELLGEIRSPSAQKAPIEVQPLPAEGALEEAPAKVEPPTVEETLAEVQPLLPPEEAP 306
 KSP+ E++SP+ K+P E + PAE ++PA+V+ P ++ AE + ++P
 Sbjct: 533 KSPA-----EVKSPAENVKSPAEEKSPAEEKSPAENVKSPATVKSPAEEKSPAEEKSP 583

Query: 307 REEARELQQLSTAME--TPAE-EAPTEFQSPLPKETTAEAS-AEIQLLAATEPPAD-ETP 361
 E + + E +PAE +P E +SP+ ++ AE S A ++ + PA+ ++P
 Sbjct: 584 AEVKSPATVKSPGAEKSPAEKSPAEVKSPEAKSPAEKSPASVKSPEAKSPAEKSP 643

Query: 362 AEARSPLSEETSAE-EAHAEVQSPLAEETTAEASAEIQLLAIEAPAD-ETPAEQSPL 419
 AE +SP + ++ E ++ AEV+SP+ ++ AE A + ++ +++PA ++P+EA+SP
 Sbjct: 644 AEVKSPATVKSPVEAKSPAEVKSPTVKSPAE-AKSPVE---VKSPASVKSPEAKSP- 697

Query: 420 SEETSAAEAPAEVQSPS-AKGVSIEEAPLELQPPSGEETTAEASAAIQLLAATEASAE 478
 + ++PAE +SP AK + ++P E +PP+ ++ AE S A A + A A+
 Sbjct: 698 ----AGAKSPAEKSPVAKSPAEKSPAEAKPPAEKSPAEKSPAE---AKSPAEAK- 749

Query: 479 APAEVQPPPAEEAPAEVQPPPAEEAP--AEVQPPPAEEAP--EVQPPPAEEAPAEVQPP 534
 +PAE + P ++P + + P E A AE + P ++P E++PP ++P + + P
 Sbjct: 750 SPAEAKSPVEVKSPEKAKSPVKEGAKSLAEKSPKAKSPVKEEIKPPAEVKSPEKAKSP 809

Query: 535 PAEEAPAEVQPPPAEEAPSEVQPPPAEEA--PAEVQSLPAEETPIEETLAHVHSPADDDV 592
 EEA + + + E + P EEA PA++S ++P +E SP ++
 Sbjct: 810 MKEEAKSPEKAKTLDVKSPEAKTPAKEEAKRPADIRSPEQVKSPAEE---AKSPEKEET 866

Query: 593 PAEEASVDKHS--PPADLLTEEFPIGEASAEVSPPPSEQTPEDEALVENVSTEFQSPQV 650
 E+ + K P + + +E P + E P + +T E+ + E Q P+
 Sbjct: 867 RTEKVAPKKEEVKSPVEEVKAKEPP--KKVEEEKTPATPKTEVKESKKDEAPKEAQKPKA 924

Query: 651 AGIPAVKLGSVVLEGEAKFEEVSK 674
 + GEAK EE +
 Sbjct: 925 EEKEPLTEKPKDSPGEAKKEEAKE 948

Score = 406 (60.9 bits), Expect = 1.7e-34, P = 1.7e-34
 Identities = 123/390 (31%), Positives = 213/390 (54%)

Query: 308 EEARELQQLSTAMETPAEEAPTEFQSPLPKETTAEASAEIQLLAATEPPADETPA---EA 364
 E+ E+Q++ E EE E Q +E AEE E A T PPA+E + E
 Sbjct: 455 EQTEEIQVT---EEVTEEDKEAQGE---EEEEAEEGGEEA---ATTSPPAEEAASPEKET 506

Query: 365 RSPLSEETSAAEHAHVQSPLAEETTAEAS-AEIQLLAIEAPAD-ETPAEQSPLSEE 422
 +SP+ EE + AE +SP ++ AE S AE++ A +++PA+ ++PAEA+SP +
 Sbjct: 507 KSPVKEEAKSP---AEAKSPAEKSPAEKSPAEVKSPEAKSPAEKSPAEKSPAEVKS 563

Query: 423 TSAE-EAPAEVQSPS-AKGVSIEEAPLELQPPSGEETTAEASAAIQLLAATEASAEAP 480
 + A ++PAE +SP+ AK + ++P ++ P GE + EA + ++ + EA ++P
 Sbjct: 564 SPATVKSPEAKSPAEKSPAEVKSPEAKSPATVKSP-GEAKSPAEKSPAEVKSPEA---KSP 619

Query: 481 AEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAEEAPAEVQPPPAEEAP 540
 AE + P + ++P E + P ++PAEV+ P ++P E + P ++P V+ P ++P
 Sbjct: 620 AEAKSPASVKSPEAKSPAEKSPAEVKSPEAKSPATVKSPVEAKSPAEVKSPTVKSPAEKSP 679

Query: 541 AEVQPPPAEEAPSEVQPPPAEEAPAEVQSLPAEETPIEETLAHVHSPAD-DVPAEEASV 599
 EV+ P + ++PSE + P ++PAE +S ++P E A PPA+ PAE S
 Sbjct: 680 VEVKSPASVKSPEAKSPAGAKSPAEKSPVAKSPAEKSPAEAKPPAEKSPAEKSP 739

Query: 600 DKHSPPADLLTEEFPIGEASAEVSPPPSEQTPEDEALVENVSTEFQSPQVAGIPAVKLG 659
 + PA+ E ++ EV P ++P E +++ E +SP+ A P VK
 Sbjct: 740 AEAKSPAEKSPAE---AKSPVEVKSPEKAKSPVKEG-AKSLA-EAKSPEKAKSP-VK-E 792

Query: 660 SVVLEGEAKFEEVSKINSVLKDLSTNDGQAPTLEIES 697
 + E K E +K S +K+ + + + +A TL+++S
 Sbjct: 793 EIKPPAEVKSPEKAK--SPMKEEAKSPE-KAKTLDVKS 827

Score = 255 (38.3 bits), Expect = 5.5e-18, P = 5.5e-18
 Identities = 124/420 (29%), Positives = 199/420 (47%)

Query: 252 ELLGEIRSPSAQKAPIEVQPLPA-----EGALEEAPAKVEPPTVEETLAEVQPLLPPEEAP 306
 ELLG+I+ A +A + + A AL E A++E TV+ TL +
 Sbjct: 236 ELLGQIQGCGAAQAQAQAEARDALKCDVTSALREIRAQLEGHTVQSTLQSEWFRVRLDR 295

Query: 307 REEARELQQLSTAMETPAEEAPTEFQSPLPKETTAEASAEIQLLAATEPPADETPAEARS 366
 EA ++ + AM + EE TE++ L TT E++ L +T+ + +E
 Sbjct: 296 LSEAAKVN-TDAMRSAQEET-TEYRRQLQARTT-----ELEALKSTKESLERQRSELED 347

Query: 367 PLSEE-TSAEEAHAHVQSPLAEETTAEASAEIQLLAIEAPAD-ETPAEQSPLSEE 422
 + S ++A ++ + L T E A+ E Q L ++ D E A + EE
 Sbjct: 348 RHQVDMASYQDAIQQLDNEL-RNTKWEAAQLREYQDLLNVKMLDIEIAAYRKLEEGEE 406

Query: 423 TSAEEAPAEV-----QSPS-AKGVSIE-EAPLELQPPSGEETT-AEEASAAIQLLA-A 471
 P+ + PS + + ++ E +++ S +ET EE + IQ+
 Sbjct: 407 CRIGFGSPFSLTEGLPKIPSMSTHIKVKSEEKIKVVEKSEKETVIVIEEQTEEIQVTEEV 466

Query: 472 TEASAEAPAEVQPPPAEEAPAEVQPP--PAEEAPAEVQPPPAEEA--PAEVQPPPA 524
 TE +EA E + AEE E PAEEA + E + P EEA PAE + P
 Sbjct: 467 TEEDKEAQGE-EEEEAEEGGEEAATSPPAEEAASPEKETKSPVKEEAKSPAEKSPAE 525

Score = 253 (38.0 bits), Expect = 9.0e-18, P = 9.0e-18
Identities = 115/364 (31%), Positives = 166/364 (45%)

Report for DKFZphtes3 17f10.3

```

SEQ      MDRSQQTSRTGYWTMMNI PPVEKV DKEQQTYFSESEIVVISRPDSSTKSKEDALKHKSS
SEG      .....
PRD      cccccccccccccccccccceehhhhhhhccccceeeecccccccchhhhhhhccc

SEQ      GKIFASEHPEFQPATNSNEEIGQKNISRTSFTQETKKGPPVLEDELREEVTVPPVQEGS
SEG      .....
PRD      cceeeccccccccccccccccccccccccccceeeecccccchhhhhhhhhheeeccccc

SEQ      AVKKVASAEIEPPSTEKFPAKIQPPLVEEATAKAEPRAETHVQVPSTEETPDAAEAT
SEG      .....
PRD      chhhhhhhccccccccccccccccchhhhhhhhhccccceeeecccccccccchhhh

SEQ      AVAENSVKVQPPPAEEAPLVEFPAEIQPPSAEESPSVELLAEILPPSAEESPSSEPPAEI
SEG      .....
PRD      hhhhhccccccccccccceeeccccccccccccccchhhhhcccccccccccccccccc

SEQ      LPPPAEKSPSVELLGEIRSPSAQKAPIEVQPLPAEGALEEAPAKVEPPTVEETLAEVQPL
SEG      .....
PRD      cccccccccccccccccccccccccccccccccchhhhhccccccccchhhhhhhhhhhc

SEQ      LPPEAPREEARELQSTAMETPAEEAPTEFQSPLPKETTAEASAEIQLLAATEPPADET
SEG      .....
PRD      cccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhcccccccc

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(No Pfam data available for DKFZphtes3 17f10.3)

DKFZphtes3_17117

group: metabolism

DKFZphtes3_17117 encodes a novel 626 amino acid protein with similarity to transketaloases (EC 2.2.1.1).

The novel protein contains a ATP/GTP-binding site motif A (P-loop). It is a new testis-specific transketolase. Transketolase requires thiamin pyrophosphate as cofactor and shows a wide specificity for both reactants, e.g. converts hydroxypyruvate and R-CHO into CO(2) and R-CHOH-CO-CH(2)OH.

The new protein can find application in modulation of metabolic pathways involving this transketolase activity and as a new enzyme for biotechnologic production processes.

strong similarity to transketolases

few EST hits (all from testis or pooled librarys containing testis)
testis specific transketolase?

Sequenced by GBF

Locus: unknown

Insert length: 2688 bp

Poly A stretch at pos. 2649, polyadenylation signal at pos. 2630

```
1  GACAAAAGAG AGATGATGGC CAACGACGCC AAGCCCGACG TGAAGACCGT
51 GCAGGTGCTG CCGGACACAG CCAACCGCCT GCGGATCCAT TCCATCAGGG
101 CCAGGTGTGC CTCTGGTTCT GGCCAGCTCA CGTCGTGCTG CAGTGCAGCG
151 GAGGTGCTGT CTGTCTCTTT CTTCCACACG ATGAAGTATA AACAGACAGA
201 CCCAGAACAC CCGGACACAG ACCGGTTCAT CCTCTCCAGG GGACATGCTG
251 CTCCTATCCT CTATGCTGCT TGGGTGGAGG TGGGTGACAT CAGTGAATCT
301 GACTTGCTGA ACCTGAGGAA ACTTCACAGC GACTTGGAGA GACACCCTAC
351 CCCGCGATTG CCGTTTGTGT ACCTGGCAAC AGGGTCCCTA GGTCAAGGAT
401 TAGCTACTGC ATGTGGAATG GCTTATACTG GCAAGTACCT TGACAAGGCC
451 AGTACCCGGG TGTTCTGCCT TATGGGAGAT GGCGAATCCT CAGAAGGCTC
501 TGTGTGGGAG GCTTTTGTCT TTGCCTCCCA CTACAACCTG GACAATCTCG
551 TGGCGGTCTT CGACGTGAAC CGCTTGGGAC AAAGTGGCCC TGCACCCCTT
601 GAGCATGGCG CAGACATCTA CCAGAATTGC TGTGAAGCCT TTGGATGGAA
651 TACTTACTTA GTGGATGGCC ATGATGTGGA GGCCTTGTGC CAAGCATTTT
701 GGCAGAACAG TCAAGTGAAG AACAAAGCCTA CTGTATAGT TGCCAAGACC
751 TTCAAAGGTC GGGGTATTCC AAATATTGAG GATGCAGAAA ATTGGCATGG
801 AAAGCCAGTG CCAAAAGAAA GAGCAGATGC AATTGTCAAA TTAATTGAGA
851 GTCAGATACA GACCAATGAG AATCTCATAC CAAAATCGCC TGTGGAAGAC
901 TCACCTCAAA TAAGCATCAC AGATATAAAA ATGACCTCCC CACCTGCTTA
951 CAAAGTTGGT GACAAGATAG CTAATCAGAA AACATATGGT TTGGCTCTGG
1001 CTAAACTGGG CCGTGCAAAT GAAAGAGTTA TTGTTCTGAG TGGTGACACG
1051 ATGAACTGCA CCTTTTCTGA GATATTCAGG AAAGAACACC CTGAGCGTTT
1101 CATAGAGTGT ATTATTGCTG AACAAAACAT GGTAAGTGTG GCACTAGGCT
1151 GTGCTACACG TGGTCGAACC ATTGCTTTTG CTGGTGCTTT TGCTGCCTTT
1201 TTTACTAGAG CATTGATGCA GCTCCGAATG GGAGCCATTT CTCAAGCCAA
1251 TATCAACCTT ATTGGTTCCC ACTGTGGGGT ATCCACTGGA GAAGATGGAG
1301 TCTCCAGATG GGCCCTGGAG GATCTAGCCA TGTTCCGAAG CATTCCCAAT
1351 TGTACTGTTT TCTATCCAAG TGATGCCATC TCGACAGAGC ATGCTATTTA
1401 TCTAGCCGCC AATACCAAGG GAATGTGCTT CATTCGAACC AGCCAACCAG
1451 AAAGTGCAGT TATTTATACC CCACAAGAAA ATTTTGAGAT TGGCCAGGCC
1501 AAGGTGGTCC GCCACGGTGT CAATGATAAA GTCACAGTAA TTGGAGCTGG
1551 AGTTACTCTC CATGAAGCCT TAGAAGCTGC TGACCATCTT TCTCAACAAG
1601 GTATTCTCTG CCGTGTCTAT GACCCATTTA CCATTAAACC CCTGGATGCC
1651 GCCACCATCA TCTCCAGTGC AAAAGCCACA GGCGGCCGAG TTATCACAGT
1701 GGAGGATCAC TACAGGGAAG GTGGCATTGG AGAAGCTGTT TGTGCAGCTG
1751 TCTCCAGGGA GCCTGATATC CTGTTCATC AACTGGCAGT GTCAGGAGTG
1801 CCTCAACGTG GGAATACTAG TGAATTGCTG GATATGTTT GAATCAGTAC
1851 CAGACACATT ATAGCAGCCG TAACACTTAC TTTAATGAAG TAAACTAGGC
1901 TTATTCTATA AAAGTCAAGT CTATTGGCTT TGGCCCAAAA GCACTGGTAT
1951 CTTTGATATA AATTCATGTT TATTGTCACA AAACCATTAT TTATACCTAT
2001 ACAGTTGTAC TGTTTCTTTT AAAGCAAAGC CATTTAACAT CTTTCTTCAT
2051 TCCTAATTTG GAAATTAAAG TTTACCTTTC TGTTAATCTA TGTATAAATG
2101 TTAAGTTGAG TATTAAATGT GGATTTTAAA ATTGTAAGCA ATAGAATAGG
2151 AAATAAAACA ACTACCTAAT ACAAATATTT CTGATAAGAC TACAAATATC
2201 TGACTGAGCT GGGGATTAAA GTAGAGGTAA CTGTATCTTA AATGAGTATG
2251 ATTTCTCTGT AATTAAAAA AATTGAAATT TAATTGTAGA CTTCAATAGT
2301 CCAAGTTTGT AAGGATGTTT GAGCTTTTGT ATAATGCCAT TTATACCTGC
2351 AGTTTTACAG ATAATGTTT ACTGCAGTTG CCTTGGAAAT TCCTCCAAGG
2401 TTTGCCCTTA TCTCTCTCT ACAGTTTGA GGTGATGGTG CAGCAGTGGA
2451 ATATCTCTTG ATGCCACCACA CTAATGTGTT TCTGTGAAGT GATGAAAGTA
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2501 TAACTGGTTC TAGTTTGCAC ACTACACACA TAGTTTGTG AAGETTCAGA
 2551 AATGTTTTTT CTTTTCCTTG TGGCCAAACC AGTTTGTAA TCTGATTATA
 2601 TTCATCTGCT AATGATACTA AAGTTAATGT AATAAAGCAT TTAAAAATCA
 2651 GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

BLAST Results

No BLAST result

Medline entries

96214928:
 Amplification of the transketolase gene in desensitization-resistant mutant
 Y1 mouse adrenocortical tumor cells.

99123875:
 Properties and functions of the thiamin diphosphate dependent enzyme transketolase.

Peptide information for frame 1

ORF from 13 bp to 1890 bp; peptide length: 626
 Category: strong similarity to known protein
 Classification: Metabolism
 Prosite motifs: ATP_GTP_A (595-603)

1 MMANDAKPDV KTVQVLRDTA NRLRIHSIRA TCASGSGQLT SCCSAAEVVS
 51 VLFFHTMKYK QTDPEHPDND RFILSRGHAA PILYAAWVEV GDISESDDLN
 101 LRKLHSDLER HPTPRLPFVD VATGSLGQGL GTACGMAYTG KYLDKASYRV
 151 FCLMGDGESE EGSVWEAFAP ASHYNLDNLV AVFDVNRLLQ SGPAPLEHGA
 201 DIYQNCCEAF GWNTYLVVDGH DVEALCQAFW QASQVKNKPT AIVAKTFKGR
 251 GIPNIEDAEN WHGKVPVKER ADAIVKLIES QIQTENLIP KSPVEDSPQI
 301 SITDIKMTSP PAYKVGDKIA TQKTYGLALA KLGRANERVI VLSGDTMNST
 351 FSEIFRKEHP ERFIECIIAE QNMVSVALGC ATRGRITIAF GAFAAFFTRA
 401 FDQLRMGAIS QANINLIGSH CGVSTGEDGV SQMALEDLAM FRISIPNCTVF
 451 YPSDAISTEH AIYLAANTKG MCFIRTSQPE TAVIYTPQEN FEIGQAKVVR
 501 HGVNDKVTVI GAGVTLHEAL EAADHLSQOG ISVRVIDPFT IKPLDAATII
 551 SSAKATGGRV ITVEDHYREG GIGEAVCAAV SREPDILVHQ LAVSGVPQQR
 601 KTSLELDMFG ISTRHIIAAV TLTLMK

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_17l17, frame 1

SWISSPROT:TKT_MOUSE TRANSKETOLASE (EC 2.2.1.1) (TK) (P68).. N = 1,
 Score = 2222, P = 2.5e-230

SWISSPROT:TKT_RAT TRANSKETOLASE (EC 2.2.1.1) (TK).. N = 1, Score =
 2202, P = 3.3e-228

TREMBL:RN09256_1 product: "transketolase"; Rattus norvegicus
 Sprague-Dawley transketolase mRNA, complete cds., N = 1, Score = 2202,
 P = 3.3e-228

SWISSPROT:TKT_HUMAN TRANSKETOLASE (EC 2.2.1.1) (TK).. N = 1, Score =
 2200, P = 5.3e-228

>SWISSPROT:TKT_MOUSE TRANSKETOLASE (EC 2.2.1.1) (TK) (P68).
 Length = 623

HSPs:

Score = 2222 (333.4 bits), Expect = 2.5e-230, P = 2.5e-230
 Identities = 417/614 (67%), Positives = 501/614 (81%)

Query: 7 KPDKVTVQVLRDTANRLRIHSIRATCASGSGQLTSCCSAAEVVSVLFFHTMKYKQTDPEH 66

Sbjct: 6 KPD + +Q L+DTANRLRI SI+AT A+GSG TSCCSAAE+++VLEFFHTM+YK DP +
6 KPDQQLQLQALKDTANRLRISSIQAATTAAGSGHPTSCCSAAEIMAVLFFHTMRYKALDPRN 65

Query: 67 PDNDRFILSRGHAAPILYA AAWVEVDISESDLLNLRKLHSDLERHPTPLPFVDVATGSL 126
P NDRF+LS+GHAAPILYA W E G + E++LLNLRK+ SDL+ HP P+ F DVATGSL

Sbjct: 66 PHNDRFVLSKGHAAPILYAVWAEAGFLPEAEELNLRKISSDLDGHPVPKQAFDVTGSL 125

Query: 127 GQGLGTACGMAYTGKYLDKASYRVFCLMGDESSEGSVWEAFASFASHYNLDNLVAVFDVN 186
GQGLG ACGMAYTGKY DKASYRV+C++GDGE SEGSVWEA AFA Y LDNLVA+FD+N

Sbjct: 126 GQGLGAACGMAYTGKYFDKASYRVYCM LGDGEVSEGSVWEAMAFAGIYKLDNLVAIFDIN 185

Query: 187 RLGQSGPAPLEHGADIYQNCCEAFGWNTYLVGDHDEALCQAFWQASQVKNKPTAIVAKT 246
RLGQS PAPL+H DIYQ CEAFGW+T +VDGH VE LC+AF QA K++PTAI+AKT

Sbjct: 186 RLGQSDPAPLQHVDIYQKRCEAFGWHTIIVDGHVSVEELCKAFGQA---KHQPTAIIAKT 242

Query: 247 FKGRGIPNIEDAENWHGKPVPKERADAIVKLIESQIQTNENLIPKSPVEDSPQISITDIK 306
FKGRGI IED E WHGKP+PK A+ I++ I SQ+Q+ + ++ P ED+P + I +I+

Sbjct: 243 FKGRGITGIEDKEAWHGKPLPKNMAEQIIQEIYSQVQSCKKILATPPQEDAPSVDIANIR 302

Query: 307 MTSPPAYKVGDKIATQKTYGLALAKLGRANERVIVLSGDTMNSTFSEIFRKEHPERFIEC 366
M +PP+YKVGDKIAT+K YGLALAKLG A++R+I L GDT NSTFSE+F+KEHP+RFIEC

Sbjct: 303 MPTPPSYKVGDKIATR KAYGLALAKLGHASDRIALDGDTKNSTFSELFKKEHPDRFIEC 362

Query: 367 IIAEQNMVSVALGCATRGRTIAFAGAFAAFFTRAFDQLRMGAISQANINLIGSHCGVSTG 426
IAEQNMVS+A+GCATR RT+ F FAAFFTRAFDQ+RM AIS++NINL GSHCGVS G

Sbjct: 363 YIAEQNMVSIAGCATRDRTVPFCSTFAAFFTRAFDQIRMAAISESNINLCGSHCGVSIG 422

Query: 427 EDGVSQMALEDLAMFRSIPNCTVFYPSDAISTEHAIYLAANTKGMCFIRTSQPETAIVIYT 486
EDG SQMALEDLAMFRS+P TVFYPSD ++TE A+ LAANTKG+CFIRTS+PE A+IY+

Sbjct: 423 EDGGSQMALEDLAMFRSVPMSTVFYPSDGVATEKAVELAANTKGICFIRTSRPNENAIYS 482

Query: 487 PQENFEIGQAKVVRHGVNDKVTIVIGAGVTLHEALEAADHLSQQGISVRVIDPFTIKPLDA 546
E+F++GQAKVV +D+VTIVIGAGVTLHEAL AA+ L + IS+RV+DPFTIKPLD

Sbjct: 483 NNEDFQVQAKVVLKSKDDQVTVIGAGVTLHEALAAAESLKKDKISIRVLDPFTIKPLDR 542

Query: 547 ATIISSAKATGGRVITVEDHYREGGIGEAVCAAVSREPDIHVHQLAVSGVPPRGKTSSELL 606
I+ SA+AT GR++TVEDHY EGGIGEAV AAV EP + V +LAVS VP+ GK +ELL

Sbjct: 543 KLILDSARATKGRILTVEDHYEGGIGEAVSAAVVGEPGVTVTRLAVSQVPRSGKPAELL 602

Query: 607 DMFGISTRHIIAAV 620
MFGI I+ AV

Sbjct: 603 KMFGIDKDAIVQAV 616

Pedant information for DKFZphtes3_17117, frame 1

Report for DKFZphtes3_17117.1

[LENGTH] 626
[MW] 67877.52
[pI] 5.90
[HOMOL] SWISSPROT:TKT_MOUSE TRANSKETOLASE (EC 2.2.1.1) (TK) (P68). 0.0
[FUNCAT] m outer membrane and cell wall [M. jannaschii, MJ0681] 3e-48
[FUNCAT] g carbohydrate metabolism and transport [H. influenzae, HI1023] 9e-36
[FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae, YPR074c] 5e-32
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YPR074c] 5e-32
[FUNCAT] 02.07 pentose-phosphate pathway [S. cerevisiae, YPR074c] 5e-32
[FUNCAT] 01.01.01 amino-acid biosynthesis [S. cerevisiae, YPR074c] 5e-32
[FUNCAT] i lipid metabolism [H. influenzae, HI1439] 3e-17
[FUNCAT] c energy conversion [H. influenzae, HI1233] 2e-09
[FUNCAT] 02.01 glycolysis [S. cerevisiae, YBR221c PDB1 - pyruvate dehydrogenase] 2e-05
[FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YBR221c PDB1 - pyruvate dehydrogenase] 2e-05
[BLOCKS] BL00801F
[BLOCKS] BL00801E
[BLOCKS] BL00801D Transketolase proteins
[BLOCKS] BL00801C Transketolase proteins
[BLOCKS] BL00801B Transketolase proteins
[BLOCKS] BL00801A Transketolase proteins
[SCOP] dltka2 3.28.1.2.1 Transketolase Transketolase, C-terminal domain 1e-21
[EC] 1.2.4.1 Pyruvate dehydrogenase (lipoamide) 8e-11
[EC] 1.2.4.4 3-Methyl-2-oxobutanoate dehydrogenase (lipoamide) 4e-10
[EC] 2.2.1.1 Transketolase 0.0
[EC] 2.2.1.3 Formaldehyde transketolase 1e-20
[PIRKW] transferase 0.0
[PIRKW] flavoprotein 2e-07
[PIRKW] Calvin cycle 1e-40
[PIRKW] heterotetramer 2e-07

SEQ	MMANDAKPDVKTVQVLRDTANRLRIHSIRATCASGSGQLTSCCSAAEVVSVLFFHTMKYK
SEG
lnsBHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHH-HHCCCT
SEQ	QTDPEHPDNDRFILSRGHAAPILYAAWVEVGDISDLLNLRLKLSDLERHPTPRLPFVD
SEG
lnsB	TTTTTTTTTCEEETGGGHHHHHHHHHHHCTTCHHHHHTTTTTTTTTTTTTTTTTTTC
SEQ	VATGSLGQGLGTACGMAYTGKYLKASRYVFCMLMGDGESSEGSVWEAFASHYNLDNLV
SEG
lnsB	CCCCTTTHHHHHHHHHHHHHHHHCBTTBTTEEECHHHHHCHHHHHHHHHHHHCTTTEE
SEQ	AVFDVNRLGQSGPALEHGADIYQNCCEAFGWNTYLVGDHDEALCQAFWQASQVKNKPT
SEG
lnsB	EEEEECCEETEEGGGCCCCCHHHHH-HHHCCEEEETTTTHHHHHHHHHHHHHTTTTCE
SEQ	AIVAKTFKGRGIPNIEDAENWHGKVPVKERADAIVKLIESQIQTNENLIPKSPVEDSPQI
SEG
lnsB	EEEEECTTTTTTCCHHHHHHHHHHTCCHHHHHHHHHHHHHHHHHHHHHHHHHHHCHHH
SEQ	SITDIKMTSPPAYKVGDKIATQKTYGLALAKLGRANERVIVLSGDTMNSTFSEIFRKEHP
SEG
lnsB	HHHHHHHHHTCCCTTTTCBCHHHHHHHHHHHHHTTTTTEEEEETTHHHHCCTTCCECCG
SEQ	ERFIECIIAEQNMVSVALGCATRGRTIAFAGAFAAFFTRAFDQLRMGAISQANINLIGSH
SEG
lnsB	GCEEETTTTHHHHHHHHHHHHHHTTTTTEEEEGGGGGGGHHHHHHHHHHHCTTTEEEEC
SEQ	CGVSTGEDGVSQMALEDLAMFRSIPNCTVFYPSDAISTEHAIIYLAANTKGMCFIRTSQPE
SEG
lnsB	CCGGGTTTTTTTTTCCHHHHHHHCTTTTTEEECCCCCHHHHHHHHHHHHTTTTCEEECCCCCB
SEQ	TAVIYTPQENFEIGQAKVVRHGVNDKVTVIGAGVTLHEALEAADHLSQQGISVRVIDPFT
SEG
lnsB	CCTTTTCHHHHHCC-CEEEETTTTTEEEECCHHHHHHHHHHHHHHHHCCCEEEE...
SEQ	IKPLDAATIISAKATGGRVITVEDHYREGGIGEAVCAAVSREPDIIVHQLAVSGVPQRG
SEG
lnsB
SEQ	KTSELDMFGISTRHIIAAVTLTLMK
SEG
lnsB

HMM_NAME Transketolase

HMM *vntIRiLaMDAVEKANSGHPGaPMGMAPMAHVLWqirMMRHNPNDPrWPN

Query	20	+N++RI ++ A + +SG +++++A++ VL++++M++++DP P+ ANRLRIHSIRATCASGSGQLTSCCSAAEVVSVLFFHTMKYKQTDPEHPD	68
HMM		RDRFVLSNGHACMLLYsMWHLYGYDMPMWDLkQFRQWHSrTPGHPEIgHT +DRF+LS GH++++LY+ W + G +++++DL+++R++HS++ +HP ++	
Query	69	NDRFILSRGHAAPILYA+AWVEVD-ISESDLNLRKLHSDLERHPTPLRP	117
HMM		PGVEVTTGTLGQGIIaNaVWMAIAERnLAATYNRRPGFDIfDHITYCFMGDG ++ +V+TG+LGQG++ +++++Y++++ D++++++C+MGDG	
Query	118	FV-DVATGSLGQGLG-----TACGMAYTGKYLDKASYRVFCLMGDG	157
HMM		CLMEGISWEACSLAGHMqLGNWiaFYDDNrISIDGdTdiWFqEDtYakRF + +EG++WEA ++A+H++L+N++A +D NR++++G++++ + D+Y+ +	
Query	158	ESSEGSVWEAFAFASHYNLDNLVAVFDVNRLGQSGPAPLEHGADIYQNCC	207
HMM		EAYGWHVIEVEndGHdVeeIcaAIEeAKaekDRPTLIiCRTVIGYGSFNk EA+GW++ +V DGHdVE++C A+ +A +K++PT+I ++T++G+G+PN	
Query	208	EAFGWNTYLV--DGHdVEALCQAFWQASQVKNKPTAIVAKTFKGRGIPNI	255
HMM		QGTHdWHGAPLGeD* ++ + WHG+P +++	
Query	256	EDAENWHGKPVPEKE 269	
HMM		*PqWePnddkIATRKAQQaLeaiGPALPEfWGGsADLTSPNLTrWKGMv P++++ +DKIAT K+++ AL+++G A +++ +S+D+ +S++++++ ++	
Query	311	PAYKV-GDKIATQKTYGLALAKLGRANERVIVLSGDTMNSTFSEIFRKE	358
HMM		WFMPSPISDTCynGNWsgRYIHYGIREHqMgAIMNGIALHGqNFRPYGGT + R+I++ I+E++M++++ G+A++G+ +++++ G	
Query	359	H-----PERFIECIIAEQNMVSVALGCATRGR-TIAFAGA	392
HMM		FMMFyDYARPAIRMAALMelPVIWVWTHDSIGLGEDGPTHQPVHHLAHR F+++F+++A++++RM A++ +++++H++++ GEDG +++++E+LA+FR	
Query	393	FAAFFTRAFDQLRMGAISQANINLIGSHCGVSTGEDGVSQMALEDLAFR	442
HMM		aIPNMsvVRPCDgNETayAWylAveRehTPtiLILSRQNLPLERnPrqf +IPN +V++P+D+ T+ A YLA+++++ +++++S ++ +++++ P +	
Query	443	SIPNCTVFYPSDAISTEHAIYLAANTKGM-CFIRTSQPETAVIYT-PQEN	490
HMM		ekvaRGGYVLkDmdnePDVILIATGSEMELavaAAKlLadEGikaRVVSM +++++++V + + + V++I++G++++A++AA+ L+ +GI +RV+++	
Query	491	FEIGQAKVVRHGVN--DKVTVIGAGVTLHEALEADHLSQQGISVRVIDP	538
HMM		PCTeWFD.....kQDeEYReSVLPdhVPqRVaVEmGvtWCWYKYVGqq ++++++D + +++++R +++DH++ +++++V ++ +++ +	
Query	539	FTIKPLDAATIISSAKATGGRVITVEDHYR-EGGIGEAVCAAVSREPDIL	587
HMM		GaIfGMNrFGESSGKAPpeVLYkMFGFTPENI* + +++ +++ ++ +L+ MFG+ +I	
Query	588	VHQLAVSGVPQR---GKTSELLDMFGISTRHI 616	

DKFZphtes3_17n12

group: transcription factors

DKFZphtes3_17n12.1 encodes a novel 804 amino acid protein which is nearly identical to mouse and trout SOX-LZ.

Sox proteins belong to the HMG box superfamily of DNA-binding proteins and are involved in the regulation of developmental processes as germ layer formation, organ development and cell type specification. Deletion or mutation of Sox proteins often results in developmental defects and congenital disease in humans. Sox proteins perform their function in a complex interplay with other transcription factors in a manner highly dependent on cell type and promoter context. The new protein is related to the SOX-LZ protein and contains an additional leucine-zipper.

The new protein can find application in modulating/blocking the expression of SOX-controlled genes.

nearly identical to mouse SOX-LZ

complete cDNA, complete cds, few EST hits
mouse and trout SOX-LZ, involved in spermatogenesis

Sequenced by GBF

Locus: unknown

Insert length: 2802 bp

Poly A stretch at pos. 2692, polyadenylation signal at pos. 2660

```
1 GGGATAGGAA AGATGAAAGG TCATGGTGAG CTTCAAGGAC ATGAAAGGTT
51 GTTGTCTCAT GTAACAATAG TAGATTGTTT TTTTCCTAA TATTCTAGC
101 CAGCCCCTAA GTCAGGTGAT GGAACAAATA CCTACAGTTT AGTCAGGTGA
151 AACAGGAGTG GGTGGAGGAA GGAAAGAAGA AAAATGGGAA GAATGTCTTC
201 CAAGCAAGCC ACCTCTCCAT TTGCCTGTGC AGCTGATGGA GAGGATGCAA
251 TGACCCAGGA TTTAACCCTA AGGGAAAAGG AAGAGGGCAG TGATCAACAT
301 GTGGCCTCCC ATCTGCCTCT GCACCCCAT A TGACACAACA AACCTCACTC
351 TGAGGAGCTA CCAACACTTG TCAGTACCAT TCAACAAGAT GCTGACTGGG
401 ACAGCGTTCT GTCATCTCAG CAAAGAATGG AATCAGAGAA TAATAAGTTA
451 TGTTCCCTAT ATTCTTCCG AAATACCTCT ACCTCACCAC ATAAGCCTGA
501 CGAAGGGAGT CGGGACCGTG AGATAATGAC CAGTGTTACT TTTGGAACCC
551 CAGAGCGCCG CAAAGGGAGT CTTGCCGATG TGGTGGACAC ACTGAAACAG
601 AAGAAGCTTG AGGAAATGAC TCGGACTGAA CAAGAGGATT CCTCCTGCAT
651 GGAAAAACTA CTTTCAAAAG ATTGGAAGGA AAAAATGGAA AGACTAAATA
701 CCAAGTAACT TCTTGGAGAA ATTAAAGGTA CACCTGAGAG CCTGGCAGAA
751 AAAGAACGGC AGCTCTCCAC CATGATTACC CAGCTGATCA GTTTACGGGA
801 GCAGCTACTG GCAGCGCATG ATGAACAGAA AAAACTGGCA GCGTCACAAA
851 TTGAGAAACA ACGGCAGCAA ATGGACCTTG CTCGCCAACA GCAAGAACAG
901 ATTGCGAGAC AACAGCAGCA ACTTCTGCAA CAGCAGCACA AAATTAATCT
951 CCTGCAGCAA CAGATCCAGG TTCAGGGTCA CATGCCTCCG CTCATGATCC
1001 CAATTTTTC ACATGACCAG CGGACTCTGG CAGCAGCTGC TGCTGCCCAA
1051 CAGGGATTCC TCTTCCCCC TGGAATAACA TACAAACCAG GTGATAACTA
1101 CCCCGTACAG TTCATTCCAT CAACAATGGC AGCTGCTGCT GCTTCTGGAC
1151 TCAGCCCTTT ACAGCTCCAG CAGCTCTATG CCGCTCAGCT GGCCAGCATG
1201 CAGGTGTCAC CTGGAGCAAA GATGCCATCA ACTCCACAG CACCAAACAC
1251 AGCAGGGACG CTCTCACCTA CTGGGATAAA AAATGAAAAG AGAGGGACCA
1301 GCCCTGTAAC TCAAGTTAAG GATGAAGCAG CAGCACAGCC TCTGAATCTC
1351 TCATCCCGAC CCAAGACAGC AGAGCCTGTA AAGTCCCCAA CGTCTCCAC
1401 CCAGAACCCT TCCCCAGCCA GCAAAACCAG CCCTGTCAAT CTGCCAAACA
1451 AAAGCAGCAT CCTAGCCCC ATTGGAGGAA GCCTGGGAAG AGGATCCTCT
1501 TTAGGTAAAT GGAAAAGTCA ACACCAGGAA GAGACTTACG AATTAGATAT
1551 CCTATCTAGT CTCAACTCCC CTGCCCTTTT TGGGGATCAG GATACAGTGA
1601 TGAAAGCCAT TCAGGAGGCG CGGAAGATGC GAGAGCAGAT CCAGCGGGAG
1651 CAACAGCAGC AACAGCCACA TGGTGTGAC GGGAAACTGT CCTCCATAAA
1701 TAATATGGGG CTGAACAGCT GCAGGAATGA AAAGGAAAAG ACGCGCTTTG
1751 AGAATTGGGG GCCCCAGTTA ACGGGAAAGT CAAATGAAGA TGGAAAAGTG
1801 GGCCCAGGTG TCATCGACCT TACTCGGCCA GAAGATGCAG AGGGAAGTAA
1851 AGCAATGAAT GGCTCTGCAG CTAAACTACA GCAGTATTAT TGTGGCCAA
1901 CAGGAGGTGC CACTGTGGCT GAAGCACGAG TCTACAGGGA CGCCCCGGC
1951 CGTGCCAGCA GCGAGCCACA CATTAAAGCG CCAATGAATG CATTATGGT
2001 TTGGGCAAGG GATGAGAGGA GAAAAATCCT TCAGGCCTTC CCCGACATGC
2051 ATAATCCAA CATTAGCAAA ATCTTAGGAT CTCGCTGGAA ATCAATGTCC
2101 AACCAGGAGA AGCAACCTTA TTATGAAGAG CAGGCCCGGC TAAGCAAGAT
2151 CCACTTAGAG AAGTACCCAA ACTATAAATA CAAACCCCGA CCGAAACGCA
2201 CCTGCAATTG TGATGGCAAA AAGCTTCGGA TTGGGGAGTA TAAGCAACTG
2251 ATGAGGTCTC GGAGACAGGA GATGAGGCAG TTCTTTACTG TGGGGCAACA
2301 GCCTCAGATT CCAATCACCA CAGGAACAGG TGTGTGTAT CCTGGTGCTA
2351 TCACTATGGC AACTACCACA CCATCGCCTC AGATGACATC TGACTGCTCT
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2401 AGCACCTCGG CCAGCCCGGA GCCCAGCCTC CCGGTCATCC AGAGCACTTA
2451 TGGTATGAAG ACAGATGGCG GAAGCCTAGC TGGAAATGAA ATGATCAATG
2501 GAGAGGATGA AATGGAATG TATGATGACT ATGAAGATGA CCCCAAATCA
2551 GACTATAGCA GTGAAAATGA AGCCCCGAG GCTGTCACTG CCAACTGAGG
2601 AGTTTTTGTG TGCTGAATTA AAGTACTCTG ACATTCACC CCCCTCCCCA
2651 ACAAAGAGTT ATTAAGAGC CCGCATGCAT TTGTGGCTCC ACAATTAAAA
2701 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2751 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2801 AA

```

BLAST Results

No BLAST result

Medline entries

95311974:

A gene that is related to SRY and is expressed in the testes encodes a leucine zipper-containing protein.

96032826:

The Sry-related HMG box-containing gene Sox6 is expressed in the adult testis and developing nervous system of the mouse.

Peptide information for frame 1

ORF from 184 bp to 2595 bp; peptide length: 804
Category: strong similarity to known protein

```

1  MGRMSSKQAT SPFACAADGE DAMTQDLTSR EKEEGSDQHV ASHLPLHPIM
51 HNKPHSEELP TLVSTIQQDA DWDSVLSSQQ RMESENNKLC SLYSFRNTST
101 SPHKPDEGSR DREIMTSVTF GTPERRKGSL ADVVDTLKQK KLEEMTRTEQ
151 EDSSCMEKLL SKDWKEKMER LNTSELLGEI KGTPESLAEK ERQLSTMITQ
201 LISLREQLLA AHDEQKKLAA SQIEKQRQQM DLARQQQEQI ARQQQQLLQQ
251 QHKINLLQQQ IQVQGHMPPPL MIPIFPHDQR TLAAAAAAQQ GFLFPPGITY
301 KPGDNYPVQF IPSTMAAAAA SGLSPLOLQQ LYAAQLASMQ VSPGAKMPST
351 PPPNTAGTV SPTGIKNEKR GTSPVTQVKD EAAQPLNLS SRPKTAEPVK
401 SPTSPTQNL FASKTSPVNL PNKSSIPSPI GGSILGRGSSL GKWKSQLHQQE
451 TYELDILSSL NSPALFGDQD TVMKAIQEAR KMREQIOREQ QQQQPHGVVDG
501 KLSSINNMGL NSCRNEKERT RFENLGPQLT GKSNEGKLG PGVIDLTRPE
551 DAEGSKAMNG SAAKLQYYC WPTGGATVAE ARVYRDARGR ASSEPHIKRP
601 MNAFMVWAKD ERRKILQAFP DMHNSNISKI LGSRWKSMNS QEKQPYEEQ
651 ARLSKIHLEK YPNYKYKPRP KRTCIVDGKK LRIGEYKQLM RSRQEMRQF
701 FTVGQQPQIP ITTGTGVVYP GAITMATTP SPQMTSDCSS TSASPEPSLP
751 VIQSTYGMKT DGGSLAGNEM INGEDEMEMY DDYEDDPKSD YSENEAPEA
801 VSAN

```

BLASTP hits

Entry MMSOXLZ2_1 from database TREMBL:

product: "SOX-LZ"; Mouse mRNA for SOX-LZ, complete cds.

Score = 3910, P = 0.0e+00, identities = 764/801, positives = 774/801

Entry I51083 from database PIR:

SOX-LZ - rainbow trout

Score = 1774, P = 1.1e-287, identities = 365/532, positives = 431/532

Entry S59121 from database PIR:

SOX6 protein - mouse

Score = 2319, P = 1.2e-240, identities = 489/660, positives = 527/660

Entry AB006330_1 from database TREMBL:

gene: "mSox5L"; product: "SOX5"; Mus musculus mSox5L mRNA, complete cds.

Score = 1212, P = 8.9e-209, identities = 274/457, positives = 324/457

Entry MMU010604_1 from database TREMBL:

gene: "sox5"; product: "L-Sox5 protein"; Mus musculus mRNA for transcription factor L-Sox5

Score = 879, P = 4.2e-195, identities = 190/281, positives = 218/281

Alert BLASTP hits for DKFZphtes3_17n12, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_17n12, frame 1

Report for DKFZphtes3_17n12.1

[LENGTH] 804
 [MW] 89332.69
 [pI] 6.97
 [HOMOL] TREMBL:MMSOXL22_1 product: "SOX-LZ"; Mouse mRNA for SOX-LZ, complete cds. 0.0

[FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YKL032c] 8e-07
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKL032c] 8e-07
 [FUNCAT] 01.07.07 regulation of vitamins, cofactors, and prosthetic groups [S. cerevisiae, YPR065w] 5e-06
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YBR089c-a] 7e-06
 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YBR089c-a] 7e-06
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YBR089c-a] 7e-06
 [FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YMR072w] 2e-04
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YMR072w] 2e-04
 [SCOP] dlhmf_1.20.1.1.1 HMG1, fragments A and B [rat/hamster (Rattus) 1e-13
 [SCOP] dllefa_1.20.1.1.6 Lymphoid enhancer-binding factor, LEF1 [mous 4e-15
 [SCOP] dlhrya_1.20.1.1.4 SRY [Human (Homo sapiens) 7e-17
 [PIRKW] DNA binding 4e-94
 [PIRKW] T-cell receptor 4e-07
 [PIRKW] leucine zipper 1e-38
 [PIRKW] alternative splicing 2e-07
 [PIRKW] transcription factor 4e-16
 [PIRKW] transcription regulation 1e-12
 [SUPFAM] HMG box homology 0.0
 [SUPFAM] unassigned HMG box proteins 4e-94
 [PROSITE] ATP_GTP_A 1
 [PROSITE] LEUCINE_ZIPPER 1
 [PROSITE] MYRISTYL 6
 [PROSITE] AMIDATION 1
 [PROSITE] CAMP_PHOSPHO_SITE 2
 [PROSITE] CK2_PHOSPHO_SITE 14
 [PROSITE] PKC_PHOSPHO_SITE 10
 [PROSITE] ASN_GLYCOSYLATION 6
 [PFAM] HMG (high mobility group) box
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 13.81 %
 [KW] COILED_COIL 3.48 %

SEQ MGRMSSKQATSPFACAADGEDAMTQDLTSREKEEGSDQHVASHLPLHPIMHNKPHSEELP
 SEG
 COILS
 Inhm-

SEQ TLVSTIQDADWDVLSQQRMESENNKLCSLYSFRNTSTSPHKPDEGSRDREIMTSVTF
 SEG
 COILS
 Inhm-

SEQ GTPERRKGLADVVDTLKQKKLEEMTRTEQEDSSCMEKLLSKDWKEKMERLNTSELLGEI
 SEG
 COILS
 Inhm-

SEQ KGTPESLAEKERQLSTMITQLISLREQLLAHDEQKKLAASQIEKQRQQMDLARQQQEIQI
 SEGXXXXXXXXXXXXXXXXXXXX
 COILSCCCCC
 Inhm-

SEQ ARQQQQQLLQQQHKNLLQQQIQVQGHMPLMIPIFPHDQRTLAAAAAQQGFLFPFGITY
 SEGXXXXXXXXXXXXXXXXXXXX
 COILSCCCCCCCCCCCCCCCCCCCC
 Inhm-

SEQ KPGDNYPVQFIPSTMAAAAASGLSPQLQLQQLYAAQLASMQVSPGAKMPSTPQPPNTAGTV
 SEGXXXXXXXXXXXXXXXXXXXX


```

COILS .....
lnhm- .....

SEQ      SPTGIKNEKRGTSPTVQVKDEAAQPLNLSSRPKTAEPVKSPTSPTQNLFPASKTSPVNL
SEG      .....
COILS    .....
lnhm-    .....

SEQ      PNKSSIPSPIGGSLGRGSSLGKWKSOHQEETYELDILSSLNSPALFGDQDTVMKAIQEAR
SEG      ...xxxxxxxxxxxxxxxxxxxxx.....
COILS    .....
lnhm-    .....

SEQ      KMREQIQREQQQQQPHGVDGKLSSINNMGLNSCRNEKERTRFENLGPQLTGKSNEDGKLG
SEG      ..xxxxxxxxxxxxxxxxxxxxx.....
COILS    .....
lnhm-    .....

SEQ      PGVIDLTRPEDAEGSKAMNGSAAKLQYYCWPTGGATVAEARVYRDARGRASSEPHIKRP
SEG      .....
COILS    .....
lnhm-    .....CCC

SEQ      MNAFMVWAKDERRKILQAFPMHNSNISKILGSRWKSMSNQEKQPYEEQARLSKIHLEK
SEG      .....x
COILS    .....
lnhm-    CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ      YPNYKYKPRPKRTCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTGVVYP
SEG      xxxxxxxxxxxxxxxx.....
COILS    .....
lnhm-    HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

SEQ      GAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKTDGGSLAGNEMINGEDEMEMY
SEG      .....xxxxxxx
COILS    .....
lnhm-    .....

SEQ      DDYEDDPKSDYSSENEAPAVSAN
SEG      xxxxxxxx.....
COILS    .....
lnhm-    .....

```

Prosites for DKFZphtes3_17n12.1

PS00001	97->101	ASN_GLYCOSYLATION	PDOC00001
PS00001	172->176	ASN_GLYCOSYLATION	PDOC00001
PS00001	388->392	ASN_GLYCOSYLATION	PDOC00001
PS00001	422->426	ASN_GLYCOSYLATION	PDOC00001
PS00001	559->563	ASN_GLYCOSYLATION	PDOC00001
PS00001	626->630	ASN_GLYCOSYLATION	PDOC00001
PS00004	126->130	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	369->373	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	5->8	PKC_PHOSPHO_SITE	PDOC00005
PS00005	28->31	PKC_PHOSPHO_SITE	PDOC00005
PS00005	94->97	PKC_PHOSPHO_SITE	PDOC00005
PS00005	136->139	PKC_PHOSPHO_SITE	PDOC00005
PS00005	203->206	PKC_PHOSPHO_SITE	PDOC00005
PS00005	299->302	PKC_PHOSPHO_SITE	PDOC00005
PS00005	390->393	PKC_PHOSPHO_SITE	PDOC00005
PS00005	512->515	PKC_PHOSPHO_SITE	PDOC00005
PS00005	530->533	PKC_PHOSPHO_SITE	PDOC00005
PS00005	692->695	PKC_PHOSPHO_SITE	PDOC00005
PS00006	28->32	CK2_PHOSPHO_SITE	PDOC00006
PS00006	129->133	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	148->152	CK2_PHOSPHO_SITE	PDOC00006
PS00006	154->158	CK2_PHOSPHO_SITE	PDOC00006
PS00006	186->190	CK2_PHOSPHO_SITE	PDOC00006
PS00006	203->207	CK2_PHOSPHO_SITE	PDOC00006
PS00006	221->225	CK2_PHOSPHO_SITE	PDOC00006
PS00006	520->524	CK2_PHOSPHO_SITE	PDOC00006
PS00006	533->537	CK2_PHOSPHO_SITE	PDOC00006
PS00006	547->551	CK2_PHOSPHO_SITE	PDOC00006
PS00006	577->581	CK2_PHOSPHO_SITE	PDOC00006
PS00006	639->643	CK2_PHOSPHO_SITE	PDOC00006
PS00006	793->797	CK2_PHOSPHO_SITE	PDOC00006
PS00008	182->188	MYRISTYL	PDOC00008
PS00008	431->437	MYRISTYL	PDOC00008

PS00008	437->443	MYRISTYL	PDOC00008
PS00008	509->515	MYRISTYL	PDOC00008
PS00008	575->581	MYRISTYL	PDOC00008
PS00008	762->768	MYRISTYL	PDOC00008
PS00009	677->681	AMIDATION	PDOC00009
PS00017	526->534	ATP_GTP_A	PDOC00017
PS00029	187->209	LEUCINE_ZIPPER	PDOC00029

Pfam for DKFZphtes3_17n12.1

HMM_NAME	HMG (high mobility group) box		
HMM	*PKRPMNAYMLWMQEMRekIKaENPNdMhNtEISKMiGEMWKnMsEEEEKm		
	+KRPMNA+M+W+++ R+KI + P DMHN++ISK++G +WK+MS +EK+		
Query	597	IKRPMNAFMVWAKDERRKILQAFP-DMHNSNISKILGSRWKSMSNQEKQ	644
HMM	PYEdMAeeEKqRYMKEMPeYK*		
	PY+++ +++ + +++ +P+YK		
Query	645	PYYEEQARLSKIHLEKYPNYK	665

DKFZphtes3_17n18

group: intracellular transport and trafficking

DKFZphtes3_17n18 encodes a novel 782 amino acid protein with weak partial similarity to known proteins.

The novel protein contains a ATP/GTP-binding site motif A (P-loop) and a TonB-dependent receptor protein signature 1. In *E. coli*, the tonB protein interacts with outer membrane receptor proteins that mediate uptake of specific substrates into the periplasmic space. In the absence of tonB these receptors bind their substrates but do not carry out active transport. The novel protein seems to be involved in ATP-dependent transport of substances into the cell.

The new protein can find application in modulation of cell-permeability and transport of suitable substrates into the cell.

unknown receptor

protein contains TONB_DEPENDENT_REC_1 Pattern and ATP_GTP_A Pattern,

Sequenced by GBF

Locus: unknown

Insert length: 2853 bp

Poly A stretch at pos. 2806, no polyadenylation signal found

```
1 GTCCTTTTAA GTCAGTAAAT TGAAGTAAAGT CGGTTATTTCG GCAAGCAGTT
51 CCTATAAAAA ACTACATGGC TAAGGTTCTT AATGATTGAC CACAAGCAGA
101 TCTTTTACCC TCGGATCTCT AGCTACAAAA GGTCCCCACA CTGAAGAAGC
151 CACTACCTCC ACCACCACCA GCACCACCAC GTCCAGTGCT GCTGGCAACC
201 ACTGGGGCAG CCAAGCGCTC CACCCTCTCT CCCACCATGG CCCGTCAGGT
251 GCGCACCCAC CAGGAGACCC TGAACAGGTT TCAGCAGCAG TCCATCCACC
301 TGCTGACGGA GCTCCTCAGA CTGAAGATGA AGGCCATGGT GGAGTCTATG
351 TCGGTGGGTG CCAACCCCTT GGACATCACC AGGCGCTTTG TGGAGGCCAG
401 CCAGCTCCTC CAGCTCAATG CCAAGGAGAT GGCCTTCAAC TGCCTGATCA
451 GCACAGCCGG GAGAAGTGGC TACAGCAGCG GACAGTTGTG GAAAGAGTCC
501 CTCGCAAAAC TGTCCGCCAT TGGGGTGAAC TCGCCTTACC AGCTGATCTA
551 CCACTCTTCC AGGCCTGTC TGAGCTTTTC TCTCTCTGCT CGAAAAGAAG
601 CCAAGAAGAA AATAGGCAAA TCTAGAACTA CAGAAGATGT CAGCATGCCG
651 CCCCTGCATC GAGGAGTGGG AACCCTGGCC AACAGCCTGG AGTTCAGCGA
701 CCCCTGCCCT GAGGCCCGGG AGAAGCTGGA GGAGTTGTGT CGCCACATAG
751 AAGCTGAAAG GGCCACATGG AAAGGGAGGA ATATCTCCTA CCCCATGATC
801 TTACGAAACT ACAAGGCAAA GATGCCCTCT CATCTAATGT TGGCCCGCAA
851 AGGAGACTCT CAGACCCCGG GTTACATTA CCCTCCCACT CAGAGTGCTC
901 AGACTCTCAG CCCCACTCT CACCCTCTT CTGCCAACCA TCATTTCAGT
951 CAGCATTGTC AAGAGGGGAA GGCACCCAAG AAGGCCTTCA AGTTTCATTA
1001 CACCTTCTAT GATGGCTCCT CCTTCGTTTA CTATCCCTCT GGAACGTCG
1051 CTGTATGTCA GATCCCCACA TGCTGCAGAG GGAGAACCAT CACCTGCCTC
1101 TTTAATGACA TACCTGGATT CTCCTTGCTG GCCCTATTCA ATACTGAAGG
1151 CCAGGGCTGT GTTCACTACA ACCTA AAAAAC CAGTTGCCCA TATGTCTTAA
1201 TCTTGGATGA GGAAGGTGGG ACCACCAATG ACCAGCAGGG CTATGTAGTC
1251 CACAAGTGGA GCTGGACTTC CAGGACAGAG ACCCTGCTTT CCCTGGAATA
1301 CAAGGTGAAT GAGGAAATGA AACTAAAGGT ACTGGGACAG GACTCCATCA
1351 CAGTCACCTT CACCTCCCTG AATGAGACAG TAACACTCAC TGTGTCGGCC
1401 AACCAATTGC CCCATGGAAT GGCATATGAC AAACGGCTGA ACCGCAGAAT
1451 CAGCAACATG GACGACAAGG TGTATAAGAT GAGCCGAGCC CTGGCTGAGA
1501 TCAAGAAGCG GTTTCAGAAG ACAGTGACTC AGTTCAATTA TTCTATCTTG
1551 CTGGCCGCAG GTCTGTTTAC CATTGAATAT CCCACCAAAA AGGAGGAGGA
1601 AGAATTTGTT CGGTTCAAGA TGAGATCCAG AACTCATCCC GAGCGGCTCC
1651 CCAAGCTAAG TTTATACTCA GGAGAAAGTC TTTTACGATC TCAGTCAGGC
1701 CACCTGGAAT CTTCAATTGC AGAGACTTTG AAGGATGAGC CTGAGTCTGC
1751 TCCTGTGAGC CCGATTCCGA AGACCACCAA AATCCACACC AAAGCCAAGG
1801 TCACATCCAG AGGGAAGGCC CGCGAGGGGC GCAGCCCCAC CAGGTGGGCG
1851 GCCTTGCCCT CAGACTGCCC GCTGGTGCTG CGGAAGCTCA TGCTCAAGGA
1901 AGACATCCAG GCTGGCTGCA AGTGCTGGT GAAGGCGCCC CTGGTCTCTG
1951 ACGTGGAGCT GGAGCGCTTC CTGTTGGCGC CCCGAGACCC CAGCCAAGTG
2001 CTGGTGTTTG GGATCATCTC AAGCCAGAAC TACACCAGCA CTGGGCAGCT
2051 CCAGTGGCTG TCTAACACTC TCTACAACCA CCAGCAGCGG GGCCGTGGCT
2101 CCCCTGTCAT CCAGTGCCGG TATGACTCCT ACCGCCTGCT GCAGTATGAC
2151 CTGGACAGCC CCGTCGAGGA GGACCCCTCC CTGATGGTGA AGAAGAATC
2201 TGTGGTGCAG GGGATGATTG TGATGTTTGC CGGGGGGAAG CTCATTTTTG
2251 GGGGCCGTGT TTTGAATGGA TATGGCCTCA GCAAGCAGAA TCTGCTGAAA
2301 CAGATCTTCC GGTCTCAACA GGATTACAAG ATGGGCTACT TCCTGCCGGA
2351 TGACTACAAA TTAGTGTTTC CCAACTCTGT CCTGAGCCTG GAGGATTCTG
2401 AATCAGTCAA GAAAGCCGAG TCAGAAGATA TCCAAGGAAG CAGCTCCTCA
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2451 TTGGCCCTGG AAGACTATGT GGAQAAGGAG TTATCTCTGG AGGCTGAGAA
2501 GACAAGAGAG CCTGAAGTGG AGCTACATCC TCTCAGCAGG GACAGCAAGA
2551 TAACTAGTTG GAAGAAGCAG GCCTCAAGA AGTAGCGCCA TCCTGGCAGC
2601 AGCCAAGTGA GCCAGGCCCC GGCCCGGGGT GCTGGGGCTT CTTGCCAGCC
2651 CAGCCCTGCC TCCCCGGTCT CCCACCCTGT CCTCCAAGCT TCTATAATAA
2701 ACCAGCGGGC CTCCAGCATT GGGGTGAGGC TCTGGGGAAG GACAAAAAAA
2751 AAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA
2801 CGGCCGAAAA AAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA
2851 CCG

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BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 237 bp to 2582 bp; peptide length: 782
 Category: putative protein
 Prosite motifs: ATP_GTP_A (122-130)
 TONB_DEPENDENT_REC_1 (1-44)

```

1 MARQVRTHQE TLNRFQQQSI HLLTELLRLK MKAMVESMSV GANPLDITRR
51 FVEASQLLHL NAKEMAFNCL ISTAGRSGYS SGQLWKESLA NMSAIGVNSP
101 YQLIYHSSTA CLSFSLSAGK EAKKKIGKSR TTEDVSMPPPL HRGVGTFPANS
151 LEFSDPCPEA REKLQELCRH IEAERATWKG RNISYPMILR NYKAKMPSHL
201 MLARKGDSQT PGLHYPTAG AQTLSPTSHP SSANHHFSQH CQEGKAPKKA
251 FKEHYTFYDG SSFVYPSGN VAVCQIPTCC RGRITITCLFN DIPGFSLLAL
301 FNTEGQGCYH YNLKTSCPYV LILDEEGGTT NDQQGYVVHK WSWTSRTETL
351 LSLEYKVNEE MKLKVLGQDS ITVTFTSLNE TVTLTVSANN CPHGMAYDKR
401 LNNRISNMDD KVKMSRALA EIKKRFQKTV TQFINSILLA AGLEFTEYPT
451 KKEEEFVRF KMRSRTHPER LPKLSLYSGE SLLRSQSGHL ESSIAETLKD
501 EPESAPVSPV RKTTKIHTKA KVTSRGKARE GRSPTRWAAL PSDCPLVLRK
551 LMLKEDTRAG CKCLVKAPLV SDVELERFLL APRDPSQVLV FGIISQNYT
601 STGQLQWLLN TLYNHQQRGR GSPCIQCRYD SYRLLQYDLD SPLQEDPPLM
651 VKKNSVVQGM ILMFAGGKLI FGGRVLNGYG LSKQNLLKQI FRSQQDYKMG
701 YFLPDDYKFS VPNSVLSLED SESVKAASE DIQSSSSSLA LEDYVEKELS
751 LEAEKTREPE VELHPLSRDS KITSWKKQAS KK

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_17n18, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_17n18, frame 3

Report for DKFZphtes3_17n18.3

```

[LENGTH]      782
[MW]           88030.16
[pI]           9.22
[BLOCKS]      BL00286 Squash family of serine protease inhibitors proteins
[PROSITE]     ATP_GTP_A      1
[PROSITE]     MYRISTYL      4
[PROSITE]     CAMP_PHOSPHO_SITE  3
[PROSITE]     CK2_PHOSPHO_SITE  14
[PROSITE]     PROKAR_LIPOPROTEIN  1
[PROSITE]     TONB_DEPENDENT_REC_1  1
[PROSITE]     PKC_PHOSPHO_SITE  10
[PROSITE]     ASN_GLYCOSYLATION  4
[KW]          Alpha_Beta

```

Prosite for DKFZphtes3 17n18.3

154. 630

PS00013	101->112	PROKAR_LIPOPROTEIN	PDOC00013
PS00017	122->130	ATP_GTP_A	PDOC00017
PS00430	1->44	TONB_DEPENDENT_REC_1	PDOC00354

(No Pfam data available for DKFZphtes3_17n18.3)

DKFZphtes3_18f3

group: testes derived

DKFZphtes3_18f3 encodes a novel 248 amino acid protein with partial similarity to human TNF-inducible protein CG12-1.

The novel protein contains two leucine zippers.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to TNF-inducible protein CG12-1

Sequenced by MediGenomix

Locus: unknown

Insert length: 4608 bp

Poly A stretch at pos. 4570, polyadenylation signal at pos. 4550

```
1 GACAGAAGTG AATGGGAATG GAGAGGCCGG CGGCCCGGGA GCCGCATGGG
51 CCCGACGCGC TCGCGCGCTT CCAGGGACTG CTGCTGGACC GCCGAGGCCG
101 GCTGCACCGC CAGGTGCTGC GCCTGCGCGA GGTGGCCCGG CGCCTGGAGC
151 GCCTGCGCAG GCGCTCCCTC GTAGCCAACG TGGCCGGCAG CTCGCTGAGC
201 GCAACGGGCG CCCTCGCCGC CATCGTGGGG CTCTCGCTCA GCCCGGTCAC
251 CCTGGGGACC TCGCTGCTGG TGTGGCCGT TCTCGCTGAT CTTCTGCAAC
301 CCGGAGGGGC CGTCACCATC ACGTCCGATC GCGGCCACCT GCCAGGACCA
351 TCCCGGGAGC TCGGAGGGT GCAGGAGATC GCGGCCACCT GCCAGGACCA
401 GATGCGAGAG ATCCTGAGCT GCCTCGAGTT TTTCTGCCCG TGGCAGGGCT
451 GCGGGGACCG CCAGCTGCTG CAGTGGGGGA GGAACGCCTC CATCGCCCTG
501 TACAATTCTG TCTACTTCAT CGTCTTCTTT GGCTCACGTG GCTTCTCAT
551 CCCCAGGCGG GCGGAGGGGG ACACCAAGGT TAGCCAGGCC GTGCTGAAGG
601 CCAAGATTCA GAAACTGGCC GAGAGCCTGG AGTCTGCAC CGGGGCTCTG
651 GACGAATCA GCGAGCAGCT GGAGTCTCGG GTTCAGCTCT GCACCAAGTC
701 CAGTCGTGGC CACGACCTCA AGATCTCTGC TGACCAGCGT GCAGGGCTGT
751 TTTTCTGAGA ACATCCTTTC CCCCTAATGA CCGAGGCCAG CAAATCATCC
801 TCATGGGATG CTCAGAAATT TGTAGCTCCC TTAGGAAAAC ACCAAGCTGG
851 GTTAGGAGCC GAAGGCAAAG GATGAGAAAA ACTGTTTTTG AAGTGGGCAG
901 GTCCCCAAAG CCTTCTTTT CCCATCACTG TGACATCTGC CTGGGCTTGA
951 GTGCTACGGA CTTTTCAGTC TTCCTAGTGG AAAAAATGTA CCCCCAACT
1001 CCTTTTCCTT TATCAAAAAC TTTCTGTCTA AACACAGCTG GGCAGGCACT
1051 CCTGTTTTAA AGTTATTTTC GGGTCCCTGA CCCTGCCCTG GTGGCTTGGC
1101 CTGAGACTGG AGAGAGTGCC ATCCTCTGGG TCCTCTCCAA GTCTACTAG
1151 TCTTTGAAGT CCTCAAAATG TGCGTGAGGA AGGCATTTGC CTCTATTCCA
1201 GAATTTCTGA TACAAAGAAC TCCAGAATCC AGAGCAAATC AGCCCTTCTC
1251 TGAACGTTGT AGGATGGTTC AGAACCAGGA GAGGACCCTG GTGCTGATAT
1301 CTCCTCCTCT TCCCTTTCCC CTCAGCTTAC TTACTCCCAG ATGCGGCCCTG
1351 GGTATGAAGT AGGCCTTTTC TGAGTGGCTC CCAATCCAGT CCTCCAAGTA
1401 CTGAGAGGGG AAGCCCGTGA AGCCGTCATC TAAGTCTGCT TCCCTCACAT
1451 GAAGCTGAGG GCCAGATAGA TGGAGCGACT GCCAACTTCA TTTCCGACA
1501 TCATTGTGTT CAGAAGAGAG TGATGGGTTT TGAGTTAGAC AGTCTGGGC
1551 TTGAGACAGG CTTTGTCACT ACTGTGTGAG TGTAGCCACC TAATCTCTCT
1601 GAGACTGTGT AAAACAAAGA TGATAAAATC TCACCCTGTT GTGAGATATT
1651 AAATGAGCCA AAGTGCCTAG CATGATGGTG CTGGCTCATA TAGTGTAGTC
1701 CCTGGAATGG CAAATTAACA TCACCAGGA ACTTGTTAGA AAGGCAAAT
1751 CTTGGACACA ACCCTCCTGA TTTATGGAAT CAGAACTCT GGCTGTGGG
1801 CCCAGCAACC TGAGTTTAAA CAATTTCTCT GGGTGGTTCT GCGGCACACT
1851 AAGGTTTGAA AATCACTACA ACAAATGCTA ACTTCTAATC CCCTTGATGA
1901 GCTTTCACGA AGTCTCACGG CTTCTCTAGG GACTCCATGG TCTTCAGAGT
1951 CGTTCACAGA TGACCAAGGA CAGACTGTGT CCCAGAAGCC AAAATGAGAG
2001 AGAGAGAGAG AGCACGCGTA CGTGCACCCT GGGGCAGTGT CTCACCGTAT
2051 GAATAAGGGA TGTAACACTA AAAGCCCAT T AGGGGGCAGT GTTCCCGCC
2101 TGTTGTAGAA ACTGTTACAG AAAGGATCCT ATATGAAGT CCTGAAACTG
2151 ACCTTTGTCT ATTATTACCT TCTCTGAAAA GTGCCAGTCC ATGTATTTTT
2201 TATTTATTTT AAGTTTGTAA TTTAATTTT AATTATTGTT TAGTGTGTC
2251 ATTTAATTTT ATTTAATCAC CACATTTAGA AAATAATAAG AGCAAGTTTC
2301 TAAATGGGAG ACTGCTGAGG CTCTTTGCAA GAGATGAGAT TAAGTTTGAG
2351 TTTCTAAGGC AGGGCATGAG CTGGAATAG CATTGCTTTC CTTGATTGTC
2401 TCTCTCCTTC AGGGAGATT TTTTCTCTA GTGTTTTAAG TGATCCTTTC
2451 AAGTAAGTGT GGAGAGTCTT GAATGGCAAG ACCAGGAGCT GAGTTTAAGC
2501 TTGTAATGGA AGCTTGCAAT GTGGGATATA TAACTGAGGA AGCATATTTC
2551 TCCTGAAGGT ATTTTGCCAG AAGGTATCAC TTGACCTGGA AAAGGAATCT
2601 ATTTAGTTCA GGAAAGATAA AAAGTTTAGA GGTATGTGAA GGAAGCACTT
2651 AGAACTTGCA AGCCTGATGT CCTATCAAGT TATGCTTCT GGGTGACAGA
2701 CAAAATAGCT TGTCTTATGG TGGTGATGTG TTGCATTTTC ACTTTGGGGT
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2751 CTGTAAGAAA CTGTCAGTGA AAATATGTAC AATTCCTTCA ATTTCCATTTC
2801 TTAACAACCTG TAATGTTGAA AAATAAGTTG AAAAGTCTTT GGGACCATAC
2851 ATGCAAAAAC GGTGCCCTCTG TTAATTAATT ATTTAATATT CTATAAATGT
2901 ACCCAATCTG TCCGCACCCT TCCCAGTGAT GGGGCAGTAT GTCTGAGGAA
2951 GTATAATTTT AGTACTGGGG TCGGGGAGAG GAGGTGATGT TTCTACATTT
3001 TTATTTTTTC TATAAATTGC AATTGGTCTG TATGCTGGTT TATTTTGAAA
3051 TTTATATTGG TTTCTTTTCA AGCTGGTGTG ATCTCCTAGA CTGTTTCACC
3101 CAGATGCTAG CATTTTTTTT TTTTTTGAGA CAGAGTCTCA CTCTGTCACC
3151 TAGGCTGGAG TTGCAGTGGT TTGATCTCGG CTCACGTCAA CCTCCGACTC
3201 CTGGGTTCAA GCAATTCTTC TGCCTCAGCC TCCTGAGTAG CTGGGATTAC
3251 AGATGTGCAC CAGCACACCC GGCTAATTTT TTGTATTTT AGTAGAGACA
3301 GGGTTTCGCC ATGTTGGCCA GGCTGGTCTT GAACTCCTGG CCTTATGTGA
3351 TCCGCCACCC TTGGCTTCCC AAAGTGCTGG GATTACAGGC ATGAGCCACC
3401 TCGCTGGGCC AGATGCTAGC ATTTTAGATC AAACAATTCA TTTTAGATGA
3451 ATTTGTTTGT TTCACAATCA TTTTAAATCA TTTTAGAATG TACTTCACAT
3501 TATTAGTTGT GTTATGGCAT AAAGGTACAA CCATTCCCTA ACTCCATCTT
3551 TTATTAATGC TTAAGTTTAA ATTATATTCT TCCAATGCCT AAGCTATTCC
3601 CTAGAATTAA ACTGGGCACT TTTGGAAGCA GCAACAGTAA CAGCAGCAGC
3651 AAACCTTTTC TCTCATTTT TGGGTGTATC AAAAGTTCTA GACTTTTGAA
3701 GTTATGATTT CAGTGGCCCA CTTTATTCTT AAGGAAGAGT GTCTACTTTG
3751 GAACGATACT TTGCACATAG TAGGAACTCA AGAAATACAT TTGAATAAAT
3801 ATAATTAACCT CTTAGCTAT CTTAATGAGA ATTTGTTGAC AACAAAAGAT
3851 CATCCATCGC CTTATGTGTG AGTAAGATTG GAGCCTCTAT CAAGATTTAG
3901 TCAAGTTCAG TTAGATTGAT TCTAGAAACA AATATTATT TCTTTCTTTT
3951 ACGGGGATGT GAATAAGGCT TTTCTTAAG GCCTTCATTC TTTAAACAAA
4001 CAGGTTGAAA TGGTATGTTG TAAAAGAGAA GACGGGAGAG AGGTATTTAG
4051 ATGATAAGTG TACTTCACAA AAATGCCAAA GTTTGAAAAA TAGGTATGTT
4101 TGTCTAAAT GTTTAAGTGC TTCTCTGTTA GGTCTGGGG CTTGCAATCA
4151 TTTGAATTGT TCTGTTTCAC AATAAAGGAG ATTCACCTGGG TTCTGCATTT
4201 TCAGGATTCA ATAGAACTGC TCCATTAAAA AAATAATCCT TAGCAAGCAT
4251 TCGAATCCTA ACTGCTTTGA TGCACCTGCC CTCGGGCACC TGTCATTTC
4301 AATATGGTAG GTGTCAAAGT CAAAAGTATT TACTGGGAGA AAAAAGAGAG
4351 GAGTGGTTGT AGAAGTCTCC CTAAATCAGA CATGCTAAGC AATCAGCCAA
4401 CGTGGTGTAT TTCTCATTCA ATATTTTAGT GTGAATTGAG AACTGAGAT
4451 AAAGACATCG TGCAGAGATA AATGGGATA CAGTTAAATG TAGCAACTCT
4501 TGAGTTCAAT TTTTCCCACT GTAGCAAAAT TAATGCTTTC TCTTTATTGA
4551 AATAAATTGC TCATTCTCCT CAAAAAATAA AAAAAAATAA AAAAAAATAA
4601 AAAAAAGG

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BLAST Results

Entry HSG27587 from database EMBL:
human STS SHGC-32548.
Score = 1951, P = 9.0e-101, identities = 411/425

Entry HS073350 from database EMBL:
human STS EST303564.
Score = 1417, P = 8.7e-58, identities = 285/287

Medline entries

No Medline entry

Peptide information for frame 2

ORF from the beginning to 580 bp; peptide length: 194
Category: questionable ORF
Classification: no clue

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_18f3, frame 2

PIR:CGB01S collagen alpha 1(I) chain - bovine (fragments), N = 1, Score = 155, P = 4.5e-10

TREMBL:HSCG1PA1_1 gene: "COL1A1"; Human proalpha 1 (I) chain of type I procollagen mRNA (partial)., N = 1, Score = 155, P = 6.5e-10

>PIR:CGB01S collagen alpha 1(I) chain - bovine (fragments)
Length = 779

HSPs:

Score = 155 (23.3 bits), Expect = 4.5e-10, P = 4.5e-10
Identities = 60/152 (39%), Positives = 67/152 (44%)

Query: 7 GEAGGPGAAWARRAAALPGTAA--GPPRPAAPPGA--APARGGPAPGAPAQALPRSQRGR 62
G+ G PG + AR PG GPP PA P GA AP G A A P SQ
Sbjct: 230 GDLGAPGPSGARGERGFPGERGVEGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQAGP 289

Query: 63 QLAERNRPRRRHRGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAAE 122
L G P RGA PG GD +GA G + G VR L + PG A
Sbjct: 290 GL---GMPGE-RGAAGLPGKGDGRDAGPKGADGAPGKDG---VRGLTGPIGPPGPAG 341

Query: 123 GAGDRGHL-P-GP-----DARDELPVFLPLAGLRGPPAA 156
GD+G P GP D +P P P AG GPP A
Sbjct: 342 APGDKGEAGPSGPAGTRGAPGDRGEPGPPG---P-AGFAGPPGA 381

Score = 121 (18.2 bits), Expect = 5.4e-05, P = 5.4e-05
Identities = 52/154 (33%), Positives = 60/154 (38%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARG-----GPAPGAPAQALPRSQRG 61
G G PGAA R P AGPP P P G ++G GPA G P + P G
Sbjct: 434 GATGFPGAA-GRVGPPGPSGNAGPPGPPGPAGKEGSKGRGETGPA-GRPGEVGP GPPG 491

Query: 62 RQLAERNRPRRRHRGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAA 121
A G P G PG PG RG G +RG R L PG +
Sbjct: 492 P--AGEKGAPGAD-GPAGAPGTGPGQGIAGQRGVVGLPGQGE---RGFPGL---PGPS 541

Query: 122 EGAGDRGHLPGPDARDPELPRVFLPLAGLRGPPAAVRE 160
G +G R P P + GL GPP + RE
Sbjct: 542 GEPGKQGPSGASGERGPPGP---MGPPGLAGPPGESGRE 577

Score = 117 (17.6 bits), Expect = 1.8e-04, P = 1.8e-04
Identities = 52/148 (35%), Positives = 62/148 (41%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARG---GPAAPARGGPAPGAPAQALPRSQRG-R 62
G G PG AR +A PG A G P A PPG + GP PG P A +G R
Sbjct: 416 GNVGAPGPKGARGSAGPPG-ATGFPGAAGRVGPPGPS-GNAGP-PGPPGPAGKEGSKGR 472

Query: 63 QLAERNRPRRRHRGALAQPUGHGDLAAGVGRGAGGGHSRRGRH--HHVRSLADLLQLPGA 120
GRP G + PG PG GA G G + ++ LPG
Sbjct: 473 GETGPAGRP---GEVGP GPPGPAGEKGAPGADGPAGAPGTGPGQGIAGQRGVVGLPGQ 528

Query: 121 AEGAGDRGH--LPGPDARDPEL-PRVFLPLAGLRGPP 154
G+RG LPGP + P +G RGPP
Sbjct: 529 R---GERGFPLPGPSGEPGKQGPS---GASGERGPP 559

Score = 117 (17.6 bits), Expect = 1.8e-04, P = 1.8e-04
Identities = 54/162 (33%), Positives = 64/162 (39%)

Query: 7 GEAGGPGAAWARRAAALPGT--AAGPPRPAAPPGAAPARG--GPA--PGAPAQALPRSQR 60
G G PG + PG A+GP P PPG G G A PG P + P +
Sbjct: 29 GPPGAPGPGQFQGPPEPGEAGSGPMGPRGPPGKNGDDGEAGKPRGPRGERGPPGPQ 88

Query: 61 G-RQLAERNRPR--RRHRGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHV--RSLADLL 115
G R L G P + HRG G GD. +G G G + R L
Sbjct: 89 GARGLPGTAGLPGMKHGRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPQMGPRLPGFP 148

Query: 116 QLPGAA--EG-AGDRGHLPGPDARDPELPRVFLPLAGLRGPPAAA 157
GAA G AG+RG +PGP P AG +CPP A
Sbjct: 149 GPKGAAGEPGKAGERG-VPGPPGAVG--PAGKDGEAGAQQPPGPA 190

Score = 113 (17.0 bits), Expect = 5.4e-04, P = 5.4e-04
Identities = 54/148 (36%), Positives = 58/148 (39%)

Query: 7 GEAGGPGAAWARRAAALPGTA-----AGPPRPAAP---PGAAPARGGPAP-GAPAQALPR 57
G AG PGA A PG A AGPP PA P PG G P P GA A P
Sbjct: 374 GFAGPPGADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGPKGARGSAGPP 433

Query: 58 SQRGRQLAERNRPRRRHRGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQL 117
G A P G PG PG +G G GR V
Sbjct: 434 GATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKEGSKGRGETGPAGRPGEVGP----- 486

Query: 118 PGAAEGAGDRGHLPGPD--ARDPELPRVFLPLAGLRG 152
PG AG++G PG D A P P +AG RG
Sbjct: 487 PGPPGPAGEKG-APGADGPAGAPGTGPP-QGIAGQRG 521

Score = 110 (16.5 bits), Expect = 1.3e-03, P = 1.2e-03

Identities = 54/151 (35%), Positives = 60/151 (39%).

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPG--AAPAR-GGPAP-GAPAQALPRSQRGR 62
 GE G G A + LPG A GPP A PG P G P P GA + +RG
 Sbjct: 194 GERGEQGPAGSPGFQGLPGPA-GPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGV 252

Query: 63 QLAERNRPRRRHREGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAEE 122
 + PR GA G GD A G+ G +G R A L PG
 Sbjct: 253 EGPPGPAGPRGANGAPGNDGAKGDAGAPGPSQGAPGLQGMPE-RGAAGL---PGPK- 307

Query: 123 GAGDRGHLPGPDARD--PELPRVFLPLAGLRGPPAAA 157
 GDRG GP D P V L G GPP A
 Sbjct: 308 --GDRGDA-GPKGADGAPGKDG V-RGLTGPIGPPGPA 340

Score = 109 (16.4 bits), Expect = 1.7e-03, P = 1.7e-03
 Identities = 55/154 (35%), Positives = 60/154 (38%)

Query: 4 NGN-GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARG-GPAPGAPAQALPRSQRG 61
 NG+ GEAG PG R P A G P A PG RG GA A P +G
 Sbjct: 67 NGDDGEAGKPGRF-GERGPPGPQARGLPAGTAGLPGMKHGRGFSGLDGAAGDAGPAGPKG 125

Query: 62 RQLAE-RNGRPRRRHREGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSL-----ADLL 115
 + NG P + G PG PG A G G G V A
 Sbjct: 126 EPGSPGENGAPGQ-MGPRGLPGFPGPKGAAGEPGKAGERGVPPGPAVGPAGKDGEAGAQ 184

Query: 116 QLPGAAGAGDRGHLPGPDARDPELPRVFLPLAGLRGPPAAA 157
 PG A AG+RG GP A P F L G GPP A
 Sbjct: 185 GPPGPAGPAGERGE-QGP-AGSPG----FQGLPGPAGPPGEA 220

Score = 104 (15.6 bits), Expect = 6.6e-03, P = 6.6e-03
 Identities = 44/131 (33%), Positives = 49/131 (37%)

Query: 2 EVNNGEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGPAP-GAPAQALPRSQR 60
 E GE G PG R LPG GP A PG A RG P P GA A +
 Sbjct: 126 EPGSPGENGAPQMGPR---GLPGFP-GPKGAAGEPGKAGERGVPPGPAVGPAGKDGEA 181

Query: 61 GRQLAERNRPRRRHREGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGA 120
 G Q P RG G PG G+ G G G+ DL PG
 Sbjct: 182 GAQPPGPAGPAGERGEQGPAGSPG--FQGLP-GPAGPPGEAGKPGEQGVPGDL-GAPGP 237

Query: 121 AEGAGDRGHLPG 132
 + G+RG PG
 Sbjct: 238 SGARGERG-FPG 248

Score = 104 (15.6 bits), Expect = 6.6e-03, P = 6.6e-03
 Identities = 43/131 (32%), Positives = 55/131 (41%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGPAPGAPAQALPRSQRGRQLAE 66
 GEAG G A R A PG G P P P G A GP PGA Q + + G A+
 Sbjct: 347 GEAGPSGPAGTRGA---PGDR-GEPGPPGPAGFA----GP-PGADGQPGAKGEPGDAGAK 397

Query: 67 RNRGRPRRRHREGALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAEGAGD 126
 + P G PG G++ A +GA G G + A + PG + AG
 Sbjct: 398 GDAGPPGPAGPAGPPGPIGNVAPGPKGARGSGAGPPGATGFPGA-AGRVGPPGPSNAGP 456

Query: 127 RGHLPGPDARD 137
 G PGP ++
 Sbjct: 457 PGP-PGPAGKE 466

Score = 104 (15.6 bits), Expect = 6.6e-03, P = 6.6e-03
 Identities = 56/162 (34%), Positives = 62/162 (38%)

Query: 7 GEAGGPGAAWARRAAALPGTAA--GPPRPAAPPGAAPARGGPAPGAPAQALPRSQRGRQL 64
 G G PGA A G GP P P G A ARG P P Q PR +G
 Sbjct: 608 GPPGAPGAPGVGPAGKSGDRGETGPAGPIGVGPAGARG---PAGP-QG-PRGBKGZTG 662

Query: 65 AERNRPRRRHREG--ALAQPUGHGDLAAGVGRGAGGGHSRRGRHHHVRSLA-DLLQ-LPG 119
 + + + HRG PG PG GA G RG S D L LPG
 Sbjct: 663 ZZGBRGIKHGRGFSGLQGPPGPSPEQGPSGASGPAGPPGSAGSPGKDG LNLPG 722

Query: 120 AEGAGDRGHL--PGPDARDPELPRVFLPLAGLRGPPAAAVREERLHRPVQ 168
 G RG GP A P P P G GPP+ L +P Q
 Sbjct: 723 FIGPPGPRGRTGDAGP-AGPPGPPG---P-PGPPGPPSGGYDLSFLPQPPQ 768

Score = 101 (15.2 bits), Expect = 1.5e-02, P = 1.5e-02
 Identities = 49/148 (33%), Positives = 55/148 (37%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGPAPGAPA----QALPRSQRGR 62
 G AG PG A R PG A GP A G A A+G P P PA + P G
 Sbjct: 152 GAAGEPGKAGERGVPPGP-AGVP---AGKDGEAGAQQPPGPAGPAGERGEQGPAGSPGF 207

Query: 63 QLAERNRPRRRHARGALAQPGHFGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAEE 122
 Q P G + G PGDL A G G RG R + PG A
 Sbjct: 208 QGLPGPAGPPGEAGKPGEGVPGDLGAP---GPSGARGERGFPGE-RGVEGP---PGPAG 260

Query: 123 GAGDRGHLPGPDARDPELPRVFLPLAGLRGPP 154
 G G PG D + P G +G P
 Sbjct: 261 PRGANG-APGNDGAKGDAGAPGAP--GSQGAP 289

Score = 100 (15.0 bits), Expect = 1.9e-02, P = 1.9e-02
 Identities = 40/130 (30%), Positives = 48/130 (36%)

Query: 7 GEAGGPGAARAAALPGT--AAGPPRPAAPPGAAPARG--GPA--PGAPAQALPRSQR 60
 G G PG + PG A+GP P PPG G G A PG P + P +
 Sbjct: 29 GPPGAPGPQGFQGPPEPGEFGASGPMGPRGPPGPGKNGDDGEAGKPRGPRGERGPPGPQ 88

Query: 61 G-RQLAERNRPR--RRHARGALAQPGHFGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQL 117
 G R L G P + HRG G GD +G G G + L
 Sbjct: 89 GARGLPGTAGLPGMKHGRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPQMGPRG-LPGF 147

Query: 118 PGAAEGAGDRG 128
 PG AG+ G
 Sbjct: 148 PGPKGAAGEPG 158

Score = 99 (14.9 bits), Expect = 2.5e-02, P = 2.5e-02
 Identities = 53/156 (33%), Positives = 61/156 (39%)

Query: 7 GEAGGPGAARAAALPGT--AAGPPRPAAPPGAAPARG--GPA---PGAPAQAL 55
 G G PGA R A PG A G P P P G + RG GPA P PA A
 Sbjct: 587 GRDGSPPAKGDRGETGPAGAPGPPGAPGAPVGPAGKSGDRGETGPAGPIGPVGPAGAR 646

Query: 56 -----PRSQRGRQLAERNRPRRRHARGALAQPGHFGDLAAGVGRGAGGGHSRRGRHHHVR 108
 PR +G + + + HRG G PG + +G G G
 Sbjct: 647 GPAGPQGPGRBKGZTGZGZBGRGKGRGFSGLQGGPPGPGSPGEGQGPSGASGPAGPRGP- 705

Query: 109 RSLADLLQLPGAEEGAGDRG--HLPDARDPELPRVFLPLAGLRGPP 154
 PG+A G G LPGP P PR AG GPP
 Sbjct: 706 -----PGSAGSPGKDGLNGLPGPIG--PFGPRGRTGDAGPAGPP 742

Score = 98 (14.7 bits), Expect = 3.3e-02, P = 3.3e-02
 Identities = 51/158 (32%), Positives = 58/158 (36%)

Query: 7 GEAGGPGAARAAALPGTAA----AGPPRPAAPPGAAPARGGPAP-GAPAQALPRSQR 60
 G G G R AA LPG AGP PG RG P G P A +
 Sbjct: 287 GAPGLQGMPPGERGAAGLPKGDGRDAGPKGADGAPGKQGVRLTGPIGPPGPAGAPGDK 346

Query: 61 GRQLAERNRPRRRHARGA---LAQPGHFGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQL 117
 G A +G P RGA +PG PG GA G +G + D
 Sbjct: 347 GE--AGPSG-PAGTRGAPGDRGEPGPPGAPGAGPPGADGQPAKGEFGDAGAKGDAGP- 402

Query: 118 PGAAEGAGDRGHLPGPDARDPELPRVFLPLAGLRGPPAAVR 159
 PG A AG G + A P+ R G G P AA R
 Sbjct: 403 PGPAGPAGPPGPIGNVGAAPGPKGARGSGAPPGATGFPGAAGR 444

Score = 96 (14.4 bits), Expect = 5.7e-02, P = 5.5e-02
 Identities = 46/152 (30%), Positives = 57/152 (37%)

Query: 6 NGEAGGPGAARAAALPGTAA--GPPRPAAPPGAAPARGGPAPGAPA-QALPRSQRGR 62
 +G G PGA + PG G PA PG A G P P PA ++ R + G
 Sbjct: 574 SREGAPGAEGSPGRDGSPPAKGDRGETGPAGAPGPPGAPGAPVGPAGKSGDRGETGP 633

Query: 63 QLAERNRPRRRHARGALAQPGHFGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAEE 122
 P RG G G+ +G G RG H R + L PG
 Sbjct: 634 AGPIGPVGPAGARGPAGPQGPGB-----KGZTGZGZBGRGKGRGFSGLQGGPPGPPG 686

Query: 123 GAGDRGHLPGPDARDPELPRVFLPLAGLRGPPAAA 157
 G++G P A P AG RGPP +A
 Sbjct: 687 SPGEQG--PS-GASGP-----AGPRGPPGSA 709

Score = 94 (14.1 bits), Expect = 9.7e-02, P = 9.2e-02
 Identities = 45/134 (33%), Positives = 56/134 (41%)

Query: 24 PGTAAGPPRPAAPPGAAPARGGPA-PGAPAQALPRSQRGRQLAERNRPRRRH--GALAQ 80
 P G P P PG +G P PG P + P RG G P ++ G +
 Sbjct: 21 PSGRPLPGPPGAPGPQGFQGPPEPGEFGASGPMGPRGP-----GPPGKNGDDGEAGK 75

Query: 81 PGHFGDLAA-GV--GRGAGGGHSRRGRHHHVRSLADLLQLPGAEEGAGDRGHL--LPGPDA 135
 PG PG+ G RG G G H R + L G A AG +G PG +
 Sbjct: 76 PGRPGERGPPGPQARGPLPGTAGLPGMKGH-RGFSGLDGAKGDAGPAGPKGEPGSPGENG 134

Query: 136 RDPDL-PRVFLPLAGLRGPPAAA 157
 ++ PR LP G GP AA

Sbjct: 135 APGQMGPGRG-LP--GFPGPKGAA 154

Score = 92 (13.8 bits), Expect = 1.7e-01, P = 1.5e-01
Identities = 52/155 (33%), Positives = 58/155 (37%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGP-APGAPAQALPRSQRGRQLA 65
GEAG G A R A G GPP PA G A G P A G P A + G
Sbjct: 347 GEAGPSGPAGTRGAPGDRGEP-GPPGPAFAGPPGADGQPGAKGEPGDAGAKGDAGPPGP 405
Query: 66 ERNGRPRRRHREGALAQPQHPGDLAAGVGRGAGGGHSRRGR--HHHVRSLADLLQLPGA-- 121
P G + PG G + GA G GR A PG A
Sbjct: 406 AGPAGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSNAGPPGPPGPAGK 465
Query: 122 EGA-GDRGHLPGDPARDPELPRVFLP-LAGLRGPPAA 156
EG+ G RG GP R E+ P AG +G P A
Sbjct: 466 EGSKGPRGET-GPAGRPEVGP GPPGPAGEKGAPGA 501

Score = 92 (13.8 bits), Expect = 1.7e-01, P = 1.5e-01
Identities = 51/156 (32%), Positives = 57/156 (36%)

Query: 7 GEAGGPGAAWARRA---AALPGT--AAGPPRPAAPPGAAPARGGPAPGAPAQAL-PRSQR 60
G G PGA R A PG A G P P PG + RG P P + P R
Sbjct: 587 GRDGSFGAKGDRGETGPAGAPGPPGAPGAPGVPAGKSGDRGETGPAGPIGPVGPAGAR 646
Query: 61 GRQLAERNRPRRRHREGALAQPQHPGDLA-AGVG--RGAGGGHSRRGRH--HHHVRSLADLL 115
G A G PR +G + G G G +G G G A
Sbjct: 647 GP--AGPQG-PRGBKGZTGZZGBRGIKHGRGFSGLQGGPPGPPGPSGEGQPSGASGPAGPR 703
Query: 116 QLPGAEGAGDRG--HLPGPDPARDPELPRVFLPLAGLRGPP 154
PG+A G G LPPG P PR AG GPP
Sbjct: 704 GPPGSAGSPGKDG LNLPGPIG--PPGPRGRTGDAGPAGPP 742

Score = 90 (13.5 bits), Expect = 2.8e-01, P = 2.5e-01
Identities = 45/134 (33%), Positives = 53/134 (39%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGPAPGAPAQALPRSQRGRQ-LA 65
G G PG A + A G A P P P G A RG G P Q R +RG L
Sbjct: 485 GPPGPPGPAGEKGAPGADGPAGAPGTPG-PQGIAGQRG--VVGLPGQ--RGERGFPLP 538
Query: 66 ERNGRPRRH--RGALAQPQHPGDLA----AGV----GR-GAGGGHSRRGRHHHVRSLADL 114
+G P + GA + G PG + AG GR GA G GR + D
Sbjct: 539 GPSGEPGKQPSGASGERGPPGPMGPPGLAGPPGESGREGAPGAEGSPGRDGSFGAKGDR 598
Query: 115 LQL-PGAAEGAGDRGHLPGP 133
+ P A G PGP
Sbjct: 599 GETGPAGAPGPPGAPGAPGP 618

Score = 83 (12.5 bits), Expect = 1.8e+00, P = 8.3e-01
Identities = 49/156 (31%), Positives = 56/156 (35%)

Query: 7 GEAGGPGAAWARRAAALPGTAA--GPPRPAAPPGAAPARG--GPAP--GAPAQALPRSQR 60
G+AG GA A + G GPP PA PG G GPA GAP R +
Sbjct: 311 GDAGPKGADGAPGKDGVRGLTGPIGPPGAPGDKGEAGPSGPAGTRGAPGD---RGEF 367
Query: 61 GRQLAERNRPRRRHREGALAQPQHPGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGA 120
G P G G PGD A G G G + ++ PG
Sbjct: 368 GPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPPGAPGAPGPPGPIGNVG---APGP 423
Query: 121 AEGAGDRGHLPGDPARDPELPRVFLP----LAGLRGPPAAVRE 160
G G PG RV P AG GPP A +E
Sbjct: 424 KGARGSAGP-PGATGFPGAAGRVGPPGPSNAGPPGPPGPAGKE 466

Score = 82 (12.3 bits), Expect = 2.3e+00, P = 9.0e-01
Identities = 46/148 (31%), Positives = 52/148 (35%)

Query: 7 GEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGPAPGAPAQALPRSQRGRQLAE 66
G+AG PGA ++ A L G G A PG RG P A P R L
Sbjct: 275 GDAGAPGAPGSQAPGLQMP-GERGAAGLPGPKGDRGDAGPKG-ADGAPGKDGVRGLTG 332
Query: 67 RNRPRRRHREGALAQPQHPGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGAEGAGD 126
G P G PG G+ G G RG A PGA G
Sbjct: 333 PIGPP----GPAGAPGDKGEAGPSGPAGTRGAPGDRGEPGPPGP-AGFAGPPGADGQPGA 387
Query: 127 RGHLPGP-DARDPELPRVFLPLAGLRGPP 154
+G PG A+ P P AG GPP
Sbjct: 388 KGE-PGDAGAKGDAGPPG--P-AGPAGPP 412

Peptide information for frame 3

ORF from 12 bp to 755 bp; peptide length: 248
Category: similarity to known protein
Classification: unset
Prosite motifs: LEUCINE_ZIPPER (17-39)
LEUCINE_ZIPPER (24-46)

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_18f3, frame 3

TREMBL:AF070675_1 product: "TNF-inducible protein CG12-1"; Homo sapiens TNF-inducible protein CG12-1 mRNA, complete cds., N = 1, Score = 135, P = 1e-06

TREMBL:HS6802_1 gene: "dJ6802.1"; product: "dJ6802.1"; Homo sapiens DNA sequence from PAC 6802 on chromosome 22. Contains apolipoprotein L, myosin heavy chain, ESTs, CA repeat, STS and GSS., N = 1, Score = 107, P = 0.0023

>TREMBL:AF070675_1 product: "TNF-inducible protein CG12-1"; Homo sapiens TNF-inducible protein CG12-1 mRNA, complete cds.
Length = 331

HSPs:

Score = 135 (20.3 bits), Expect = 1.0e-06, P = 1.0e-06
Identities = 30/103 (29%), Positives = 55/103 (53%)

Query: 30 RLHRQVLRRLREVARRLRLRRSLVANVAGSSLSATGALAAIVGLSLSPVTLGTSLLVSA 89
++ + +LR +A +E + R ++NV SS A + ++ GL L+P T GTSL ++A
Sbjct: 91 KIQESIEKLRLALANGIEVHRGCTISNVVSSSTGAASGIMSLAGLVLPFTAGTSLALTA 150
Query: 90 VGLGVATAGGAVTITS DL-SLIFCNSRELRRVQEIAATCQDQMR 132
G+G+ A IT+ + + +S E + AT D+++
Sbjct: 151 AGVGLGAASAVTGITTSIVEHSYTSSAEAE-ASRLTATSIDRLK 193

Pedant information for DKFZphtes3_18f3, frame 2

Report for DKFZphtes3_18f3.2

[LENGTH] 193
[MW] 19708.24
[pI] 11.90
[KW] All_Alpha
[KW] LOW_COMPLEXITY 55.44 %

SEQ TEVNGNGEAGGPGAAWARRAAALPGTAAGPPRPAAPPGAAPARGGPAPGAPAQALPRSQR
SEGxx
PRD ccc

SEQ GRQLAERNRPRRRHRGALAQP GHPGDLAAGVGRGAGGGHSRRGRHHHVRSLADLLQLPGA
SEGxx
PRD hhhhhhcc

SEQ AEGAGDRGHLPGPDARDPELPRVFLPLAGLRGPPAAAVREERLHRPVQFCLLHRLWLWTW
SEGxx
PRD ccc

SEQ LPHPQAGGGGHQ
SEG xxxxxxxxxxxxxxxx
PRD ccccccccccccccc

(No Prosite data available for DKFZphtes3_18f3.2)

(No Pfam data available for DKFZphtes3_18f3.2)

Pedant information for DKFZphtes3_18f3, frame 3

Report for DKFZphtes3_18f3.3

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[LENGTH]      248
[MW]           27162.56
[pI]           9.92
[PROSITE]      LEUCINE_ZIPPER 2
[KW]           TRANSMEMBRANE 1
[KW]           LOW_COMPLEXITY  30.65 %
[KW]           COILED_COIL    12.10 %

SEQ    MGMPERPAAREPHGPDALRRFQGLLLDRRGRLHRQVLRLEVARRLERLRRSLVANVAGS
SEG    .....XXXXXXXXXXXXXXXXXXXXX.XXXXXXXXXXXXXXXXXXXXXX.XXX
PRD    cccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccc
COILS  .....
MEM    .....

SEQ    SLSATGALAAIVGLSLSPVTLGTSLLVSAVGLGVATAGGAVTITSDLSLIFCNSRELRRV
SEG    xxxxxxxxxxxx.....XXXXXXXXXXXXXXXXXXXXXXXXXXXXX.....
PRD    cchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....
MEM    .....MMMMMMMMMMMMMMMMMM.....

SEQ    QEIAATCQDQMREILSCLEFFCRWQCGDRQLQCGRNASIALYNSVYFIVFFGSRGFLI
SEG    .....
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....
MEM    .....

SEQ    PRRAEGDTKVSQAVLKAKIQKLAESLESCTGALDELSEQLESRVQLCTKSSRGHDLKISA
SEG    .....
PRD    cccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  .....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....
MEM    .....

SEQ    DQRAGLFF
SEG    .....
PRD    hhhhcccc
COILS  .....
MEM    .....

```

Prosites for DKFZphtes3_18f3.3

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PS00029      17->39  LEUCINE_ZIPPER      PDOC00029
PS00029      24->46  LEUCINE_ZIPPER      PDOC00029

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(No Pfam data available for DKFZphtes3_18f3.3)

DKFZphtes3_1817

group: cell structure and motility

DKFZphtes3_1817 encodes a novel 1050 amino acid protein with weak partial similarity to ankyrins.

The novel protein contains an ATP/GTP-binding site motif A (P-loop) and an Ank repeat. Ankyrins are peripheral membrane proteins which interconnect integral proteins with the spectrin-based membrane skeleton. Thus the novel protein seems to be involved in coupling of cyto skeleton and cell membrane.

The new protein can find application in modulation of cyto skeleton-membrane interactions.

similarity to ankyrins

Sequenced by MediGenomix

Locus: unknown

Insert length: 4501 bp

Poly A stretch at pos. 4423, no polyadenylation signal found

```
1  GATCGCCGCG CGAGGGTGGT GGGCATCGAG GTCCCAGCAG CGGACGAGGG
51 AGGTGCCGCC GTGCCCCAGG ATGGGCTGGG AATGAAGCGA TGTAGCCTTT
101 TAAGAGATTT GCTCTGACCC ATCTGAAGTC CATATGGCTC TGTATGATGA
151 AGACCTCCTG AAAAATCCTT TCTATCTGGC TCTGCAAAAG TGCCGCCCTG
201 ACTTGTGCAG CAAAGTGGCC CAAATCCATG GCATTGTCTT AGTACCCTGC
251 AAAGGAAGCC TGTCGAGCAG CATCCAGTCT ACTTGTCACT TTGAGTCCTA
301 CATTTTGATA CCTGTGGAAG AGCATTTTCA GACCTTAAAT GGAAAGGATG
351 TCTTTATTCA AGGGAACAGG ATTAATTAG GAGCTGGTTT TGCCTGTCTT
401 CTCTCAGTGC CCATTCTCTT TGAAGAACT TTCTACAATG AAAAAGAAGA
451 GAGTTTCAGC ATCCTGTGTA TAGCCCATCC TTTGGAAAAG AGAGAGAGTT
501 CAGAAGAGCC TTTGGCACCC TCAGATCCCT TTTCCCTGAA AACCATTGAA
551 GATGTGAGAG AGTTCTTGGG AAGACACTCC GAGCGATTTG ACAGGAACAT
601 CGCCTCTTTC CATCGAATC TCCGAGAATG CGAGAGAAAG AGCCTCCGTC
651 ACCACATAGA CTCAGCGAAT GCTCTCTACA CCAATGCCT CCAGCAGCTT
701 CTGAGGGACT CTCACCTGAA AATGCTCGCC AAGCAGGAGG CCCAGATGAA
751 CCTGATGAAG CAGGCAGTGG AGATATACGT CCATCATGAA ATTTACAACC
801 TGATCTTTAA ATACGTGGGG ACCATGGAGG CAAGTGAGGA TCGCGCCTTT
851 AACAAAATCA CAAGAAGCCT TCAAGATCTT CAGCAGAAAG ATATTGGTGT
901 GAAACCGGAG TTCAGCTTTA ACATACCTCG TGCCAAAAGA GAGCTGGCTC
951 AGCTGAACAA ATGCACCTCC CCACAGCAGA AGCTTGCTCG CTTGCGAAAA
1001 GTGGTGCAGC TCATTACACA GTCTCCAAGC CAGAGAGTGA ACCTGGAGAC
1051 CATGTGTGCT GATGATCTGC TATCAGTCTT GTTATACTTG CTGTGAAAAA
1101 CGGAGATCCC TAATTGGATG GCAAATTTGA GTTACATCAA AAACCTCAGG
1151 TTTAGCAGCT TGGCAAAGGA TGAATGGGGA TACTGCCTGA CCTCATTCGA
1201 AGCTGCCATT GAATATATTC GGCAAGGAAG CCTCTCTGCT AAACCCCTG
1251 AGTCTGAGGG ATTTGGAGAC AGGCTGTTCC TTAAGCAGAG AATGAGCTTA
1301 CTCTCTCAGA TGACTTCGTC TCCCACCGAC TGCCTGTTA AGCACATTGC
1351 ATCAGGTAAC CAGAAAGAAG TGGAGAGACT TCTGAGCCAA GAGGACCATG
1401 ATAAAGATAC CGTCCAAAAG ATGTGTCACC CTCTCTGCTT CTGCGATGAC
1451 TGTGAGAAAC TCGTCTCTGG GAGGTGGAAT GATCCCTCAG TTGTCACTCC
1501 ATTTCTCCAG TACGACAGGG GGCACACCCC TCTCCATGTG GCTGCTGTCT
1551 GTGGGCAGGC ATCCCTCATC GACCTCCTGG TTTCCAAGGG CGCCATGGTA
1601 AATGCCACAG ACTACCATGG GGCCACTCCG CTCCACCTGG CCTGTCAGAA
1651 GGGCTACCAG AGCGTGACGC TGCTGCTGCT GCACTACAAG GCCAGCGCGG
1701 AAGTGCAGGA CAACAATGGG AATACGCCAC TCCACCTGGC CTGCACCTAC
1751 GGCCACGAGG ACTGTGTGAA GGCTCTGGTT TACTACGACG TGGAGTCGTG
1801 CAGACTTGAC ATTGGCAATG AGAAAGGAGA CACCCCTCTA CACATTGCTG
1851 CCCGCTGGGG CTACCAAGGC GTCATAGAGA CATTGCTGCA GAACGGAGCG
1901 TCCACCGAGA TCCAGAACAG ACTGAAGGAG ACGCCCTCA AGTGTGCATT
1951 AAACCTCAAAG ATTCTGTCTG TAATGGAAGC CTATCACETG TCCTTCGAGA
2001 GGAGGCAGAA GTCGTCCGAG GCCCCTGTGC AGTCCCCGCA GCGCTCCGTG
2051 GACTCCATCA GCCAAGAGTC CTCCACTTCC AGCTTCTCCT CCATGTCAGC
2101 GCGCTCAAGG CAGGAGGAGA CCAAGAAGGA CTACAGAGAG GTAGAAAAC
2151 TTTTGAGAGC AGTTGCTGAT GGAGATCTAG AAATGGTGCG TTACCTGTTG
2201 GAATGGACAG AGGAGGACCT GGAGGATGCG GAGGACACTG TCAGTGCAGC
2251 AGACCCCGAA TTCTGTACC CGTTGTGCCA GTGCCCCAAG TGTGCCCCAG
2301 CTCAGAAGAG GCTGGCGAAG GTTCTTGCCA GTGGGCTTGG TGTGAACGTG
2351 ACCAGCCAGG ACGGCTCCTC CCCGCTGCAT GTCGCGCGCC TGCACGCGCG
2401 GCGGACCTC ATCCGCTCC TGCTGAAGCA CGGGGCCAAC GCAGGTGCCA
2451 GGAACGCAGA CCAAGCCGTC CCGCTCCACC TGGCCTGCCA GCAGGGCCAC
2501 TTTTCAGGTG TGAAGTGTCT GTTAGATTCC AATGCAAAAC CCAATAAGAA
2551 GGACCTCAGT GGAACACGC CCCTCATTTA CGCTGTCTCC GGTGGCCATC
2601 ACGAGCTTGT GGCAGTGTG CTACAGCACG GGGCCTCCAT TAACGCTTCT
2651 AACAAATAAG GCAACACAGC GCTGCACGAG GCTGTGATTG AAAAGCACGT
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2701 CTTCTGGGTA GAGCTGCTTC TGCTCCACGG AGCGTCAGTT CAGGTGCTGA
2751 ACAAGCGGCA GCGCACGGCT GTAGACTGTG CTGAACAGAA TTCAAAAATA
2801 ATGGAATTGC TTCAGGTGCT ACCAAGCTGT GTTGCTTCAT TAGATGATGT
2851 GGTGAAACT GACCGCAAGG AGTATGTCAC TGTTAAGATC AGGAAAAAAT
2901 GGAACCTCAA ACTGTATGAT CTACCAGATG AGCCTTTTAC AAGACAGTTT
2951 TACTTTGTCC ACTCAGCTGG TCAGTTTAAG GGAAAGACTT CAAGGGAGAT
3001 TATGGCAAGA GATAGAAGTG TCCCTAATTT AACCGAAGGT TCTTTGCATG
3051 AGCCAGGGAG GCAAAGTGTC ACACCTGAGAC AGAATAACCT GCCAGCTCAG
3101 AGTGGATCTC ATGCTGCTGA GAAAGGCAAC AGCGACTGGC CAGAGAGGCC
3151 TGGACTGACA CAGACTGGCC CTGGACACAG ACGGATGCTG CGGAGACACA
3201 CGGTAGAGGA TGCGGTCGTG TCCAGGGGCC CGGAGGCTGC TGGCCCCCTC
3251 TCCACTCCCC AAGAGGTTAG TGCTTCCCGG TCCTAACAGG AATGAGGAGT
3301 TGTGTAACCC ACTGCTAGGA AGCAAGGATG CAACAAGATG ATGCTGAGCG
3351 TGAACACATC TGAGAACTAA ATGTGCTTCC ATGAGACTGG CTTGAGAAGT
3401 CTTTCAGCAC AAGTTCCTGA AAGCTTTTCT GTGGCAGGAA AGAATGCAAC
3451 AAAAAAGTTA ACCACCACCA TCTCTCTCCT CTTCAAAGCT AATGAATACA
3501 ATTGAAACAG ACAAATAATC CAGTAGCATC CAGATCCTTA AGCCAGAGGT
3551 GCATGCTTCT TTTTAAGTAT GAGGGTTTGT TGCTCAGAT GGGAGAGGTT
3601 TCACCACCGC ATTCTGACCT CCTCCTCCCA AAAGGTGCTA AACCTCTCTG
3651 ACCTGTGTAC ATTCACAAAC CACAGCTAGA ATTCCTCCAC CTAGGATTAA
3701 GCTGGAGAGA AGTAAGTAAT TTAGGTTTCA TGGTACTGTA GAGGCCAGGC
3751 TGAATGTGCA TATCTGAAGG AAGAAAGCAG CAGCTGGACA ATGTTTCTTT
3801 GCAAAGCAAC ACTCGAACCA AAAGATGCCT CAATCCCAT TGTATATTCA
3851 TTTTAGTGAA AGGATGCATC AGACCTGTTC CACATCATGC ACATGGGAAA
3901 GGGTGGTTAT CATTTTCTT CTAACAAGTA GGTACAGATA TTCGGTTACT
3951 ACACGTGCAC CTGTAGCAGT ATTTCTAGAA ACATCCCTTT TTGTTGAGAA
4001 CCTCCCTTGA ATGTCTGTCA CACTCACACC TGACGGGATG GTTACTGGAT
4051 TAGAGAGTAG ATTTGGCACA TCTTTTCTTA GTCTTTTGAT TCAAATTCAA
4101 AACTTAACAG CACAAACCAG GTCAGAGTTA CTTTCGGTTA GAATTTATTG
4151 CCATTTATTC CTTTTATAA ATTTCTATAG ATTATACTGT TATTTTATG
4201 TTATTGGCCT AGAGCTACAC GTATATGGGT TTGTCTGAG TCCGTTTTCA
4251 AATGACCTTG TGATAGGGAA ATGGTTTTGT CCATGTTCTT GGAAATACTT
4301 GTGTATGTAC AGAAGGAAGG GAGGGATTAT TTTTCTACAA AGTAATTTAT
4351 GATTTCTAAT TTTCTAATGT GCCTTGGATA TGTGCCAAAT GATGGAAAAG
4401 AAACAGTAAA CTTTATGATT CTTAAAAAAA AAAAAAAAAA AAAAAAAAAA
4451 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
4501 G
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 134 bp to 3283 bp; peptide length: 1050

Category: similarity to known protein

Classification: Cell structure/motility

Prosites motifs: ATP_GTP_A (945-953)

```
1 MALYDEDLLK NPFYALQKC RPDLCCKVAQ IHGIVLVPC KSLSSSIQST
51 CQFESYILIP VEEHFQTLNG KDVFIQGNRI KLGAGFACLL SVPILFEEFT
101 YNEKEESFSI LCIAHPLEKR ESSEELPLAPS DPFLSKTIED VREFLGRHSE
151 RFRNRIASFH RTFRECERKS LRHHIDSANA LYTKCLQQLL RDSHLKMLAK
201 QEAQMNLMKQ AVEIYVHHEI YNLIFKYVGT MEASEDAAFN KITRSLQDLQ
251 QKDIGVKPEF SFNIPRAKRE LAQLNKCTSP QOKLVCLRKV VOLITQSPSQ
301 RVNLETMCAD DLLSVLLYLL VKTEIPNWMA NLSYIKNFRF SSLAKDELGY
351 CLTSFEAAIE YIRQGSLSAK PPESEFGGDR LFLKQRMSSL SQMTSSPTDC
401 LFKHIASGNQ KEVERLLSQE DHDKDTVQKM CHPLCFCDCC EKLVSGRLND
451 PSVVTPFSRD DRGHTPLHVA AVCGQASLID LLVSKGAMVN ATDYHGATPL
501 HLACQKGYQS VTLLLLHYKA SAEVQDNNGN TPLHLACTYG HEDCVKALVY
551 YDVESCLLDI GNEKGDTPH IAARWGYQGV IETLLQNGAS TEIQNRKKT
601 PLKCALNSKI LSVMEAYHLS FERRQKSSEA PVQSPQRSVD SISQESSTSS
651 FSSMSAGSRQ EETKKDYREV EKLLRAVADG DLEMVRYLLE WTEEDLEDAE
701 DTVSAADPEF CHPLCQCPKC APAQKRLAKV PASGLGVNVT SQDGSPLHV
751 AALHGRADLI RLLKKGANA GARNADQAVP LHLACQGHF QVVKCLLDSN
801 AKPNKKDLGS NTPLIYACSG GHHELVALLL QHGASINASN NKGNTALHEA
851 VIEKHVFVVE LLLHLGASVQ VLNKRQRTAV DCAEQNSKIM ELLQVVPSCV
```


901 ASLDDVAETD RKEYVTVKIR KKWNSKLYDL PDEPFTRQFY FVHSAGQFKG
 951 KTSREIMARD RSVPNLTEGS LHEPGRQSVT LRQNNLPAQS GSHAAEKGNS
 1001 DWPERPGLTQ TGPGRHRLR RHTVEDAVVS QGPEAAGPLS TPQEVASRS

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_1817, frame 2

TREMBL:HSU43965.1 gene: "ANK3"; product: "ankyrin G119"; Human ankyrin G119 (ANK3) mRNA, complete cds., N = 2, Score = 287, P = 3.7e-21

PIR:I49502 ankyrin - mouse, N = 3, Score = 365, P = 2.2e-27

TREMBL:HSANKY_2 product: "alt. ankyrin (variant 2.2)"; Human mRNA for ankyrin (variant 2.1), N = 2, Score = 380, P = 7.3e-31

SWISSPROT:ANK1_HUMAN ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)., N = 2, Score = 380, P = 8.2e-31

PIR:SJHUK ankyrin 1, erythrocyte splice form 1 - human, N = 2, Score = 380, P = 8.2e-31

>TREMBL:HSANKY_2 product: "alt. ankyrin (variant 2.2)"; Human mRNA for ankyrin (variant 2.1)
 Length = 1,719

HSPs:

Score = 380 (57.0 bits), Expect = 7.3e-31, Sum P(2) = 7.3e-31
 Identities = 139/447 (31%), Positives = 207/447 (46%)

Query: 462 RGHTPLHVAACGQASLIDLLVSKGAMVNATDYHGATPLHLACQKGYSVTLLLLHYKAS 521
 +G+T LH+AA+ GQ ++ LV+ GA VNA G TPL++A Q+ + V LL A+
 Sbjct: 77 KGNTALHIAALAGQDEVVRELNVYGANVNAQSQKGFPLYMAAQENHLEVVKFLENGAN 136

Query: 522 AEVODNNGNTPLHLACTYGHEDCVKALVYYDVES-CRL----- 558
 V +G TPL +A GHE+ V L+ Y + RL
 Sbjct: 137 QNVATEDGFTPLAVALQQGHENVVAHLINYGTKGKVRPLPALHIAARNDDTRTAAVLLQND 196

Query: 559 ---DIGNEKGDTPHLIAARWGYQGVIETLLQNGASTEIQNRLKETPLKCALNSKILSVME 615
 D+ ++ G TPLHIAA + V + LL GAS + TPL A S+ +V+
 Sbjct: 197 PNPDVLSKTGFTPLHIAAHYENLNVAQLLLNRGASVNFTFQNGITPLHIA--SRRGNVIM 254

Query: 616 AYHLSFERROKSSEAPVQSPQRSVDSISQESSTS-SFSSMSAGSR-QEETKKDYREVEKL 673
 L +R + E + + ++ S + G+ Q +TK +
 Sbjct: 255 V-RLLLDRGAQI-ETKTKDELTPHCAARNGHVRRISEILLDHGAPIQAKTKNGLSPIHM- 311

Query: 674 LRAVADGD-LEMVRYLLEWTEEDLEDAEDTVSAADPEFCHPLCQCPKCAPAQKRLAKVPA 732
 A GD L+ VR LL++ E ++D T+ P H C R+AKV
 Sbjct: 312 ---AAQGDHLDCVRLLLQYDAE-IDDI--TLDHLTP--LHVAACH-----GHHRVAKVLL 358

Query: 733 S-GLGVNVTSDQGSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGGHFQ 791
 G N + +G +PLH+A ++ LLLK GA+ A PLH+A GH
 Sbjct: 359 DKGAKPNSRALNGFTPLHIACKKNHVRVMEILLKTGASIDAVTESGLTPLHVASFMGHLP 418

Query: 792 VVKCLDSNAKPNKKDLSGNTPLIYACSGGHHELVALLQHGASINASNKNGNTALHEAV 851
 +VK LL A PN ++ TPL A GH E+ LLQ+ A +NA T LH A
 Sbjct: 419 IVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDQTPHCAA 478

Query: 852 IEKHVFVVELLLLHGASVQVLNKRQRTAVDCAEQNSKIMELLQVV 896
 H +V+LLL + A+ + T + A + + +L ++
 Sbjct: 479 RIGHTNMVKLLLENNANPNLATTAGHTPLHIAAREGHVETVLALL 523

Score = 378 (56.7-bits), Expect = 1.2e-30, Sum P(2) = 1.2e-30
 Identities = 130/447 (29%), Positives = 195/447 (43%)

Query: 465 TPLHVAACGQASLIDLLVSKGAMVNATDYHGATPLHLACQKGYSVTLLLLHYKASAEV 524
 TPLH AA G + ++L+ GA + A +G +P+H+A Q + LLL Y A +
 Sbjct: 274 TPLHCAARNGHVRRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDCVRLLLQYDAEIDD 333

Query: 525 QDNNGNTPLHLACTYGHEDCVKALVYYDVE-----SCR----- 557
 + TPLH+A GH K L+ + +C+
 Sbjct: 334 ITLDHLTPHVAACHGHHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVMEILLKT 393

Query: 558 ---LDIGNEKGDTPHLIAARWGYQGVIETLLQNGASTEIQNRLKETPLKCALNSKILSV 614
 +D E G TPLH+A+ G+ +++ LLQ GAS + N ETPL A + V
 Sbjct: 394 GASIDAVTESGLTPLHVASFMGHLPVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVA 453

Query: 615 EAYHLSFERRQKSSEAPVQSPQRSVDSISQESSTSSFSMSAGSRQEETKKDYREVEKLL 674
 + Y L + + + Q+P I + +A T L
 Sbjct: 454 K-YLLQNKAKVNAKAKDDQTPHCAARIGHTNMVKLLLENNANPNLATTAGH----TPLH 508

Query: 675 RAVADGDLEMVRYLLEWTEEDLEDAEDTVSAADPEFCHPLCQCPKCAPAQKRLAKVPASG 734
 A +G +E V LLE ++ A T P H + K A+ L +
 Sbjct: 509 IAAREGHVETVLALLE---KEASQACMTKKGFTP--LHVAAYKGVRAELLER----D 559

Query: 735 LGVNVTSQDGSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGHFQVVK 794
 N ++G +PLHVA H D+++LLL G + + + PLH+A +Q +V +
 Sbjct: 560 AHPNAAAGKNGLTPLHVAHVHNNLDIVKLLPRGGSPHSPAUNGYTPLHIAAKQNQVEVAR 619

Query: 795 CLLDSNAKPNKKDLSGNTPLIYACSGGHELVALLQHGASINASNNGNTALHEAVIEK 854
 LL N + + G TPL A GH E+VALL A+ N N G T LH E
 Sbjct: 620 SLLQYGGSSANAESVQGVTPHLAAQEGHAEMVALLSKQANGNLGNKSGLTPLHLVAQEG 679

Query: 855 HVFVVELLLLHGASVQVLNKRQRTAVDCAEQ--NSKIMELL 893
 HV V ++L+ HG V + T + A N K+++ L
 Sbjct: 680 HVPVADVLIKGVMDATTRMGYTPLHVASHYGNIKLVKFL 720

Score = 367 (55.1 bits), Expect = 1.8e-29, Sum P(2) = 1.8e-29
 Identities = 131/489 (26%), Positives = 210/489 (42%)

Query: 404 HIAS--GNQKEVERLLSQEDHDKDTVQKMCHPL-CFCDDCEKLVSGRLNDPSVVT PFSRD 460
 HIAS GN V LL + + + PL C + +S L D ++
 Sbjct: 244 HIASRRGNVIMVRLLLDRGAQIETKTDELTPHCAARNGHVRRISEILLDHGAPIQ-AKT 302

Query: 461 DRGHTPLHVAAVCGQASLIDLVSXGAMVNATDYHGATPLHLACQKGYQSVTLLLLHYKA 520
 G +P+H+AA + LL+ A ++ TPLH+A G+ V +LL A
 Sbjct: 303 KNGLSPIHMAAQGDHLDCVRLLLQYDAEIDDITLDHLLTPHVAACHGHRVAKVLLDKGA 362

Query: 521 SAEVQDNNGNTPLHLACTYGHEDCVKALVYDVESCRDLIGNEKGDTPHIAARWGYQGV 580
 + NG TPLH+AC H ++ L+ +D E G TPLH+A+ G+ +
 Sbjct: 363 KPNSRALNGFTPLHIACKKNHVRVMELLK---TGASIDAVTESGLTPLHVASFMGHLPI 419

Query: 581 IETLLQNGASTEIQNRLKETPLKCAL---NSKILSVMEAYHLSFERRQKSSEAPVQSPQR 637
 ++ LLQ GAS + N ETPL A ++++ + + K + P+ R
 Sbjct: 420 VKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDQTPHCAAR 479

Query: 638 ----SVDSISQESSTSSFSMSAGSRQEETKKDYREVEKLLRAVADGDLEMVRYLLEWTE 693
 ++ + E++ + +AG VE +L + + +T
 Sbjct: 480 IGHNTNMVKLLLENNANPNLATTAGHTPLHIAAREGHVETVLALLEKEASQACMTKKGFTP 539

Query: 694 EDLEDAEDTVSAAD---PEFCHPLCQ-----CP-KCAPAQKRLAKVPA---SGLGVNVTS 741
 + V A+ HP P A L V G + +
 Sbjct: 540 LHVAAYKGVRAELLERDAHPNAAAGKNGLTPLHVAHVHNNLDIVKLLPRGGSPHSPA 599

Query: 742 QDGSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGHFQVVKCLLDSNA 801
 +G +PLH+AA + ++ R LL++G +A A + PLHLA Q+GH ++V LL A
 Sbjct: 600 WNGYTPLHIAAKQNQVEVARSLQYGGSSANAESVQGVTPHLAAQEGHAEMVALLSKQA 659

Query: 802 KPNKKDLSGNTPLIYACSGGHELVALLQHGASINASNNGNTALHEAVIEKHVFVVEL 861
 N + SG TPL GH + +L++HG ++A+ G T LH A ++ +V+
 Sbjct: 660 NGNLGNKSGLTPLHLVAQEGHVPVADVLIKGVMDATTRMGYTPLHVASHYGNIKLVKFL 719

Query: 862 LLLHGASVQVLNK 874
 LL H A V K
 Sbjct: 720 LLQHQAADVNAKTK 732

Score = 345 (51.8 bits), Expect = 4.2e-27, Sum P(2) = 4.2e-27
 Identities = 146/506 (28%), Positives = 233/506 (46%)

Query: 404 HIAS--GNQKEVERLLSQEDHDKDTVQK---MCHPLCFCDDCEKLVSGRLNDPSVVT PFS 458
 H+AS G+ K V LL +E + T +K H +++V +N + V +
 Sbjct: 50 HLASKEGHVKMVVELLHKEIILETTTKKGNTALHIAALAGQ-DEVVRELNVYGANVN--A 106

Query: 459 RDDRGTPLHVAAVCGQASLIDLVSXGAMVNATDYHGATPLHLACQKGYQSVTLLLLHY 518
 + +G TPL++AA ++ L+ GA N G TPL +A Q+G+++V L++Y
 Sbjct: 107 QSQKGFTPLYMAAQENHLEVVKFLLENGANQNVATEDGFTPLAVALQGHENVAHLIN 166

Query: 519 KASAEVQDNNGNTPLHLACTYGHEDCVKALVYDVESCRDLIGNEKGDTPHIAARWGY 577
 +V+ P LH+A ++D A V + D+ ++ G TPLHIAA +
 Sbjct: 167 GTKGKVR-----LPALHIAAR--NDOTRTAAVLLQNDP-NPDVLSKTGFTPLHIAAHYEN 218

Query: 578 QGVITLLQNGASTEIQNRLKETPLKCAL---NSKILSVMEAYHLSFERRQKSSEAPVQS 634
 V + LL GAS + TPL A N ++ ++ E + K P+
 Sbjct: 219 LNVAQLLLNRGASVNETPQNGITPLHIAARRGNVIMVRLLLDRGAQIETKTDELTPHLC 278

Query: 635 PQRSVDSISQESSTSSFSMSAGSRQEETKKDYREVEKLLRAVADGD-LEMVRYLLEWTE 693
 R+ E + + A +TK + A GD L+ VR LL++
 Sbjct: 279 AARNGHVRRISEILLDHGAPIQA-----KTKNGLSPIHM---AAQGDHLDCVRLLLQYDA 329

Query: 694 EDLEDAE-DTVSAAD-PEFC---HPLCQC-----PK-----CAPAQKRLAK 729
 E ++D D ++ C H ++ P C R+ +
 Sbjct: 330 E-IDDITLDHLTPLHVAACHGHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVME 388

Query: 730 VPA-SGLGVNVTSDQGSSPLHVAALHGRADLIRLLLLKHGANAGARNADQAVPLHLACQOG 788
 + +G ++ ++ G +PLHVA+ G +++ LL+ GA+ N PLH+A + G
 Sbjct: 389 LLLKTGASIDAVTESGLTPLHVASFHGLPIVKNLLQRGASPNVSNVKVETPLHMAARAG 448

Query: 789 HFQVVKCLLDSNAKPNKKDLSGNTPLIYACSGGHELVALLLQHGASINASNNGNTALH 848
 H +V K LL + AK N K TPL A GH +V LLL++ A+ N + G+T LH
 Sbjct: 449 HTEVAKYLLQNKAKVNAKAKDDQTPLHCAARIGHTNMVKLLENNANPNLATTAGHTPLH 508

Query: 849 EAVIEKHVFVVELLLHGVSVQVLNKRQRTAVDCAEQNSKIM--ELL 893
 A E HV V LL AS + K+ T + A + K+ ELL
 Sbjct: 509 IAAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYKVRVAELL 555

Score = 243 (36.5 bits), Expect = 1.6e-14, Sum P(2) = 1.6e-14
 Identities = 64/199 (32%), Positives = 97/199 (48%)

Query: 404 HIAS--GNQKEVERLLSQEDHDKDVTQKMCPLCFDCEKLVSGRLNDPSVVTFFSRDD 461
 H+A+ G + E LL ++ H + PL L +L P +P S
 Sbjct: 541 HVAARYGKVRVAELLERDAHPNAGKNGLTPLHVAVHHNNLDIVKLLPRGGSPHSPAW 600

Query: 462 RGHTPLHVAACVCGQASLIDLVSKGAMVNATDYHGATPLHLACQKGYQSVTLLLLHYKAS 521
 G+TPLH+AA Q + L+ G NA G TPLHLA Q+G+ + LLL +A+
 Sbjct: 601 NGYTPLHIAAKQNQVEVARSLLOYGGSANAESVQGVTPHLHAAQEGHAEMVALLLSKQAN 660

Query: 522 AEVDQNNNGNTPLHLACTYGHEDCVKALVYYDVESCRDLIGNEKGDTPHLIAARWGYQGV 581
 + + +G TPLHL GH L+ + V +D G TPLH+A+ +G ++
 Sbjct: 661 GNLGNKSGLTPLHLVAQEGHVPVADVLIKHG---MVDATTRMGYTPLHVASHYGNIKLV 717

Query: 582 ETLLQNGASTEIQNRKLTPL 602
 + LLQ+ A + +L +PL
 Sbjct: 718 KFLQHQADVNAKTKLGYSP 738

Score = 242 (36.3 bits), Expect = 5.0e-29, Sum P(2) = 5.0e-29
 Identities = 63/176 (35%), Positives = 92/176 (52%)

Query: 734 GLGVNVTSDQGSSPLHVAALHGRADLIRLLLLKHGANAGARNADQAVPLHLACQOGHFQVV 793
 G VN T Q+G +PLH+A+ G ++RLLL GA + D+ PLH A + GH ++
 Sbjct: 229 GASVNFTPQNGITPLHIASRRGNVIMVRLLLDRGAQIETKTKDELTPHCAARNGHVRIS 288

Query: 794 KCLLDSNAKPNKKDLSGNTPLIYACSGGHELVALLLQHGASINASNNGNTALHEAVIE 853
 + LLD A K +G +P+ A G H + V LLLQ+ A I+ T LH A
 Sbjct: 289 EILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVRLLLQYDAEIDITLDHLTPLHVAACH 348

Query: 854 KHVFVVELLLHGA--SVQVLNKRQRTAVDCAEQNSKIMELLQVVPSCVASLDDVAET 909
 H V ++LL GA + + LN + C + + +MELL AS+D V E+
 Sbjct: 349 GHHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVMEMLLKTG---ASIDAVTES 403

Score = 242 (36.3 bits), Expect = 3.3e-14, Sum P(2) = 3.3e-14
 Identities = 80/284 (28%), Positives = 129/284 (45%)

Query: 404 HIAS--GNQKEVERLLSQEDHDKDVTQKMCPLCFDCEKLVSGRLNDPSVVTFFSRDD 461
 HIA+ G+ + V LL +E +K PL K+ L P +
 Sbjct: 508 HIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAARYGKVRVAELLERDAHPNAGK 567

Query: 462 RGHTPLHVAACVCGQASLIDLVSKGAMVNATDYHGATPLHLACQKGYQSVTLLLLHYKAS 521
 G TPLHVA ++ LL+ +G ++ ++G TPLH+A ++ V LL Y S
 Sbjct: 568 NGLTPLHVAVHHNNLDIVKLLPRGGSPHSPAWNNGYTPLHIAAKQNQVEVARSLLOYGGS 627

Query: 522 AEVDQNNNGNTPLHLACTYGHEDCVKALVYYDVESCRDLIGNEKGDTPHLIAARWGYQGV 581
 A + G TPLHLA GH + V L+ ++GN+ G TPLH+ A+ G+ V
 Sbjct: 628 ANAESVQGVTPHLHAAQEGHAEMVALLLSKQANG---NLGNKSGLTPLHLVAQEGHVPVA 684

Query: 582 ETLLQNGASTEIQNRKLTPLKCAL---NSKILSVMEAYHLSFERROKSSEAPV-QSPQR 637
 + L+++G + R+ TPL A N K++ + + + K +P+ Q+ Q+
 Sbjct: 685 DVLIKHGVMVDATTRMGYTPLHVASHYGNIKLVKFLQHQADVNAKTKLGYSPHQAQQ 744

Query: 638 S-VDSISQ--ESSTSSFSMSAGSRQEETK--DYREVEKLLRAVAD 679
 D ++ ++ S S G+ K Y V +L+ V D
 Sbjct: 745 GHTDIVTLLKNGASPNEVSSDGTTPLAIAKRLGYISVTDVLKVVD 791

Score = 235 (35.3 bits), Expect = 7.9e-34, Sum P(2) = 7.9e-34
 Identities = 58/165 (35%), Positives = 83/165 (50%)

Query: 734 GLGVNVTSDQGSSPLHVAALHGRADLIRLLLLKHGANAGARNADQAVPLHLACQOGHFQVV 793
 G N S G +PLH+AA G A+++ LLL AN N PLHL Q+GH V
 Sbjct: 625 GGSANAESVQGVTPHLHAAQEGHAEMVALLLSKQANGNLGNKSGLTPLHLVAQEGHVPVA 684

Query: 794 KCLLDSNAKPNKKDLSGNTPLIYACSGGHHELVALLLQH GASINASNKNGNTALHEAVIE 853
 L+ + G TPL A G+ +LV LLQH A +NA G + LH+A +
 Sbjct: 685 DVLIKHGVMVDATTRMGYTPLHVASHYGNIKLVKFLQLQH QADVNAKTKLGYSPHLHQAAQQ 744

Query: 854 KHVFVVELLLLHGASVQVLNKRQRTAVDCAEQNS--KIMELLQVV 896
 H +V LLL +GAS ++ T + A++ + ++L+VV
 Sbjct: 745 GHTDIVTLLKNGASPNVSSDGTTPLAIAKRLGYISVTDVLKVV 789

Score = 233 (35.0 bits), Expect = 7.9e-34, Sum P(2) = 7.9e-34
 Identities = 67/202 (33%), Positives = 100/202 (49%)

Query: 404 HTAS-GNQKEVERLLSQEDHDKDTVQKMCH--PLCFDDC-EKLVSGRLNDPSVVTFSR 459
 H+A+ G+ + RLL Q D + D + + H PL C V+ L D P SR
 Sbjct: 310 HMAAQGDHLDCVRLLLQYDAEIDDIT-LDHLTPLHVAAHCGHHRVAKVLLDKGA-KPNSR 367

Query: 460 DDRGHTPLHVAAVCGQASLIDLLVSKGAMVNATDYHGATPLHLACQKGYQSVTLLLLHYK 519
 G TPLH+A +++LL+ GA +A+ G TPLH+A G+ + LL
 Sbjct: 368 ALNGFTPLHIAKKNHVRVMELLKKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRG 427

Query: 520 ASAEVQDNNGNTPLHLACTYGHEDCVKALVYYDVESCRLDIGNEKGDTPHLIAARWGYQG 579
 AS V + TPLH+A GH + K L+ +++ + TPLH AAR G+
 Sbjct: 428 ASPNVSNVKVETPLHMAARAGHTEVAKYLLQ---NKAKVNAKAKDDQTPHLCAARIGHTN 484

Query: 580 VIETLLQNGASTEIQNRLKETPLKCA 605
 +++ LL+N A+ + TPL A
 Sbjct: 485 MVKLLLENNANPNLATTAGHTPLHIA 510

Score = 226 (33.9 bits), Expect = 7.0e-33, Sum P(2) = 7.0e-33
 Identities = 53/153 (34%), Positives = 83/153 (54%)

Query: 743 DGSSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGHFQVVKCLLDSNAK 802
 +G +PLH+AA + ++ R LL++G +A + + PLHLA Q+GH ++V LL A
 Sbjct: 601 NGYTPLHIAAKQNVARSLLQYGGSSANAESVQGVTPHLHAAQEGHAEMVALLLSKQAN 660

Query: 803 PNKKDLSGNTPLIYACSGGHHELVALLLQH GASINASNKNGNTALHEAVIEKHVFVVELL 862
 N + SG TPL GH + +L++HG ++A+ G T LH A ++ +V+ L
 Sbjct: 661 GNLGKNSGLTPLHLVAQEGHVPVADVLIKHGVMVDATTRMGYTPLHVASHYGNIKLVKFL 720

Query: 863 LLHGASVQVLNKRQRTAVDCAE--NSKIMELL 893
 L H A V K + + A Q ++ I+ LL
 Sbjct: 721 LQH QADVNAKTKLGYSPHLHQAAQQGHTDIVTLL 753

Score = 198 (29.7 bits), Expect = 2.5e-11, Sum P(2) = 2.5e-11
 Identities = 51/157 (32%), Positives = 82/157 (52%)

Query: 737 VNVTSQDGSSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGHFQVVKCL 796
 + T++ G++ LH+AAL G+ +++R L+ +GAN A++ PL++A Q+ H +VVK L
 Sbjct: 71 LETTTKKGNTALHIAALAGQDEVRRLVNYGANVNAQSQKGFTPLYMAAQENHLEVVKFL 130

Query: 797 LDSNAKPNKKDLSGNTPLIYACSGGHHELVALLLQH GASINASNKNGNTALHEAVIEKHV 856
 L++ A N G TPL A GH +VA L+ +G ALH A
 Sbjct: 131 LENGANQNVATEDGFTPLAVALQGHENVVVAHLINYGTK---GKVRPLALHIAARNDDT 186

Query: 857 FVVELLLLHGASVQVLNKRQRTAVDCAE--QNSKIMELL 893
 +LL + + VL+K T + A +N + +LL
 Sbjct: 187 RTAAVLLQNDPNPDVLSKTGFTPLHIAAHYENLNVAQLL 225

Score = 186 (27.9 bits), Expect = 6.6e-29, Sum P(2) = 6.6e-29
 Identities = 55/143 (38%), Positives = 68/143 (47%)

Query: 463 GHTPLHVAAVCGQASLIDLLVSKGAMVNATDYHGATPLHLACQKGYQSVTLLLLHYKASA 522
 GHTPLH+AA G + L+ K A G TPLH+A + G V LLL A
 Sbjct: 503 GHTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRVAELLERDAHP 562

Query: 523 EVQDNNGNTPLHLACTYGHEDCVKALVYYDVESCRLDIGNEKGDTPHLIAARWGYQGVIE 582
 NG TPLH+A + + D VK L+ S N G TPLHIAA+ V
 Sbjct: 563 NAAGKNGLTPLHVAVHHNNLDIVKLLPRG-GSPHSPAWN--GYTPLHIAAKQNVQVEAR 619

Query: 583 TLLQNGASTEIQNRLKETPLKCA 605
 +LLQ G S ++ TPL A
 Sbjct: 620 SLLQYGGSSANAESVQGVTPHLA 642

Score = 182 (27.3 bits), Expect = 2.9e-28, Sum P(2) = 2.9e-28
 Identities = 54/185 (29%), Positives = 89/185 (48%)

Query: 738 NVTSQDGSSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGHFQVVKCLL 797
 N+ ++ G +PLH+ A G + +L+KHG A PLH+A G+ ++VK LL
 Sbjct: 662 NLGNKNSGLTPLHLVAQEGHVPVADVLIKHGVMVDATTRMGYTPLHVASHYGNIKLVKFL 721

Query: 798 DSNAPNKKDLSGNTPLIYACSGGHHELVALLLQH GASINASNKNGNTALHEAVIEKHVF 857
 A N K G +PL A GH ++V LLL++GAS N ++ G T L A ++

Sbjct: 722 QHQADVNAKTKLGYSPHLHQAQQGHTDIVTLLKNGASPNVSSDGTTPLAIAKRLGYIS 781
 Query: 858 VVELLLLHGASVQVLNKRQRTAVDCAEQNSKIMELLQVVPSCVASLDDVAETDRKEYVTV 917
 V ++L + V ++ V + S P V + DV+E + +E ++
 Sbjct: 782 VTDVLKV-----VTDETSFVLVSDKHRMS-----FPETVDEILDVSEDEGEELISF 827
 Query: 918 KIRKK 922
 K ++
 Sbjct: 828 KAERR 832

Score = 180 (27.0 bits), Expect = 5.0e-29, Sum P(2) = 5.0e-29
 Identities = 41/121 (33%), Positives = 67/121 (55%)

Query: 486 GAMVNATDYHGATPLHLACQKGYQSVTLLLLHYKASAEVQDNNNGNTPLHLACTYGHEDCV 545
 G +N + +G LHLA ++G+ + + LH + E GNT LH+A G ++ V
 Sbjct: 35 GVDINTCNQNGNLNGLHLASKEGHVMMVVELLHKEIILETTTCKGNTALHIAALAGQDEVV 94
 Query: 546 KALVYYDVESCRLDIGNEKGDTPHLIAARWGYQGVETLLQNGASTEIQNRLKETPLKCA 605
 + LV Y ++ ++KG TPL++AA+ + V++ LL+NGA+ + TPL A
 Sbjct: 95 RELVNY---GANVNAQSQKGFPLYMAAQENHLEVVKFLENGANQNVATEDGFTPLAVA 151
 Query: 606 L 606
 L
 Sbjct: 152 L 152

Score = 166 (24.9 bits), Expect = 3.4e-06, Sum P(2) = 3.4e-06
 Identities = 89/318 (27%), Positives = 140/318 (44%)

Query: 448 LNDPSVVTFSRDDRGTPLHVAACVQASLIDLLVSKGAMVNATDYHGATPLHLACQKG 507
 L + + V ++DD+ TPLH AA G +++ LL+ A N G TPLH+A ++G
 Sbjct: 457 LQNKAKVNAKAKDDQ--TPLHCAARIGHTNMVKLLLENNANPNLATTAGHTPLHIAAREG 514
 Query: 508 YQSVTLLLLHYKASAEVQDNNNGNTPLHLACTYGHEDCVKALVYYD----- 552
 + L LL +AS G TPLH+A YG + L+ D
 Sbjct: 515 HVETVLALLEKEASQACMTKKGFTPLHVAAYGKVRVAELLERDAHPNAAKNGLTPLH 574
 Query: 553 --VESCRDI-----GNE-----KGDTPLHIAARWGYQGVETLLQNGASTEIQNRL 597
 V LDI G+ G TPLHIAA+ V +LLQ G S ++
 Sbjct: 575 VAVHHNNLDIVKLLPRGGSPHSPAWNNGYTPLHIAAKQNVARSLLQYGGSSANAESVQ 634
 Query: 598 KETPLKCALNSKILSVMEAYHLSFERRQKSSEAPVQSPQSVDSISQESSTSSFSSM-SA 656
 TPL A M A LS +Q + +S + ++QE +
 Sbjct: 635 GVTPLHLAAQEGHAE-MVALLS---KQANGNLGNKSGLTPLHLVAQEGHVPVADVLIKH 690
 Query: 657 GSRQEETKKDYREVEKLLRAVADGDLEMVRYLLEWTEEDLEDAEDTVSAADPEFCHPLCQ 716
 G + T + L A G++++V++LL+ + D+ +A+ + + PL Q
 Sbjct: 691 GVMVDATTR--MGYTPLHVASHYGNIKLVKFLQH-QADV-NAKTKLGY-----PLHQ 740
 Query: 717 CPKCAPAQKRLAKVPASGLGVNVTSQDGSSPLHVA 751
 + + +G N S DG++PL +A
 Sbjct: 741 AAQQGHTDI-VTLLKNGASPNVSSDGTTPLAIA 774

Score = 162 (24.3 bits), Expect = 1.8e-07, Sum P(2) = 1.8e-07
 Identities = 48/149 (32%), Positives = 71/149 (47%)

Query: 737 VNVTSQDGSSPLHVAALHGRADLIRLLKKGANAGARNADQAVPLHLACQGGHFQVVKCL 796
 V D ++ AA G D L+G + N + LHLA ++GH ++V L
 Sbjct: 5 VGFREDAATSFLRAARSGNLDKALDHLRNGVDINTCNQNGNLNGLHLASKEGHVMMVVEL 64
 Query: 797 LDSNAKPNKDLSGNTPLIYACSGGHHELVALLLQH GASINASNNGNTALHEAVIEKHV 856
 L GNT L A G. E+V L+ +GA++NA + KG T L+ A E H+
 Sbjct: 65 LHKEIILETTTCKGNTALHIAALAGQDEVVRELVNYGANVNAQSQKGFPLYMAAQENHL 124
 Query: 857 FVVELLLLHGASVQVLNKRQRTAVDCAEQ 885
 VV+ LL +GA+ V + T + A Q
 Sbjct: 125 EVVKFLENGANQNVATEDGFTPLAVALQ 153

Score = 158 (23.7 bits), Expect = 5.7e-26, Sum P(2) = 5.7e-26
 Identities = 38/135 (28%), Positives = 65/135 (48%)

Query: 460 DDRGTPLHVAACVQASLIDLLVSKGAMVNATDYHGATPLHLACQKGYQSVTLLLLHYK 519
 + G LH+A+ G ++ L+ K ++ T G T LH+A G V L++Y
 Sbjct: 42 NQNGNLNGLHLASKEGHVMMVVELLHKEIILETTTCKGNTALHIAALAGQDEVVRELVNYG 101
 Query: 520 ASAEVQDNNNGNTPLHLACTYGHEDCVKALVYYDVESCRLDIGNEKGDTPHLIAARWGYQG 579
 A+ Q G TPL++A H + VK L+ ++ E G TPL +A + G++
 Sbjct: 102 ANVNAQSQKGFPLYMAAQENHLEVVKFLE---NGANQNVATEDGFTPLAVALQOQHEN 158
 Query: 580 VIETLLQNGASTEIQ 594
 V+ L+ G +++
 Sbjct: 159 VVAHLINYGTKGKVR 173

Score = 115 (17.3 bits), Expect = 1.8e-21, Sum P(2) = 1.8e-21
Identities = 37/119 (31%), Positives = 58/119 (48%)

Query: 497 ATPLHLACQKGYQSVTL LLLHYKASAEVQ--DNNGNTPLHLACTYGHEDCVKALVYYDVE 554
AT A + G ++ L H + ++ + NG LHLA GH V L++ ++
Sbjct: 13 ATSF LRAARG--NLDKALDHLRNGVDINTCNQNLNGLHLASKEGHVKM VVELLHKEII 70

Query: 555 SCRLDIGNEKGDTPHLIAARWGYQGV IETLLQNGASTEIQNRLKETPLKCALNSKILSVM 614
L+ +KG+T LHIAA G V+ L+ GA+ Q++ TPL A L V+
Sbjct: 71 ---LETTT KGN TALHIAALAGQDEVVREL VNYGANVNAQSQKGFTPLYMAAQENHLEV 127

Query: 615 E 615
+
Sbjct: 128 K 128

Score = 106 (15.9 bits), Expect = 1.8e-01, Sum P(2) = 1.6e-01
Identities = 34/121 (28%), Positives = 54/121 (44%)

Query: 769 NAGARNADQAVPLHLACQQGHFQVVKCLLDSNAKPNKKDLSGNTPLIYACSGGHHELVAL 828
+ G R AD A A + G+ L + N + +G L A GH ++V
Sbjct: 4 SVGFREADAATSFLRAARSGNLDKALDHLRNGVDINTCNQNLNGLHLASKEGHVKM VVE 63

Query: 829 LLQHGASINASNKGN TALHEAVIEKHVFVVELLLLHGASVQVLNKRQRTAVDCAEQNSK 888
LL + + KGN TALH A + VV L+ +GA+V +++ T + A Q +
Sbjct: 64 LLHKEIIILETTT KGN TALHIAALAGQDEVVREL VNYGANVNAQSQKGFTPLYMAAQENH 123

Query: 889 I 889
+
Sbjct: 124 L 124

Score = 40 (6.0 bits), Expect = 1.6e-14, Sum P(2) = 1.6e-14
Identities = 11/56 (19%), Positives = 23/56 (41%)

Query: 622 ERRQKSSEAPVQSPQRSVDSISQESSTSSFSSMSAGSRQEETKKDYREVEKLLRAV 677
+RRQ+ E VQ + + + Q + + Q ++ +K++R V
Sbjct: 1614 DRRQQQEEQVQEAKNTFTQVVQGNFQNI PGEQVTEEQFTDEQGNIVTKKIIRKV 1669

Score = 38 (5.7 bits), Expect = 2.6e-14, Sum P(2) = 2.6e-14
Identities = 6/12 (50%), Positives = 10/12 (83%)

Query: 806 KDLSGNTPLIYA 817
+D++G T L+YA
Sbjct: 1186 EDITGTTKLVA 1197

Pedant information for DKF2phtes3_1817, frame 2

Report for DKF2phtes3_1817.2

[LENGTH] 1050
[MW] 117013.72
[pI] 6.47
[HOMOL] TREMBL:DMANKY_1 product: "ankyrin"; Drosophila melanogaster ankyrin mRNA,
complete cds. 2e-45
[FUNCAT] 08.19 cellular import [S. cerevisiae, YOR034c] 5e-13
[FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YDR264c]
3e-12
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins
[S. cerevisiae, YDR264c] 3e-12
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YIL112w] 2e-11
[FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YGR232w] 8e-10
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YIR033w] 2e-08
[FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YIR033w] 2e-08
[FUNCAT] 01.04.04 regulation of phosphate utilization [S. cerevisiae, YGR233c]
3e-08
[FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YML097c] 5e-05
[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YML097c]
5e-05
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YML097c] 5e-05
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YML097c]
5e-05
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YER111c] 3e-04
[FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YER111c] 3e-04
[BLOCKS] BL00901A Cysteine synthase/cystathionine beta-synthase P-phosphate att
[SCOP] dlawcb 1.91.3.1.2 GA binding protein (GABP) alpha GA bindini 4e-12
[EC] 3.1.3.53 Myosin-light-chain-phosphatase 1e-12
[PIRKW] phosphotransferase 1e-19
[PIRKW] nucleus 1e-13

[PIRKW] potassium channel 5e-15
 [PIRKW] early protein 2e-13
 [PIRKW] tumor suppressor 1e-09
 [PIRKW] duplication 1e-14
 [PIRKW] tandem repeat 1e-19
 [PIRKW] heterodimer 1e-14
 [PIRKW] potassium transport 5e-15
 [PIRKW] cell cycle control 1e-10
 [PIRKW] serine/threonine-specific protein kinase 1e-19
 [PIRKW] transmembrane protein 5e-15
 [PIRKW] transport protein 5e-15
 [PIRKW] DNA binding 2e-11
 [PIRKW] oncogene 1e-08
 [PIRKW] ATP 1e-19
 [PIRKW] protein kinase inhibitor 1e-09
 [PIRKW] voltage-gated ion channel 5e-15
 [PIRKW] phosphoprotein 4e-38
 [PIRKW] apoptosis 1e-19
 [PIRKW] liver 4e-09
 [PIRKW] integrin binding 3e-16
 [PIRKW] differentiation 2e-12
 [PIRKW] transforming protein 1e-08
 [PIRKW] alternative splicing 1e-40
 [PIRKW] coiled coil 1e-14
 [PIRKW] peripheral membrane protein 2e-38
 [PIRKW] transcription factor 4e-16
 [PIRKW] transcription regulation 2e-16
 [PIRKW] nucleotide binding 5e-15
 [PIRKW] phosphoric monoester hydrolase 1e-12
 [PIRKW] cytoskeleton 8e-39
 [PIRKW] calmodulin binding 1e-19
 [PIRKW] smooth muscle 1e-12
 [SUPFAM] ankyrin 1e-40
 [SUPFAM] death-associated protein kinase 1e-19
 [SUPFAM] ankyrin repeat homology 1e-40
 [SUPFAM] protein kinase homology 1e-19
 [SUPFAM] vaccinia virus 27.4K HindIII-C protein homology 3e-07
 [SUPFAM] int-3 transforming protein 1e-08
 [SUPFAM] unassigned ankyrin repeat proteins 2e-38
 [SUPFAM] notch protein 2e-12
 [SUPFAM] fowlpox virus BamHI-ORF7 protein 2e-13
 [SUPFAM] rel homology 2e-11
 [SUPFAM] EGF homology 2e-12
 [PROSITE] ATP_GTP_A 1
 [PFAM] Ank repeat
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 3.05 %

SEQ MALYDEDLLKNPFYALQKCRPDLCISKVAQIHGIVLPCKGSLSSSIQSTCQFESYILIP
 SEG
 lawcB

 SEQ VEEHFQTLNGKDVFIQGNRIKLGAAGFACLLSVPIPFETFYNEKEESFSLCIAHPLEKR
 SEG
 lawcB

 SEQ ESSEEPLAPSDPFSKLTIEDVREFLGRHSEFDRNIASFHRTFRECEKSLRHHIDSANA
 SEG
 lawcB

 SEQ LYTKCLQQLLRDHLKMLAKQEAQNMNMKQAVEIYVHHEIYNLIFKYVGTMEASEDAAFN
 SEG
 lawcB

 SEQ KITRSLQDLQKQDIGVKPEFSFNIIPRAKRELAQLNKCTSPQQLVCLRKVVQLITQSPSQ
 SEG
 lawcB

 SEQ RVNLETMCADDLLSVLLYLLVKTEIPNWMANLSYIKNFRFSSSLAKDELGYCLTSFEAAIE
 SEG
 lawcB

 SEQ YIRQGSLSAKPPESEGFGRDLFLKQRMSSLLSQTSSPTDCLFKHIASGNQKEVERLLSQE
 SEG
 lawcB

 SEQ DHDKDTVQKMCHPLCFDDCEKLVSGRLNDPSVVTFFSRDDRGHTPLHVAAVCGQASLID
 SEG
 lawcB

```

SEQ    LLVSKGAMVNATDYHGATPLHLACQKGYQSVTLTLLHLYKASAEVQDNNNGNTPLHLACTYG
SEG    .....
lawcB  .....

SEQ    HEDCVKALVYYDVESCRLDIGNEKGDTPHLIAARWGYQGVIETLLQNGASTEIQNRLKET
SEG    .....
lawcB  .....

SEQ    PLKCALNSKILSVMEAYHLSFERRQKSSEAPVQSPQRSVDSISQESSTSSFSSMSAGSRQ
SEG    .....
lawcB  .....

SEQ    EETKKDYREVEKLLRAVADGDLEMVRYLLEWTEEDLEDAEDTVSAADPEFCHPLCQCPKC
SEG    .....
lawcB  .....

SEQ    APAQKRLAKVPASGLGVNVTSQDGSSPLHVAALHGRADLIRLLKKGANAGARNADQAVP
SEG    .....
lawcB  .....

SEQ    LHLACQQGHFQVVKCLDSNAKPNKKDLSGNTPLIYACSGGHHELVALLLQH GASINASN
SEG    .....
lawcB  .....

SEQ    NKGNTALHEAVIEKHVFVVELLLLHGASVQVLNKRQRTAVDCAEQNSKIMELLQVVPSCV
SEG    .....
lawcB  .....

SEQ    ASLDDVAETDRKEYVTVKIRKKWNSKLYDLPDEPFTRQFYFVHSAGQFKGKTSREIMARD
SEG    .....
lawcB  .....

SEQ    RSVPNLTEGSLHEPGRQSVTLRQNNLPAQSGSHAAEKGNSDWPERPGLTQTGPGRHRRMLR
SEG    .....
lawcB  .....

SEQ    RHTVEDAVVSQGPEAAGPLSTPQEV SASRS
SEG    .....
lawcB  .....

```

Prosites for DKFZphtes3_1817.2

PS00017 945->953 ATP_GTP_A PDOC00017

Pfam for DKFZphtes3_1817.2

```

HMM_NAME      Ank repeat

HMM            *GyTPLHIAARYNNvEMVrllLQHGADIN*
               G+TPLH+AA  ++  +++LL+++GA +N
Query          463  GHTPLHVAAVCGQASLIDLVS KGAMVN      490

32.12 (bits) f: 496 t: 523 Target: dkfzphes3_1817.2 similarity to ankyrins
Alignment to HMM consensus:
Query          *GyTPLHIAARYNNvEMVrllLQHGADIN*
               G TPLH+A++ +  ++  LLL + A+
dkfzphes3      496  GATPLHLACQKGYQSVTLTLLHLYKASAE      523

Query          f: 529 t: 556 Target: dkfzphes3_1817.2 similarity to ankyrins
Alignment to HMM consensus:
HMM            *GyTPLHIAARYNNvEMVrllLQHGADIN*
               G+TPLH+A+ Y+++++V+ L+ +
Query          529  GNTPLHLACTYGHEDCVKALVYYDVESC      556

42.65 (bits) f: 565 t: 592 Target: dkfzphes3_1817.2 similarity to ankyrins
Alignment to HMM consensus:
Query          *GyTPLHIAARYNNvEMVrllLQHGADIN*
               G+TPLHIAAR +  +++  LLQ+GA+
dkfzphes3      565  GDTPLHIAARWGYQGVIETLLQNGASTE      592

Query          f: 744 t: 771 Target: dkfzphes3_1817.2 similarity to ankyrins
Alignment to HMM consensus:
HMM            *GyTPLHIAARYNNvEMVrllLQHGADIN*
               G +PLH+AA  +++  +++RLLL+HGA+
Query          744  GSSPLHVAALHGRADLIRLLKKGANAG      771

```


36.38 (bits) f: 777 t: 804 Target: dkfzptes3_1817.2 similarity to ankyrins

Alignment to HMM consensus:

Query *GyTPLHIAARYNNvEMVrllLLQHGA⁺DIN*
PLH+A++++ ++V+ LL+ +A +N
dkfzptes3 777 QAVPLHLACQGHFQVVKCLLDSNAKPN 804

Query f: 810 t: 837 Target: dkfzptes3_1817.2 similarity to ankyrins

Alignment to HMM consensus:

HMM *GyTPLHIAARYNNvEMVrllLLQHGA⁺DIN*
G+TPL++A+ ++ E+V LLLQHGA+IN
Query 810 GNTPLIYACSGGHHELVALLLQHGA⁺SIN 837

44.62 (bits) f: 843 t: 870 Target: dkfzptes3_1817.2 similarity to ankyrins

Alignment to HMM consensus:

Query *GyTPLHIAARYNNvEMVrllLLQHGA⁺DIN*
G+T+LH A+++ +V +V+LLL HGA++
dkfzptes3 843 GNTALHEAVIEKHVFVVELLLLHGASVQ 870

DKFZphtes3_19f19

group: testes derived

DKFZphtes3_19f19 encodes a novel 254 amino acid protein with weak similarity to *S. cerevisiae* protein YFL046w.

The protein contains a RGD cell attachment site.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to YFL046w

localisation: 3 STS match perfect but HS1292427 matches to chromosome 4

Sequenced by MediGenomix

Locus: /map="405.0/.3 cR from top of Chr11 linkage group"

Insert length: 1395 bp

Poly A stretch at pos. 1367, no polyadenylation signal found

```

1 GGGACCAACGG TGGCGCCTGC GCTGGGAGGT GAGCTTGTGA CAGAGCGAAA
51 ACTACAATTCC CCAGCATTCCT TGTGGTGCCA GAACTACCTT GCCCGAAAAGC
101 CTGTGCGAGA TTTACCCCGT CTTCCGCCTC CCTCCCACCG GAAAACCTCTG
151 AGGACATGAA TAGTCGCCAG GCTTGGCGGC TCTTTCTCTC CCAAGGCAGA
201 GGAGATCGTT GGGTTTCAAG GCCCGCGGG CATTCTCGC CGGCCCTGCG
251 GAGAGAGTTC TTTACTACCA CAACCAAGGA GGGATATGAT AGGCGGCCAG
301 TGGATATAAC TCCTTTAGAA CAAAGGAAAT TAACCTTTGA TACCCATGCA
351 TTGGTTCAGG ACTTGGAAAC TCATGGATTT GACAAAACAC AAGCAGAAAC
401 AATTGTATCA GCGTTAACTG CTTTATCAAA TGTCAGCCTG GATACTATCT
451 ATAAAGAGAT GGTCACTCAA GCTCAACAGG AAATAACAGT ACAACAGCTA
501 ATGGCTCATT TGGATGCTAT CAGGAAAGAC ATGGTCATCC TAGAGAAAAG
551 TGAATTGCA AATCTGAGAG CAGAGAATGA GAAAATGAAA ATTGAATTAG
601 ACCAAGTTAA GCAACAACTA ATGCATGAAA CCAGTCGAAT CAGAGCAGAT
651 AATAAACTGG ATATCAACTT AGAAAGGAGC AGAGTAACAG ATATGTTTAC
701 AGATCAAGAA AAGCAACTTA TGGAAACAAC TACAGAATTT ACAAATAAGG
751 ATACTCAAAC CAAAAGTATT ATTTACAGAG CCAGTAATAA AATTGACGCT
801 GAAATTGCTT CCTTAAAAAC ACTGATGGAA TCTAACAAAC TTGAGACAAT
851 TCGTTATCTT GCAGCTTCGG TGTTCCTTG CCTGGCAATA GCATTGGGAT
901 TTTATAGATT CTGGAAGTAG TATTAATGCT CATCCTGCTG TGGCTGTTGG
951 CTTCTTAGAA CACCAAACCG GGAGAGATTT ACTTTGAACA TTGTCAAGTTG
1001 CAGCAAAAAT TTTACTACCA AGATTATTCG AAGTGTATAC GGAATAAAG
1051 AGGAAGTGTT TTAGAATGAG AAGAGATACT GTGTCTTTAT TGTGTGTGTG
1101 TGAGTGCAGG TGTGTGCTT TATTATATTG AAAAGCTGTC ACTCAGACCT
1151 CGTTTGAGAT AGAAGAGCAT TTTGTCCTTT TGATAGTTAA TAGAAATTGA
1201 ACCAGAGTTT TCTTATGTTT GCTTGAACAG TTGTGTAAAT CATAACAGGAT
1251 TTTGTGGGTA TTGGTTGAAT ATTTGTAAAC CATTCCCTAG CCTACATATT
1301 TATTACTGAA TTAACCTTCC TGATAACCAT TGCATAATTA CATTTTCTTA
1351 TAAATGAAA GATTATTACA ACAAATAAAA AAAAAAATAA AAAAA

```

BLAST Results

Entry HS419346 from database EMBL:

human STS WI-13569.

Score = 2154, P = 8.6e-91, identities = 446/459

Entry HS1292427 from database EMBL:

human STS SHGC-50338.

Score = 1737, P = 7.2e-72, identities = 359/369

Entry HS253344 from database EMBL:

human STS WI-13893.

Score = 1578, P = 1.0e-64, identities = 358/397

Medline entries

No Medline entry

```

1  MNSRQAWRLF  LSQGRGDRWV  SRPRGHFSPA  LRREFFTTT  KEGYDRRPVD
51  ITPLEQRRLT  FDTHALVQDL  ETHGFDKTA  ETIVSALTAL  SNVSLDTIYK
101 EMVTOAQKEI  TVQQLMAHLV  AIRKDMQILE  KESFANLRAE  NEKMKIELDQ
151 VKQQLMHETS  RIRADNKLDI  NLERSVYTM  FTDQEQQLME  TTTEFTKKDT
201 QTKSISETS  NKIDAEIASL  KTLMESNKL  TIRYLAASVF  TCLAIALGFY
251 RWFK

```

BNSDOCID: <WO 0112659A2 I >

Prosites for DKFZphtes3 19f19.3

(No Pfam data available for DKFZphtes3_19f19.3)

DKFZphtes3_19j17

group: testes derived

DKFZphtes3_19j17 encodes a novel 436 amino acid protein with partial similarity to C.elegans Y40B1A.2 protein.

The novel protein contains two Prosite WW/rsp5/WWP domain signatures. The WW domain (or rsp5 or WWP domain) has been originally discovered as a short conserved region in a number of unrelated proteins, such as dystrophin, utrophin, vertebrate YAP protein, mouse NEDD-4 and yeast RSP5. The domain is repeated up to 4 times in some proteins. It has been shown to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. It appears to contain beta-strands grouped around four conserved aromatic positions; generally Trp. The name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to C.elegans Y40B1A.2

there are two long ORFs in this cDNA according to EST:
HS12146/HS75086/AA923755/MMAA17335 remaining intron at Bp 1506-1733

Sequenced by MediGenomix

Locus: unknown

Insert length: 2762 bp
Poly A stretch at pos. 2740, no polyadenylation signal found

```
1 ATTCTCAGCC AAATTTTTTT ATTTTGTGCA GAATCAGTGT GCAAGGTGGT
51 TTATAAGATA ATGGAGTGGT TTTTTTTTGT GTTTAGTGTG ATTGTTATC
101 AGGAGTCTTA TTGTAACGCT TAAGCATTAG GTTTTTTGTG TGAGAACTT
151 TAAAGAGTAA AGCAGAAATTG AAAGTGGAAA TTTTAATTTT GTAAGTTCAT
201 AAAATTTAAT GATAATACAC CAAAGTTTAT GTTTAAATTA GGGAGTTTAA
251 GGTTTCAATT CTTTCTCTTT TTTTTTGGGG GGGTGATGTT TTAAGGCAC
301 TTAAGTATTC ATCGAAGAGT CACCCAGTA GCGGTGATCA CAGACATGAA
351 AAGATGCGAG CGCCGGGAGA TCCTTCACCA CCAATAAAA TGTTGCGGAG
401 ATCTGATAGT CCTGAAAACA AATACAGTGA CAGCACAGGT CACAGTAAGG
451 CCAAAAATGT GCATACTCAC AGAGTTAGAG AGAGGGATGG TGGGACCACT
501 TACTCTCCAC AAGAAAATTC ACACAACCAC AGTGCTCTTC ATAGTTCAAA
551 TTCACATTCT TCTAATCCAA GCAATAACCC AAGCAAACT TCAGATGCAC
601 CTTATGATTC TGCAGATGAC TGGTCTGAGC ATATTAGCTC TTCTGGGAAA
651 AAGTACTACT ACAAATGTTC AACAGAAGTT TCACAATGGG AAAAACCAAA
701 AGAGTGGCTT GAAAGAGAAC AGAGACAAA AGAAGCAAAC AAGATGGCAG
751 TCAACAGCTT CCAAAAAGAT AGGGATTACA GAAGAGAGGT GATGCAAGCA
801 ACAGCCACTA GTGGGTTTGC CAGTGGAATG GAAGACAAGC ATTCCAGTGA
851 TGCCAGTAGT TTGCTCCAC AGAATATTT GTCTCAACA AGCAGACACA
901 ATGACAGAGA CTACAGACTG CCAAGAGCAG AGACTCACAG TAGTTCTACG
951 CCACTACAGC ACCCATCAA ACCAGTGGT CATCCAAGT CTACCCCAAG
1001 CACTGTCTCT TCTAGTCCAT TTACGCTACA GTCTGATCAC CAGCCAAAGA
1051 AATCATTTGA TGCTAATGGA GCATCTACTT TATCAAACT GCCTACACC
1101 ACATCTTCTG TCCCTGCACA GAAAACAGAA AGAAAAGAAT CTACATCAGG
1151 AGACAAACCC GTATCACATT CTGCAACAAC TCCTTCCAG TCTTCTGCCT
1201 CTGGACTGAA CCCCACATCT GCACCTCCAA CATCTGCTTC AGCGGTCCCT
1251 GTTCTCTCTG TTCCACAGTC GCCAATACCT CCCTTACTTC AGGACCCAAA
1301 TCTTCTTAGA CAATTGCTTC CTGCTTTGCA AGCCACGCTG CAGCTTAATA
1351 ATTCTAATGT GGACATATCT AAAATAAATG AAGTTCTTAC AGCAGCTGTG
1401 ACACAAGCCT CACTGCAGTC TATAATTCAT AAGTTTCTTA CTGCTGGACC
1451 ATCTGCTTTC AACATAACGT CTCTGATTTC TCAAGCTGCT CAGTCTCTA
1501 CACAAGATAT CCCTCTTCAT GAAGGTATCC AAATGGAGAG AGATACACAT
1551 AGGAGCAAAT GGAAGTGAA AGGGTCACTT TGTGAGAAAG CTGATAAACA
1601 GCAGGAATGC CTTGTCTGGA ATGGAAGTAT AATGGTGCAA AGACTCTTGC
1651 AACCTCTGG CTAGCCTCAT GAGCAGGAGA CTGCGTGGGA TACCTGGGCC
1701 TAAATGTAGA ATAGAAAGA AGAAATAAGG ATGCCCAGCC ATCTAATCAG
1751 TCTCCGATGT CTTTAACATC TGATGCGTCA TCCCCAAGAT CATATGTTTC
1801 TCCAAGAATA AGCACACCTC AAACATAACAC AGTCCCTATC AAACCTTTGA
1851 TCAGTACTCC TCTGTTTCA TCACAGCCAA AGGTTAGTAC TCCAGTAGTT
1901 AAGCAAGGAC CAGTGTCA CA GTCAGCCACA CAGCAGCCTG TAACTGCTGA
1951 CAAGCAGCAA GGTTCATGAAC CTGTCTCTCC TCGAAGTCTT CAGCGCTCAA
2001 GCCAGAGAAG TCCATCACCT GGTCCCAATC ATACTTCTAA TAGTAGTAAT
2051 GCATCAAAATG CAACAGTTGT ACCACAGAAT TCTTCTGCCC GATCCACGTG
```

```

2101 TTCATTAACG CCTGCACTAG CAGCACACTT CAGTGAAAAT CTCATAAAAC
2151 ACGTTCAAGG ATGGCCTGCA GATCATGCAG AGAAGCAGGC ATCAAGATTA
2201 CGCGAAGAAG CGCATAACAT GGGAACTATT CACATGTCCG AAATTTGTAC
2251 TGAATTAAAA AATTTAAGAT CTTTAGTCCG AGTATGTGAA ATTCAAGCAA
2301 CTTTGCGAGA GCAAAGGATA CTATTTTGA GACAACAAAT TAAGGAACTT
2351 GAAAAGCTAA AAAATCAGAA TTCCTTCATG GTGTGAAGAT GTGAATAATT
2401 GCACATGGTT TTGAGAACAG GAACTGTAAA TCTGTTGCC AATCTTAACA
2451 TTTTGTAGCT GCATTTAAGT AGACTTTGGA CCGTTAAGCT GGGCAAAGGA
2501 AATGACAAGG GGACGGGGTC TGTGAGAGTC AATTCAGGGG AAAGATACAA
2551 GATTGATTTG TAAAACCCCTT GAAATGTAGA TTTCTTGTAG ATGTATCCTT
2601 CACGTTGTAA ATATGTTTGT TAGAGTGAAG CCATGGGAAG CCATGTGTAA
2651 CAGAGCTTAG ACATCCAAAA CTAATCAATG CTGAGGTGGC TAAATACCTA
2701 GCCTTTTACA TGTAACCTG TCTGCAAAAT TAGCTTTTTC AAAAAAAAAA
2751 AAAAAAAAAA AA

```

BLAST Results

Entry AC005876 from database EMBLNEW:
Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1,
complete sequence.
Score = 2130, P = 0.0e+00, identities = 426/426
12 exons matching Bp 492-2740

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 1757 bp to 2383 bp; peptide length: 209
Category: questionable ORF
Classification: no clue

```

1 MSLTSDASSP RSYVSPRIST PQTNTVPIKP LISTPPVSSQ PKVSTPVVKQ
51 GPVSQSATQQ PVTADKQOGH EPVSPRSLQR SSQRSPSPGP NHTSNSSNAS
101 NATVVPQNSS ARSTCSLTPA LAAHFSENLI KHVQGWPAH AEKQASRLRE
151 EAHNMGTIHM SEICTELKNL RSLVRVCEIQ ATLREQRILF LRQIQIKELEK
201 LKNQNSFMV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_19j17, frame 2

No Alert BLASTP hits found

Peptide information for frame 3

ORF from 354 bp to 1661 bp; peptide length: 436
Category: similarity to unknown protein
Classification: unclassified
Prosite motifs: WW_DOMAIN_1 (90-116)
WW_DOMAIN_1 (90-116)

```

1 MRDAGDPSP NKMLRRSDSP ENKYSdstGH SKAKNVHTHR VRERDGGTSY
51 SPQENSHNHS ALHSSNSHSS NPSNNPSKTS DAPYDSADDW SEHSSSGKK
101 YYNCRTEVS QWEKPKEWLE REQRQKEANK MAVNSEPKDR DYRREVMQAT
151 ATSGFASGME DKHSSDASSL LPQNILSQTs RHNDRDYRLP RAETHSSSTP
201 VQHPKPKPVVH PTATPSTVPS SPFTLQSDHQ PKKSFdANGA STLSKLPTPT
251 SSVPAQKTER KESTSGDKPV SHSCTTPSTS SASGLNPTSA PPTSASAVPV
301 SPVPSPIPP LLQDPNLLRQ LLPALQATLQ LNNSNVDISK INEVLTAATV
351 QASLQSIHK FLTAGPSAFN ITSLISQAAQ LSTQDIPLHE GIQMERDTHR
401 SKWEVKGSLC QKADKQOECL VWNGSIMVQR LLQPSG

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_19j17, frame 3

TREMBL:CEY40B1A_2 gene: "Y40B1A.2"; Caenorhabditis elegans cosmid Y40B1A, N = 1, Score = 144, P = 1.8e-09

>TREMBL:CEY40B1A_2 gene: "Y40B1A.2"; Caenorhabditis elegans cosmid Y40B1A
Length = 120

HSPs:

Score = 144 (21.6 bits), Expect = 1.8e-09, P = 1.8e-09
Identities = 30/67 (44%), Positives = 43/67 (64%)

Query: 90 WSEHISSSGKYYNCRTEVSQWEKPKEW-LEREQRQKEANKMAVNSFPK---DRDYRRE 145
W+E +SSSGK YYYN +TE+SQW+KP EW E +++ K VN P+ DR Y
Sbjct: 11 WTEQMSSSGKMYYNKKTEISQWDKPAEWPAEGGSAERDKPKGGVNEKPRFAEDR-YNEY 69

Query: 146 VMQATATS 153
+ Q +++S
Sbjct: 70 IGQLSSSS 77

Pedant information for DKFZphtes3_19j17, frame 2

Report for DKFZphtes3_19j17.2

[LENGTH] 209
[MW] 22873.85
[pI] 9.95
[KW] All_Alpha
[KW] LOW_COMPLEXITY 13.40 %

SEQ MSLTSDASSPRSYVSPRISTPQTNTVPIKPLISTPPVSSQPKVSTPVVKQGPVSQSATQQ
SEG
PRD ccc

SEQ PVTADKQQGHEPVSPRSLQRSSQSPSPGPNHTSNSSNASNATVVPQNSSARSTCSLTPA
SEGxx.....
PRD cchh

SEQ LAAHFSENLIKHVQGWPADHAEQASRLREEAHNMGTIHMSEICTELKNLRS LRVVCEIQ
SEG
PRD hhhhhhhcchhhhhccccchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhh

SEQ ATLREQRILFLRQQIKELEKLKNQNSFMV
SEG
PRD hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccc

(No Prosite data available for DKFZphtes3_19j17.2)

(No Pfam data available for DKFZphtes3_19j17.2)

Pedant information for DKFZphtes3_19j17, frame 3

Report for DKFZphtes3_19j17.3

[LENGTH] 436
[MW] 47716.62
[pI] 8.71
[HOMOL] TREMBL:CEY40B1A_2 gene: "Y40B1A.2"; Caenorhabditis elegans cosmid Y40B1A 6e-08

[FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YKL012w] 2e-04
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKL012w] 2e-04
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YPR152c] 6e-04
[BLOCKS] BL01159 WW/rsp5/WWP domain proteins
[PROSITE] WW DOMAIN 1 2
[PFAM] WW/rsp5/WWP domain containing proteins
[KW] All_Alpha
[KW] LOW_COMPLEXITY 22.48 %

```

SEQ      MRDAGDPSPPNKMLRRSDSPENKYSdstghsKAKNVHthrvRERDGGTSYSPOENSHNHS
SEG      .....XXXXXXXX
PRD      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ      ALHSSNSHSSNPSPNPKSTSDAPYDSADDWSEHISSSGKKYYNCRTEVSQWEKPKEWLE
SEG      XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHH

SEQ      REQRQKEANKMAVNSFPKDRDYRREVQATATSGFASGMEDKHSSDASSLLPQNILSQTs
SEG      .....
PRD      hhhhhhhhhhhhhccccccccchhhhhhhhhhhcccccccccccccccccccccccccc

SEQ      RHNDRDYRLPRAETHSSSTPVQHPIKPVVHPTATPSTVPSSPFTLQSDHQPKKSFdANGA
SEG      .....XXXXXXXXXXXXXXXXXXXX
PRD      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ      STLskLPTPTSSVPAQKTERKESTSGDKPVSHSCTTPSTSSASGLNPTSAPPTSASAVPV
SEG      XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ      SPVPQSPiPPLLQDPNLLRQLLPALQATLQLNNSNVDISKINEVLTAAVTQASLQSIHK
SEG      XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD      CCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

SEQ      FLTAGPSAFNITSLISQAAQLSTQDIPLHEGIQMERDTHRSKWEVKGSLCQKADKQQECL
SEG      .....
PRD      hhccccccceehhhhhhhhhhhccccccccccccccccccccccccceehhhhhhhhhccee

SEQ      VWNGSIMVQRLLQPSG
SEG      .....
PRD      eeccchhhhhhhcccc

```

Prosites for DKFZphtes3_19j17.3

PS01159	90->116	WW_DOMAIN_1	PDOC50020
PS01159	90->116	WW_DOMAIN_1	PDOC50020

Pfam for DKFZphtes3_19j17.3

HMM_NAME	WW/rsp5/WWP domain containing proteins		
HMM	*LPsGWEeHWDpsGRpWYYWNHETkTTQWEpP*		
	+ ++W EH++ SG+ YY+N T+ +QWE+P		
Query	86	SADDWSEHISSSGKK-YYNCRTEVSQWEK	115

DKFZphtes3_lcl

group: signal transduction

DKFZphtes3_lcl encodes a novel 632 amino acid putative GTPase-activating protein, related to drosophila rotund transcript and human n-chimaerin.

rac small GTPase is associated with type-I phosphatidylinositol 4-phosphate 5-kinase and regulating the production of phosphatidylinositol 4,5-bisphosphate. The new protein is expected to activate p21rac-related small GTPases.

The new protein can find application in modulating/blocking the response to a cellular receptor.

similarity to GTPase-activating proteins

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 3237 bp

Poly A stretch at pos. 3227, no polyadenylation signal found

```
1  GCGAAGTGAA  GGGTGGCCCA  GGTGGGGCCA  GGCTGACTGA  ATGTATCTCC
51  TAGCTATGGA  CTAAATAATA  CATGGGGGGA  AATAAACAAG  TATTCATGAG
101 GGTGAAATG   TGACCCAGCA  GGAAAATTAC  AACTATTTTC  AATTGACGTT
151 GAATAGGATG  AGTCATGGAA  TTAAAGTGAT  TTACTGAAGA  TTATACTACT
201 GGATAGATAGA  AGAGCTAAAG  AAAGATGGAT  ACTATGATGC  TGAATGTGCG
251 GAATCTGTCT  GAGCAGCTTG  TGGCGCGGGT  GGAGATTCTC  AGTGAAGGAA
301 ATGAAGTGCA  ATTTATCCAG  TTGGCGAAGG  ACTTTGAGGA  TTTCCGTAAA
351 AAGTGGCAGA  GGACTGACCA  TGAGCTGGGG  AAATACAAGG  ATCTTTTGAT
401 GAAAGCAGAG  ACTGAGCGAA  GTGCTCTGGA  TGTTAAGCTG  AAGCATGCAC
451 GTAATCAGGT  GGATGTAGAG  ATCAAACGGA  GACAGAGAGC  TGAGGCTGAC
501 TGGCAAAAGC  TGGAAACGACA  GATTCAAGCTG  ATTCGAGAGA  TGCTCATGTG
551 TGACACATCT  GGCAGCATTC  AACTAAGCGA  GGAGCAAAA  TCAGCTCTGG
601 CTTTTCTCAA  CAGAGGCCAA  CCATCCAGCA  GCAATGCTGG  GAACAAAAGA
651 CTATCAACCA  TTGATGAATC  TGGTTCCATT  TTATCAGATA  TCAGCTTTGA
701 CAAGACTGAT  GAATCACTGG  ATTGGGACTC  TTCTTTGGTG  AAGACTTTCA
751 AACTGAAGAA  GAGAGAAAAG  AGGCGCTCTA  CTAGCCGACA  GTTTGTTGAT
801 GGTCCCCCTG  GACCTGTAAA  GAAAACTCGT  TCCATTGGCT  CTGCAGTAGA
851 CCAGGGGAAT  GAATCCATAG  TTGCAAAAC  TACAGTGACT  GTTCCCAATG
901 ATGGCGGGCC  CATCGAAGCT  GTGTCCACTA  TTGAGACTGT  GCCATATTGG
951 ACCAGGAGCC  GAAGGAAAAC  AGGTACTTTA  CAACCTTGGA  ACAGTGACTC
1001 CACCCTGAAC  AGCAGGCAGC  TGGAGCCAAG  AACTGAGACA  GACAGTGTGG
1051 GCACGCCACA  GAGTAATGGA  GGGATGCGCC  TGCATGACTT  TGTCTCTAAG
1101 ACGGTTATTA  AACCTGAATC  CTGTGTTCCA  TGTGGAAAGC  GGATAAAATT
1151 TGGCAAAATTA  TCTCTGAAGT  GTCGAGACTG  TCGTGTGGTG  TCTCATCCAG
1201 AATGTCGGGA  CCGCTGTCCC  CTTCCCTGCA  TTCCTACCCT  GATAGGAACA
1251 CCTGTCAAGA  TTGGAGAGGG  AATGCTGGCA  GACTTTGTGT  CCCAGACTTC
1301 TCCAATGATC  CCTCCATTG  TTGTGCATTG  TGTAATGAG  ATTGAGCAAA
1351 GAGGTCTGAC  TGAGACAGGC  CTGTATAGGA  TCTCTGGCTG  TGACCGCACA
1401 GTAAAGAGAG  TGAAAGAGAA  ATTCCCTCAG  GTGAAACTG  TACCCCTCCT
1451 CAGCAAAGTG  GATGATATCC  ATGCTATCTG  TAGCCTTCTA  AAAGACTTTC
1501 TTCGAAACCT  CAAAGAACCT  CTTCTGACCT  TTCGCCTTAA  CAGAGCCTTT
1551 ATGGAAGCAG  CAGAAATCAC  AGATGAAGAC  AACAGCATAG  CTGCCATGTA
1601 CCAAGCTGTT  GGTGAACCTG  CCCAGGCCAA  CAGGGACACA  TTAGCTTTCC
1651 TCATGATTCA  CTTGCAGAGA  GTGGCTCAGA  GTCCACATAC  TAAAATGGAT
1701 GTTGCCAATC  TGGCTAAAGT  CTTTGGCCCT  ACAATAGTGG  CCCATGCTGT
1751 GCCCAATCCA  GACCCAGTGA  CAATGTTACA  GGACATCAAG  CGTCAACCCA
1801 AGGTGGTTGA  GCGCCTGCTT  TCCTTGCCCT  TGGAGTATTG  GAGTCAGTTC
1851 ATGATGGTGG  AGCAAGAGAA  CATTGACCCC  CTACATGTCA  TTGAAAACCT
1901 AAATGCCTTT  TCAACACCAC  AGACACCAGA  TATTAAGTGA  AGTTTACTGG
1951 GACCTGTGAC  CACTCCTGAA  CATCAGCTTC  TCAAGACTCC  TTCATCTAGT
2001 TCCCTGTCAC  AGAGAGTCCG  TTCCACCCTC  ACCAAGAACA  CTCCTAGATT
2051 TGGGAGCAAA  AGCAAGTCTG  CCACTAACCT  AGGACGACAA  GGCAACTTTT
2101 TTGCTTCTCC  AATGCTCAAG  TGAAGTCACA  TCTGCCTGTT  ACTTCCCAGC
2151 ATTGACTGAC  TATAAGAAAG  GACACATCTG  TACTCTGCTC  TGCAGCCTCC
2201 TGTACTCTAT  ACTACTTTTA  GCATTCTCCA  GGCTTTTACT  CAAGTTTAAT
2251 TGTGCATGAG  GGTTTTATTA  AAATATATA  TATCTCCCTT  TCCTTCTCCT
2301 CAAGTCACAT  AATATCAGCA  CTTTCTGCTG  GTCATTGTTG  CGAGCTTTTA
2351 GATGAGACAT  CTTTCCAGGG  GTAGAAGGGT  TAGTATGGAA  TTGGTTGTGA
2401 TTCTTTTGG  GGAAGGGGGT  TATTGTTTCT  TTGGCTTAAA  GCCAAATGCT
2451 GCTCATAGAA  TGATCTTTCT  CTAGTTTCAT  TTAGAAGTGA  TTTCCGTGAG
2501 ACAATGACAG  AAACCTTACC  TATCTGATAA  GATTAGCTTG  TCTCAGGGTG
2551 GGAAGTGGGA  GGGCAGGGCA  AAGAAAGGAT  TAGACCAGAG  GATTTAGGAT
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```

2601 GCCTCCTTCT AAGAACCAGA AGTTCTCATT CCGGATTATG AACTGAGCTA
2651 TAATATGGAG CTTTCATAAA AATGGGATGC ATTGAGGACA GAACTAGTGA
2701 TGGGAGTATG CGTAGCTTTG ATTTGGATGA TTAGGTCTTT AATAGTGTG
2751 AGTGGCACAA CCTTGTAAT GTGAAAGTAC AACTCGTATT TATCTCTGAT
2801 GTGCCGCTGG CTGAACCTTG GGTTCATTG GGGTCAAAGC CAGTTTTTCT
2851 TTTAAATTG AATTCATTCT GATGCTTGGC CCCCATACCC CCAACCTTGT
2901 CCAGTGGAGC CCAACTTCTA AAGGTCAATA TATCATCCTT TGGCATCCCA
2951 ACTAACAAATA AAGAGTAGGC TATAAGGGAA GATTGTCAAT ATTTTGTGGT
3001 AAGAAAAGCT ACAGTCATTT TTTCTTTGCA CTTTGGATGC TGAAATTTT
3051 CCCATGGAAC ATAGCCACAT CTAGATAGAT GTGAGCTTT TCTTCTGTTA
3101 AAATTATTCT TAATGTCTGT AAAAACGATT TTCTTCTGTA GAATGTTTGA
3151 CTTCTGATTG ACCCTTATCT GTAAACACC TATTTGGGAT AATATTTGGA
3201 AAAAAAGTAA ATAGCTTTT CAAAATGAAA AAAAAA

```

BLAST Results

Entry U82984 from database EMBLEST:
Homo sapiens DRES 56 mRNA sequence.
Score = 8775, P = 0.0e+00, identities = 1757/1758
matches 3' end

Medline entries

93074974:
Developmental regulation and neuronal expression of the mRNA of rat
n-chimaerin, a
p21rac GAP:cDNA sequence.

93024458:
A Drosophila rotund transcript expressed during spermatogenesis and
imaginal disc
morphogenesis encodes a protein which is similar to human Rac
GTPase-activating
(racGAP) proteins.

Peptide information for frame 3

ORF from 225 bp to 2120 bp; peptide length: 632
Category: similarity to known protein

```

1 MDTMMLNVRN LFEQLVRRVE ILSEGNEVQF IQLAKDFEDF RKKWQRTDHE
51 LGKYKDLLMK AETERSALDV KLKHARNQVD VEIKRRQRAE ADCEKLERQI
101 QLIREMLMCD TSGSIQLSEE QKSALAFLNR GQSSSNAGN KRLSTIDEG
151 SILSDISFDK TDESLOWDSS LVKTFKLKKR EKRRSTSRQF VDGPPGPVKK
201 TRSIGSAVDQ GNEIVAKTT VTPNDGGPI EAVSTIETVP YWTRSRRKTG
251 TLQPWNDSST LNSRQLEPRT ETDSVGTPOS NGGMLRHDFV SKTVIKPESC
301 VPCGKRIKFG KLSLKCRDCR VVSHPECRDR CPLPCIPTLI GTPVKIGEGM
351 LADFVSQTSP MIPSIVVHCV NEIEQRGLTE TGLYRISGCD RTVKELKEKF
401 LRVKTVPLLS KVDDIHAICS LLKDFLRNLK EPLLTFRNLN AFMEAAEITD
451 EDNSIAAMYQ AVGELPQANR DTLAFLMIHL QRVAQSPHTK MDVANLAKVF
501 GPTIVAHAVP NPDVPTMLQD IKRQPKVVER LLSLPLEYWS QFMMVEQENI
551 DPLHVIENSN AFSTPQTPDI KVSLLGPVTT PEHQLLKTPS SSSLSQVRVS
601 TLTKNTPREFG SKSKSATNLG RQGNFFASPM LK

```

BLASTP hits

Entry CEK08E3_4 from database TREMBLNEW:
gene: "K08E3.6"; Caenorhabditis elegans cosmid K08E3
Score = 452, P = 2.6e-48, identities = 126/377, positives = 189/377

Entry A48122 from database PIR:
GTPase-activating protein Rac homolog, splice form clone pcl.7 - fruit
fly (Drosophila melanogaster) (fragment)
Score = 480, P = 9.2e-46, identities = 111/270, positives = 155/270

Entry B48122 from database PIR:
GTPase-activating protein Rac homolog, splice form clone pcl.7d - fruit
fly (Drosophila melanogaster)
Score = 480, P = 9.2e-46, identities = 111/270, positives = 155/270

Entry DM22539_1 from database TREMBL:
 gene: "rotund"; product: "rnracGAP"; *Drosophila melanogaster* rnracGAP
 (rotund) gene, complete cds.
 Score = 480, P = 9.2e-46, identities = 111/270, positives = 155/270

Entry S29128 from database PIR:
 N-chimerin - rat
 Score = 336, P = 8.8e-30, identities = 86/253, positives = 128/253

Alert BLASTP hits for DKFZphtes3_lcl, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_lcl, frame 3

Report for DKFZphtes3_lcl.3

[LENGTH] 632
 [MW] 71026.84
 [pI] 9.08
 [HOMOL] PIR:B48122 GTPase-activating protein Rac homolog, splice form clone pcl.7d -
 fruit fly (*Drosophila melanogaster*) 2e-46
 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YBR260c] 3e-12
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YER155c] 2e-11
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YER155c] 2e-11
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YER155c]
 2e-11
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDL240w] 3e-09
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YOR134w] 4e-09
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YOR134w] 4e-09
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins
 [S. cerevisiae, YOR127w] 5e-09
 [FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae, YPL115c] 3e-08
 [FUNCAT] 10.02.09 regulation of g-protein activity [S. cerevisiae, YPL115c] 3e-08
 [BLOCKS] BL00479B Phorbol esters / diacylglycerol binding domain proteins
 [BLOCKS] BL00479A Phorbol esters / diacylglycerol binding domain proteins
 [SCOP] dlpba_1.83.1.1.2 p85 alpha subunit RhoGAP domain [human (Homo sapiens)] 1e-55
 [SCOP] dlrgp_1.83.1.1.1 p50 RhoGAP domain [human (Homo sapiens)] 1e-49
 [PIRKW] breakpoint cluster region 1e-19
 [PIRKW] transmembrane protein 7e-08
 [PIRKW] brain 3e-22
 [PIRKW] alternative splicing 1e-19
 [PIRKW] P-loop 2e-25
 [SUPFAM] CDC24 homology 3e-22
 [SUPFAM] bcr protein 3e-22
 [SUPFAM] myosin motor domain homology 2e-25
 [SUPFAM] pleckstrin repeat homology 4e-10
 [SUPFAM] LIM metal-binding repeat homology 2e-09
 [SUPFAM] protein kinase C zinc-binding repeat homology 5e-29
 [PROSITE] MYRISTYL 6
 [PROSITE] AMIDATION 1
 [PROSITE] CAMP_PHOSPHO_SITE 3
 [PROSITE] CK2_PHOSPHO_SITE 13
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 9
 [PROSITE] ASN_GLYCOSYLATION 1
 [PROSITE] DAG_PE_BINDING_DOMAIN 1
 [PFAM] Phorbol esters / diacylglycerol binding domain
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 2.22 %
 [KW] COILED_COIL 8.54 %

SEQ MDTMMLNVRNLFQVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELKGYKDLLMK
 SEG
 COILSCCCCCCCCCCCC
 lrqp-
 SEQ AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE
 SEG
 COILS CC
 lrqp-
 SEQ QKSALAFNLNRGPSSSNAGNKRSLTIDESGSILSDISFDKTDSESLDWSSSLVKTFLKRR
 SEG
 COILS

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lrgp- .....
SEQ      EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDDGGPIEAVSTIETVP
SEG      .....
COILS    .....
lrgp- .....

SEQ      YWTRSRRKGTGLQPWNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC
SEG      .....
COILS    .....
lrgp- .....

SEQ      VPCGKRIKFGKLSLKCRCRVSHPEDCRCLPCIPTLIGTPVKIGEGMLADFSQTSF
SEG      .....
COILS    .....
lrgp- .....

SEQ      MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
SEG      .....
COILS    .....
lrgp-    .CCHHHHHHHHHHHHHHTTTTTTTTCCCHHHHHHHHHHHHHCCCCCG-GGCCCCHHHHH

SEQ      LLKDFLRNLKEPLLTFRNLRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMLIHL
SEG      .....
COILS    .....
lrgp-    HHHHHHHHTTTTTTTGGGHHHHHHHTTTT-CGGGHHHHHHHHHHHCCCHHHHHHHHHHHHH

SEQ      QRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMLQDIKRPKVVERLLSLPLEYWS
SEG      .....
COILS    .....
lrgp-    HHHHHHHHHCCCHHHHHHHHGGGCC.....

SEQ      QFMMVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTSPSSSSLSQRVRS
SEG      .....
COILS    .....
lrgp-    .....

SEQ      TLTKNTPRFGSKSKSATNLGRQGNFFASPMK
SEG      xxx.....
COILS    .....
lrgp-    .....

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Prosites for DKFZphtes3_lcl.3

PS00001	212->216	ASN_GLYCOSYLATION	PDOC00001
PS00004	141->145	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	182->186	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	246->250	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	63->66	PKC_PHOSPHO_SITE	PDOC00005
PS00005	174->177	PKC_PHOSPHO_SITE	PDOC00005
PS00005	186->189	PKC_PHOSPHO_SITE	PDOC00005
PS00005	245->248	PKC_PHOSPHO_SITE	PDOC00005
PS00005	313->316	PKC_PHOSPHO_SITE	PDOC00005
PS00005	392->395	PKC_PHOSPHO_SITE	PDOC00005
PS00005	435->438	PKC_PHOSPHO_SITE	PDOC00005
PS00005	595->598	PKC_PHOSPHO_SITE	PDOC00005
PS00005	606->609	PKC_PHOSPHO_SITE	PDOC00005
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	66->70	CK2_PHOSPHO_SITE	PDOC00006
PS00006	144->148	CK2_PHOSPHO_SITE	PDOC00006
PS00006	206->210	CK2_PHOSPHO_SITE	PDOC00006
PS00006	234->238	CK2_PHOSPHO_SITE	PDOC00006
PS00006	270->274	CK2_PHOSPHO_SITE	PDOC00006
PS00006	323->327	CK2_PHOSPHO_SITE	PDOC00006
PS00006	387->391	CK2_PHOSPHO_SITE	PDOC00006
PS00006	392->396	CK2_PHOSPHO_SITE	PDOC00006
PS00006	410->414	CK2_PHOSPHO_SITE	PDOC00006
PS00006	449->453	CK2_PHOSPHO_SITE	PDOC00006
PS00006	489->493	CK2_PHOSPHO_SITE	PDOC00006
PS00006	579->583	CK2_PHOSPHO_SITE	PDOC00006
PS00007	46->55	TYR_PHOSPHO_SITE	PDOC00007
PS00007	376->385	TYR_PHOSPHO_SITE	PDOC00007
PS00008	131->137	MYRISTYL	PDOC00008
PS00008	150->156	MYRISTYL	PDOC00008
PS00008	276->282	MYRISTYL	PDOC00008
PS00008	377->383	MYRISTYL	PDOC00008
PS00008	388->394	MYRISTYL	PDOC00008
PS00008	623->629	MYRISTYL	PDOC00008
PS00009	303->307	AMIDATION	PDOC00009

PS00479 287->336 DAG_PE_BINDING_DOMAIN PDOC00379

Pfam for DKFZphtes3_1c1.3

HMM_NAME	Phorbol esters / diacylglycerol binding domain		
HMM	*HrFmrHTFrqPTWCDHCgeFIWGWgKQGYQCQnCgMNCHKRCHelVPmm		
	H+F+ +T + P +C CG +I +GK ++C +C+++ H +C+ + P		
Query	287	HDFVSKTVIKPESCVPCGKRI-KFGKLSLKCRDCRVVSHPECRDRCPLP	334
HMM		C*	
		C	
Query	335	C	335

DKFZphtes3_lgl3

group: intracellular transport and trafficking

DKFZp DKFZphtes3_lgl3 encodes a novel 1007 amino acid protein with similarity to human 256 kD golgin.

The new protein contains 7 leucine zippers and seems to be involved in protein-protein-interaction in the golgi apparatus. The very similar rat cpl51 shows haploid-specific transcription in mus musculus testis.

The new protein can find application in modulating protein traffic in the golgi apparatus, especially in human haploid germ cells.

similarity to 256 kD golgi, strong similarity to rat "cpl51"

21 exons encoded on AC004682

EST from a testis library, two mouse ESTs of a testis cDNA library, rat cpl51 shows haploid-specific transcription!
testis or haploid-specific transcription

Sequenced by DKF2

Locus: map="16q22.2"

Insert length: 3405 bp

Poly A stretch at pos. 3394, polyadenylation signal at pos. 3373

```

1 GGGATAGGGG ATGTGGTTTG TTACAAAGGA TGAGTATTTT GATAGCTTCT
51 CATTCTTGA ACTATTCTGC AGGTTTATAA CAAAGCTCAG AAAATACTAA
101 AGGTTAAAGG AGAATTGAGA GCTGCCAAGG AAATGAAAGA TGAGGCGGGG
151 GAGAGAGACA GAGAAGTGAG CAGCCTGAAC AGCAAGCTGT TAAGCCTGCA
201 ACTTGACATC AAGAATCTGC ACGATGTCTG CAAGAGACAG AGGAAGACCT
251 TGCAGGACAA TCAGCTCTGC ATGGAGGAGG CAATGAACAG CAGCCACGAC
301 AAGAAGCAAG CACAGGCATT AGCATTGAGG GAGTCAGAGG TGGAAATTTGG
351 GTCCAGTAAA CAGTGTCTATC TGAGACAACCT CCAGCAACTG AAGAAAAAAT
401 TGCTGGTCTT TCAACAAGAA CTGGAGTTTC ACACAGAGGA GTTGCAGACT
451 TCTTACTATT CTCTCCGCCA GTATCAGTCC ATCTAGAGAG AGCAGACTTC
501 CGACCTGGTT CTCTGCACCC ATCACTGCAA ACTGAAAGAA GATGAGGTGA
551 TTCTCTATGA GGAGGAAATG GGAAATCACA ACGAGAACAC AGGGGAGAAG
601 CTCCATTTGG CGCAGGAGCA ACTCGCCTTG GCCGGGGACA AGATCGCCTC
651 TCTAGAGAGG AGCTTAAACC TCTACAGGGA TAAATACCAG TCTTCCCTGA
701 GCAACATCGA GTTACTAGAA TGCCAAGTGA AGATGTTGCA GGGGGAACCTC
751 GGCGGGATCA TGGGTCAGGA GCCTGAGAAC AAGGGTGATC ATTCAAAGGT
801 ACGGATATAC ACTTCTCCTT GCATGATTCA AGAGCATCAG GAGACTCAGA
851 AACGACTGTC TGAAGTCTGG CAAAAGGTCT CTCAACAGGA TGATCTCATT
901 CAAGAAGTTC GAAATAAGCT GGCCTGCAGT AACGCTTTGG TTCTGGAGCG
951 TGAAAAGGCT TGTATAAACC TACAAGCCGA TTTTGCTTCC TGTACAGCCA
1001 CCCACAGATA CCTCCTAGC TCCTCAGAAG AGTGTGAAGA CATCAAAAAG
1051 ATACTGAAGC ACTTGCAGGA GCAGAAAGAC AGCCAGTGCC TGCATGTGGA
1101 GGAGTACCCAG AACCTGGTGA AGGATCTGCG CGTGGAACCTA GAGGCCGTGT
1151 CGGAACAGAA GAGAAACATC ATGAAGGACA TGATGAAGCT GGAGCTGGAC
1201 CTGCACGGAC TGCGGGAGGA GACATCTGCC CACATTGAGA GGAAGGATAA
1251 GGACATCACC ATCTTGCACT GCCGGCTGCA GGAGCTGCAG CTGGAGTTCA
1301 CCGAGACCCA AAAGCTCACT TTGAAGAAAG ACAAGTTTCT CCAAGAGAAA
1351 GATGAGATGC TGCAAGAGCT GGAGAAGAAA CTGACACAGG TTCAGAACAG
1401 CCTCTGAAA AAGGAGAAGG AGCTGGAGAA GCAGCAGTGC ATGGCCACAG
1451 AACTTGAAT GACAGTCAAG GAGGCTAAGC AGGACAAGTC CAAGGAGGCG
1501 GAGTGCAAGG CCCTGCAGGC TGAGGTCCAG AAGCTGAAGA ACAGTCTCGA
1551 AGAGGCCAAG CAGCAGGAGA GGCTGGCTGC TCAGCAAGCA GCCCAGTGCA
1601 AAGAAGAGGC TGCACTGGCA GGCTGTCACT TGGAGGACAC CCAGAGGAAA
1651 CTGAGAAGG GTCTCTCCTT GGACAAGCAG AAGGCAGACA CCATCCAGGA
1701 ACTACAGAGA GAACTTCAGA TGCTGCAGAA GGAGTCTCTG ATGGCTGAGA
1751 AGGAACAAC CTCCAACAGA AAACGGGTGG AGGAGCTGTC ATTAGAACTC
1801 TCTGAAGCCC TGAGGAAGCT TGAAAATTCA GACAAGGAAA AGAGGCAGCT
1851 TCAGAAGACA GTGGCTGAGC AGGATATGAA AATGAATGAC ATGCTTGATC
1901 GTATCAAGCA CCAGCACAGG GAGCAAGGCT CCATCAAATG CAAGTTAGAA
1951 GAAGATCTTC AGGAGGCCAC AAAGCTTCTG GAGGACAAAC GGGAGCAGTT
2001 GAAGAAGAGC AAAGAGCATG AGAAGCTGAT GGAGGGAGAA CTTGAAGCTT
2051 TGCGGCAGGA ATTTAAAAAG AAAGACAAGA CGTTGAAAGA GAATTCAGGA
2101 AAGTTGAGG AAGAAAATGA GAATCTCCGA GCAGAGCTAC AGTGTGTGTC
2151 TACACAACCT GAATCTCTCT TCAACAAATA CAACACCAGC CAGCAAGTCA
2201 TCCAAGACTT GAATAAAGAG ATAGCCCTTC AGAAGGAGTC CTTAATGAGC
2251 CTGACAGCCC AGCTGGACAA AGCTCTGCAG AAGGAGAAGC ACTATCTCCA
2301 GACTACCATC ACCAAAGAAG CCTATGATGC ATTATCCCGG AAGTCAGCCG
2351 CCTGCCAGGA TGACCTGACA CAAGCCCTCG AGAAGCTCAA TCACGTGACC
2401 TCAGAGACAA AGAGCCTGCA GCAAAGCTTG ACACAGACCC AAGAGAAGAA

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2451 AGCTCAGCTG GAAGAGGAAA TCATTGCTTA TGAGGAAAGG ATGAAAAAGC
2501 TCAATACGGA ATTAAGAAAA CTGCGGGGCT TCCACCAGGA GAGTGAGCTG
2551 GAGGTGCACG CCTTTGACAA GAAGCTAGAG GAGATGAGCT GCCAGGTGCT
2601 GCAGTGGCAG AAGCAACACC AGAATGACCT CAAGATGCTG GCAGCCAAAG
2651 AGGAGCAGCT CAGGGAGTTC CAGGAGGAGA TGGCCGCCCT AAAAGAGAAC
2701 CTCCTTGAGG ACGATAAGGA GCCCTGCTGC CTGCCCCAGT GGTCTGTGCC
2751 CAAAGACACC TGTAGGCTCT ACCGAGGGAA TGATCAGATT ATGACCAACT
2801 TGGAGCAATG GGCAAAACAG CAGAAGGTCG CCAATGAGAA ACTAGGAAAC
2851 CAGCTCCGAG AGCAGGTGAA CTACATTGCC AAGCTGAGTG GCGAAAAGGA
2901 CCACCTCCAC AGTGTAAATGG TCCACTTGCA GCAGGAAAAC AAGAAGCTGA
2951 AGAAGGAGAT AGAAGAGAAG AAGATGAAAG CCGAGAACAC AAGGCTATGC
3001 ACCAAAGCCC TAGGCCCAG CAGAACGGAG TCCACACAGA GGGAGAAAGT
3051 GTGCGGCACC TTGGGCTGGA AGGGGTTGCC CCAGGATATG GGTCAAAGAA
3101 TGGACCTCAC CAAGTACATC GGGATGCCCC ACTGCCCGGG TTCTTCATAC
3151 TGCTAGAATC CAGTCTAGC CCTGAGCAGC ATTTCCACGG GTGTTTCTTC
3201 AGAGGACAGT GAGTTCCTAG CCCTCCCTCT CTCTTGACCT GGATCAGCTC
3251 TTACAGGAGT ATATCAGCGT CCCAGCCTAT TTTGCAAGAC ACTAATTTT
3301 GTTGAGTTTT TGCCACTTCC TGCCATGGAG TGAGCTTTAG AACCATACTA
3351 CCATCTCCAG GCCCAAACCT TGAAATAAAG ACATGAGCAT GAGCAAAAAA
3401 AAAAA

```

BLAST Results

Entry AC004682 from database EMBLNEW:
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete
sequence.
Score = 1291, P = 0.0e+00, identities = 265/272

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 133 bp to 3153 bp; peptide length: 1007
Category: similarity to known protein
Prosites motifs: LEUCINE_ZIPPER (83-105)
LEUCINE_ZIPPER (90-112)
LEUCINE_ZIPPER (97-119)
LEUCINE_ZIPPER (104-126)
LEUCINE_ZIPPER (403-425)
LEUCINE_ZIPPER (410-432)
LEUCINE_ZIPPER (918-940)

```

1 MKDEAGERDR EVSSLNSKLL SLQLDIKNLH DVCKRQRKTL QDNQLCMEEA
51 MNSSHDKKQA QALAFEESEV EFGSSKQCHL RQLQQLKKKL LVLQOELEFH
101 TEELQTSYYS LRQYSILEK QTSDLVLLHH HCKLKEDEVI LYEEEMGNHN
151 ENTGEKLHLA QEQLALAGDK IASLERSLNL YRDKYQSSLS NIELLECQVK
201 MLQGLGGIM GQEPENKGDH SKVRIYTPC MIQEHQETQK RLSEVWQKVS
251 QDDLIQELR NKLACSNALV LEREKALIKL QADFASCTAT HRYPPSSSEE
301 CEDIKILKH LQEQKDSQCL HVEEYQNLVK DLRVELEAVS EQKRNIMKDM
351 MKLELDLHGL REETSAHIER KDKDITILC RLOELOLEFT ETOKLTLKKD
401 KFLQEKDEML QELEKKLTQV QNSLLKKEKE LEKQQCMATE LEMTVKEAKQ
451 DKSKEAECKA LQAEVQKLKN SLEEAQOQER LAAQQAQCK EEAALAGCHL
501 EDTQRKLQKG LLLDKQKADT IQELQRELQM LQKESSMAEK EQTSNRKRVE
551 ELSLELSEAL RKLENSDKEK RQLQKTVAEQ DMKMNDMLDR IKHQHREQGS
601 IKCKLEEDLO EATKLEDKR EQLKKSKEHE KLMEGELEAL ROEFKKKDKT
651 LKENSRLKEE ENENLRAELQ CCSTQLESSL NKYNTSQQVI QDLNKEIALQ
701 KESLMSLQAK LDKALQKEKH YLQTTITKEA YDALSRSAA QDDDLTQALE
751 KLNHVTSETK SLQQSLTQTQ EKKAQLEEEI IAYEERMKKL NTELKRLRGF
801 HQESELEVHA FDKKLEEMSC QVLQWQKHQ NDLKMLAAKE EQLREFQEEM
851 AALKENLLED DKPECCLPQW SVPKDTCLRL RGNDQIMTNL EQWAKQKQVA
901 DEKLGQLRE QVNYIAKLSG EKDHLSVMV HLQENKCLK KEIEEKKMKA
951 ENTRLCTKAL GPSRTESTQR EKVCGTLGWK GLPQDMGQRM DLTKYIGMPH
1001 CPGSSYC

```

BLASTP hits

Entry HS417401_1 from database TREMBL:
product: "trans-Golgi p230"; Human trans-Golgi p230 mRNA, complete

cds.

Score = 411, P = 3.9e-34, identities = 212/862, positives = 420/862

Entry SCINTANA_1 from database TREMBL:

Saccharomyces cerevisiae integrin analogue gene, complete cds.

Score = 404, P = 6.2e-34, identities = 199/897, positives = 423/897

Entry HS6802_2 from database TREMBL:

gene: "MYH9"; product: "dJ6802.2"; Homo sapiens DNA sequence from PAC 6802 on chromosome 22. Contains apolipoprotein L, myosin heavy chain, ESTs, CA repeat, STS and GSS.

Score = 404, P = 1.9e-33, identities = 231/1028, positives = 469/1028

Entry AF092090_1 from database TREMBL:

product: "cp151"; Rattus norvegicus cp151 mRNA, partial cds.

Score = 2523, P = 3.0e-262, identities = 506/733, positives = 611/733

Alert BLASTP hits for DKFZphtes3_lgl3, frame 1

TREMBL:HSGOLGIN_1 product: "256 kD golgin"; H.sapiens mRNA for golgin,
N = 1, Score = 411, P = 4.4e-34

TREMBL:HS417401_1 product: "trans-Golgi p230"; Human trans-Golgi p230
mRNA, complete cds., N = 1, Score = 411, P = 4.5e-34

TREMBL:SCINTANA_1 Saccharomyces cerevisiae integrin analogue gene,
complete cds., N = 1, Score = 404, P = 7.1e-34

>TREMBL:HSGOLGIN_1 product: "256 kD golgin"; H.sapiens mRNA for golgin
Length = 2,185

HSPs:

Score = 411 (61.7 bits), Expect = 4.4e-34, P = 4.4e-34
Identities = 212/816 (25%), Positives = 420/816 (51%)

```

Query:   145 EMGNHNEN-TGEKLHLAQEQLALAGDKIASLERSLNLYRDKYQSSLSNIELLECQVKMLQ 203
          +M +  E+  G   L +EQL  ++ +ERSL+ YR KY  ++ ++L+ + K LQ
Sbjct:   119 DMDSEADLVGNSDSLKEQLI---QRLRRMERSLSSYRGKYSLVLTAYQMLQREKKKLQ 175

Query:   204 GELGGIMGOEPENKGDHSHKVRIYTPSPCMIQEHQETQKRLESEVWQ-KVSQQDDLIQELRNK 262
          G   I+ Q   D S RI   +Q Q+ +K L E +  + +D I L+ +
Sbjct:   176 G----ILSQSQ----DKSLRRIAELREELQMDQAKKHLOEEFDASLEEKDQYISVLQTO 227

Query:   263 LAC-----SNALVLEREKALIKLQADFASCTATHRYPPSSSEEC-ED--IKKILKHLQE 313
          ++   + + ++ K L +L+  A   P S E  ED  K L+ LQ+
Sbjct:   228 VSLKQRLRNGPMNVVDVLPKPLPQLEPQ-AEVFTKEENPESDGEFVVEDGTSVKTLETLOQ 286

Query:   314 QKDSQ-----CLH-VEEYQNLVKDLRVELEAVSEQKRNIMKDMMKLELDLHGLREETS 366
          +  Q   C  ++ ++  L E EA+ EQ  +++ K++ DLH + E+T
Sbjct:   287 RVKRQENLLKRCKETIQSHKEQCTLLTSEKEALQEQLDERLQELEKIK-DLH-MAEKT 344

Query:   367 HIERKDKDITILQCRQLQELQLEFTETQKTLTKKDKFLQEKDEMLQELEKLTQV--QNSL 424
          + +D  I Q  Q+ +  ET++  +  + L+ K+E + +L ++ Q+ Q
Sbjct:   345 ITQLRDAKNLIEQLE-QDKGMVIAETKR---QMHTLEMKEEEIAQLRSRIKQMTTQGE 400

Query:   425 LKKEKELEKQQCMATELEMTVKEAKQDKSKEAECKALQAEVOKLKSLEEAKQOERLAAQ 484
          L+++KE + ++  ELE + A+ K++EA K L+AE+ +  ++E+ ++ER++ Q
Sbjct:   401 LREQKE-KSERAAFEELKALSTAQ--KTEEARRK-LKAEMDEQIKTIEKTSEEERISLQ 456

Query:   485 QA-AQCKEEAA-LAGCHLEDTQKRLQKGLLLDKQKADTIQELQRELQMLQKESMAEKEQ 542
          Q ++ K+E  +  E+  KLQK L +K+ A  QEL ++LQ ++E  E+ +
Sbjct:   457 QELSRVQEVVDVMKKSSEEQIAKLQK--LHEKELARKEQELTKKLQTRERE--FQEQMK 512

Query:   543 TSNRKRVEELSLELSEALRKLNSDKEKRQLQKT--VAEQDMKMNDMLDRIKHQHREQGS 600
          + K  E L++S+  + E+  E+ +LQK  + E + K+ D+  +
Sbjct:   513 VALEKSQSEY-LKISQEKEQESLALLELELQKKAILTESENKLRDLQQAETYRTRILE 571

Query:   601 IKCKLEEDLQEATKLLD-----KREQLKKSKEHEKLMEG---ELEALR-QEFKKKDKTL 651
          ++ LE+ LQE  +D  + E+ K +KE  ++E  ELE+L+ Q+  + L
Sbjct:   572 LESSLEKSLQENKNQSKDLAVHLEAKNKHNEITVMVEKHKTELESKKHQDALWTEKL 631

Query:   652 KENSRKLEENENLRAELQCCSTQLESSL-NKYNTSQVQIDLNKE----IALQKESLMS 706
          +  ++ + E E LR +  C + E+ L +K  Q I+++N++  + +++ L S
Sbjct:   632 QVLKQYQTEMEKLRK---CEQEKETLLKDKKEIFQAHEEMNEKTLEKLDVQKTELES 688

Query:   707 LQAQLDKALQKEKHLYQT--TITKEAYDALSRKSAACQDDLTQALEKLNHVTSETKSLQ 764
          L ++L + L K +H L+  ++ K+  D + ++  A D+  Q   V S K  +

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Sbjct: 689 LSSELSSEVL-KARHKLEELSVLKDQTDKMKQELEAKMDE--QKNHHQQQVDSIIKEHEV 745

Query: 765 SLTQTOEKKAQLEEEIIAYEERMKKLNTELRLRGFHOESELEVHAFDKKLEEMSCQVLQ 824
S+ +T+ KA L+++I E +K+ + L++ + + E ++ + +L++ S ++

Sbjct: 746 SIQRTE--KA-LKDQINQLELLLLKERDKHLKEHQAHVENLEADIKRSEGELQQASAKLDV 802

Query: 825 WQKQHNDLKMMLAAKEEQLEFQEEMAALKENLLEDDKEPCCLPQW-----SVPKDTC-R 878
+Q +Q+ A EQ + ++E++A L++ LL+ + E L + + + KD C

Sbjct: 803 FQS-YQS-----ATHEQTAYEEQLAQLQKLLDLETERILLTKQVAEVEAQKQDVCTE 855

Query: 879 LYRGNDQIMTNLEQWAKQKQVANERLGNLREQVNYIAKLS-GEKDLHLSVMVHLQENK 937
L Q+ ++Q KQ +K+ + QV Y +KL G K+ + + ++EN

Sbjct: 856 LDAHKIQVDLMQOLEKQNSEMEQKVKSLT--QV-YESKLEDGNKEQEQTKQILVEKENM 912

Query: 938 KLK-KEIEEKKMKAENTRLCTK 958
L+ +E ++K+++ +L K

Sbjct: 913 ILQMRGQKKEIEILTQKLSAK 934

Score = 338 (50.7 bits), Expect = 3.1e-26, P = 3.1e-26
Identities = 216/953 (22%), Positives = 468/953 (49%)

Query: 2 KDEAGERDRE--VSSLNS-KLL-SLQLDIKNLHDVCKRQRKTLQDN-QLCM-----EEAM 51
K+E E D E V S K L +LQ +K ++ KR ++T+Q + + C +EA+

Sbjct: 260 KEENPESDGEPPVEDGTSVKTLETLOQRVVRQENLLKCKETIQSHKEQCTLLTSEKEAL 319

Query: 52 NSSHDKKQAALAFESEVEFGSSKQCHLRQ----LQQLK--KKLLVLQOELEFHTTELO 105
D++ + ++ + + LR ++QL+ K +++ + + + H E L+

Sbjct: 320 QEQLDERLQELEKIKDLHMAEKTCLITQLRDAKNLIEQLEQDKGMVIAETKRQMH-ETLE 378

Query: 106 TSYSLRQYQSILEKQTSIDLVLHHHCKLKEDEVILYEEEMGNHNENTGEKLHLAQEQL- 164
+ Q +S +++ T+ L K K + E E +T +K A+ +L

Sbjct: 379 MKEEEIAQLRSRIKQMTTQGEELREQ-KEKSERAFAEELEKAL---STAQKTEEARRKLK 434

Query: 165 ALAGDKIASLERSLNLRYDKYQSSLSNI--ELLEQVVKMLQELGGIMQEPENKGDHKS 222
A ++I ++E++ R Q LS + E+++ K + ++ + Q+ K K

Sbjct: 435 AEMDEQIKTIEKTSEEERISLQELSRVQEVVDVMKKSSEEQIAKL--QKLHEKELARK 492

Query: 223 VRIYTPCMIOEHQETQKRLSEVWQKVSQDDLIQELRNKLACSNAVLEREKALIKLQA 282
+ T +E +E Q+++ +K SQ + L ++ + +L LE ++LQ

Sbjct: 493 EQELTKKLQTRE-REFQEQMKVALEK-SQSEYL--KISQEKEQQESLALAE---LELQK 544

Query: 283 DFASCTATHRYPPSSSEECEDIKKILKHLQEQQDSQCLHVEEYQNLVKDLRVELEAV-SE 341
A T + +E E + + L+ + ++E +N KDL V LEA ++

Sbjct: 545 K-AILTESENKLRLDLQQAETRYTRILESSLEKS---LQENKNQSKDLAVHLEAEKNK 600

Query: 342 QKRNMKDMKLELDLHGLREETSABIERKDKDITI-LQCRLOLEQLEFTETQKLTCLKD 400
+ I + K + +L L+ + A K + + Q +++L+ E E +K TL KD

Sbjct: 601 HNKEITVMVEKHKTELESCLKHQDALWTEKLQVLKQYQTEMEKLR-EKCEQEKETLLKD 659

Query: 401 K-----FLQEKDEM-LQELEKLTQVQNSLLKKEKELEKQOCMATELEMTVKEAKQDKS 453
K ++E +E L++L+ K T+++ SL + E+ K + E E++V + + DK

Sbjct: 660 KEIIFQAHEEMNEKTLEKLDVQKTELE-SLSSELSSEVLKARHKLEE-ELSVLKDQTDKM 717

Query: 454 K-EAECKALQAEVQKLNLSLEEAKQERLAAQQAQC-KEEAALAGCHLEDTQRKLQKGL 511
K E E K + + + ++ ++ ++ Q+ + K++ L++ + L++

Sbjct: 718 KQELEAK-MDEQKNHHQQQVDSIIKEHEVSIQRTEKALKDQINQLELLLLKERDKHLKEHQ 776

Query: 512 L-LDKQKADTIQELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLKLENSDKEK 570
++ +AD I+ + ELQ + + + Q++ ++ + +L++ +KL + + E+

Sbjct: 777 AHVENLEAD-IKRSEGELQQASAKLDVFSYSQATHEQTAYEEQLAQLQKLLDLETER 835

Query: 571 RQLQKTVAEQDMKMNDM---LD--RIKHQHQREQSGIK--CKLEEDLQEATKLEDKREQL 623
L K VAE + + D+ LD +I+ Q Q K ++E+ ++ T++ E K E

Sbjct: 836 ILLTKQVAEVEAQKQDVCTELDAHKIQVDLMQOLEKQNSEMEQKVKSLTQVYESKLEDG 895

Query: 624 KKSKEHEK--LMEGELEALRQEFKKDKTLKENSRLKEEENENLRAELQCCSTQLESLN 681
K +E K L+E E L+ +K-K ++ ++KL + +++ - + T+ ++

Sbjct: 896 NKEQEQTKQILVEKENMILQMRGQK-KEIEILTQKLSAKEDSIHILNEEYETKFKNQEK 954

Query: 682 KYNTSQQVIQDLNKEIALQKESLMSLQAQLDKALQEKHYLQTTITKEAYDALSRKSAAC 741
K +Q +++ + + K+ L+ +A+L K L E L+ + ++ ++A + A

Sbjct: 955 KMEKVKQKAKEMQETL---KKLLLDQEAKLKEL--ENTALELSQEKQFNAKMLEMAQA 1009

Query: 742 QD-DLTQALEKLNHVTSETKSLOQSLTQTOEKKAQLEEEIIAYEERMKKLNTELRLRGF 800
++ A+ +L T++ + ++ SLT+ + +L + I +E KKLN + +L+

Sbjct: 1010 NSAGISDAVSRLE--TNQKEQIE-SLTEVHRR--ELNDVISIWE---KKLNQQAELQEI 1061

Query: 801 HOESELEVHAFDKKLEEMSCQVLQW--QKQHNDLKMMLAAKEEQLEFQEEMAALKENLL 858
H E+++ +++++ E+ ++L + +K+ N ++ KEE +++ + L+E L

Sbjct: 1062 H---EIQLQEKEQEVAEKQKILLFGCEKEEMNK-EITWLKEEGVKQ-DTTLNELQEQLK 1116

Query: 859 EDDKEPCGLPQWSPKDTCLRLYRGNDQIMTNLEQ--WAKQKQVANEKLGQNLREQVNYI- 915
 + L Q K L + + +L++ + ++Q V + L + + +V+ +
 Sbjct: 1117 QKSAHVNSLAQ-DETKLKAHLEKLEVDLNKSLKENTFLQEQLVELKMLAEEDKRVSELT 1175

Query: 916 AKLSGEKDLHLSVMVHLQQENKKLK-KEIEEKKMKAE 951
 +KL + S+ ++ NK L+ K +E KK+ E
 Sbjct: 1176 SKLKTDEEFQSLKSSHEKSNKSLKEDKSLEFKKLSSE 1212

Score = 337 (50.6 bits), Expect = 4.0e-26, P = 4.0e-26
 Identities = 215/951 (22%), Positives = 433/951 (45%)

Query: 10 REVSSLSNKLKSLQDLIKNLHDVCKRQKTLQDNQLCMEAMNSSHDKKQAQALAFESE 69
 +E + +++L L+ ++ K Q K L + EA + H+K+ + E+ +
 Sbjct: 560 QEAETYRTRILESSLEKSLQENKNQSKDLAVHL----EAEKNKHKEIT--VMVEKHK 613

Query: 70 VEFSSSKQCHLRQLQQLKKLLVLQQLLEFHTTEELQTSYSLRQYSILEKQTSQDLVLLH 129
 E S K H +Q +KL VL+Q+ + E+L+ Q + L K +++
 Sbjct: 614 TELESK--H-QQDALWTEKLQVLKQQYQTEMEKLEK---CEQKETLLKD-KEIIFQA 666

Query: 130 HHCKLKE---DEVILYEEEMGNHNENTGEKL---HLAQEQLALAGDKIASLERSINLYRD 183
 H ++ E +++ + + E+ + + E L H +E+L++ D+ +++ L D
 Sbjct: 667 HIEEMNEKTLEKLDVQTELESLSSESEVLKARHKEEELSVLKDQTDKMKQLEAKMD 726

Query: 184 K---YQSSLSNIELLECQVKMLQGE--LGGIMGQEPENKGDHRSKVRIYTPCMIQEHQE 237
 + Q + +I + E +V + + E L + Q + K + ++ +
 Sbjct: 727 EQKNHHQQQVDSI-IKEHEVSIQRTKALKDQINQLELLLLKERDK-HLKEHQAHVENLEA 784

Query: 238 TQKRLSEVWQKVSQDDLIQELRNKLACSNAVLEREKALIKLOADFASCTATHRYPPSS 297
 KR Q+ S + D+ Q ++ ++ E+ L +LQ T R
 Sbjct: 785 DIKRSEGELQASAKLDVFQSYQS---ATHEQTKAYEEQLAQLQKLLDLE-TERIL--- 837

Query: 298 SEECEDIKKILKHLQEQKDSQCLHVEEYQNLVKDLRVELEAVSEQKRNIMKDMMKL-ELD 356
 + K + ++ QK C ++ ++ V+DL +LE + + +K + ++ E
 Sbjct: 838 -----LTKQVAEVEAQKQKDVCTELDAHKIQVQDLQMLEKQNSEMEQKVKSLTOVYESK 891

Query: 357 LH-GLREETSASIERKDKDITILQCLRL-QELQLEFTETQKLTLLKDKF--LQEKDEM-LQ 411
 L G +E+ +K+ ILQ R Q+ ++E TQKL+ K+D L E+ E +
 Sbjct: 892 LEDGNKEQEQTQKILVEKENMILQMQREGQKKEIEIL-TQKLSAKEDSIHILNEEYETKFK 950

Query: 412 ELEKLTQVQNSLLK-----KEKELEKQCCMATELEMTVKEAQDKSKEAECKALQAEVQ 466
 EKK+ +V+ + K+K L+++ + ELE T E Q K K+ K L+ Q
 Sbjct: 951 NQEKMEKVKQKAKEMQETLKKLLDQEAALKKELENTALELSQ-KEKQFNAKMLEM-AQ 1008

Query: 467 KLKNSLEEAKQQLERLAAQQAQCKEEAALAGCHLEDTRKRLQKGLLLDKQKADTIQELQR 526
 + A RL Q Q + + L D +K L Q+A+ +QE+
 Sbjct: 1009 ANSAGISDAVS--RLETNQKEQIESLTVHRRELNDVISIWEKKL---NQQAELQEIH- 1062

Query: 527 ELQMLQKESMAEKEQT-----SNRKR---EELSLELSEALRKLENSDKERQLQ 574
 E+Q+ +KE +AE +Q K + +E ++ L +L+ K+K
 Sbjct: 1063 EIQLQKEQEVAELKQKILLFGCEKEEMKEITWLKEEGVKQDITLNLQELQKQSAHV 1122

Query: 575 KTVAEQDMKMNMDLRIKHQHREQSGIKCKLEEDLQEAATKLEEDKREQLKKSKEHEKLME 634
 ++A+ + K+ L++++ + L+E L E L E+ + ++ + K +
 Sbjct: 1123 NSLAQDETCLKAHLEKLEVDLNKSLKENTFLQEQLVELKMLAEEDKRVSELTSLKTTD 1182

Query: 635 GELEALRQEFKKDKTLKENSRLKEEENENLRAELQCCSTQLESSLNKYNTSQQVIQDLN 694
 E ++L+ +K +K+L++ S + ++ +E L +L C + E+ L T++ + +
 Sbjct: 1183 EEFQSLKSSHEKSNKSLKEDKSLEFKKLSSELAIQLDICCKKTEALLEA-KTNELINISS 1241

Query: 695 KEIALQKESLMSLQAQLDKALQEKHYLQTTITKEAYDALSRKSAACQDDLT----QALE 750
 K A+ + Q + K KE ++T E +A R+ Q+ L QA
 Sbjct: 1242 KTNAILSRLSHCQHRRTKV--REALIKTCTVSEL-EAQLRQLTEEQNTLNISFQQATH 1297

Query: 751 KLNHVTSSETKSLQOSLTQTEKKAQLEEEIIAYEERMKKLN---TELK--LRGFHQESE 805
 +L ++ KS++ + +K L++E ++ + T+L+K + +
 Sbjct: 1298 QLEEKENQIKSMKADIESLVTEKEALQKEGGNQQAASEKESCITQLKKELSENINAVTL 1357

Query: 806 LEVHAFDKKLE--EMSCQVLQWQKHQNDLKMMLAAKEEQLREFQEEAALKENLLEDDKE 863
 ++ ++K+E +S Q+ Q QN + L+ KE + ++ K LL D +
 Sbjct: 1358 MKEELKEKKVEISSLSKQLTDLNVQLQNSIS-LSEKEAAISSLRKQYDEEKCELL-DQVQ 1415

Query: 864 PCCLPQWSPKDTCLRLYRGNDQIMTNLEQWAKQKQVANEKLGQNLRE--QVNYIAKLSG 920
 ++ K+ D +W K+ + + N ++E Q+ +K +
 Sbjct: 1416 DLSFKVDTLSEKISALEQVDDWSNKFSEWKKKQSRFTQHNTVKELQIQLELKSKEAY 1475

Query: 921 EKDH-LHSVMVHLQQENKK---LKKEIEEKKMKAE 951
 EKD ++ + L Q+NK+ LK E+E+ K K E
 Sbjct: 1476 EKDEQINLLKEELDQQNKRFDCLEKEMEDDKSKME 1510

Score = 332 (49.8 bits), Expect = 1.4e-25, P = 1.4e-25
 Identities = 209/953 (21%), Positives = 438/953 (45%)

Query: 1 MKDEAGERDREVSSLSKLLSLQLDIKNLHDVCKRQKTLQDNQOLCMEAMNS----SHD 56
 MK + E+ ++ L+ K L+ + + + + R+R+ + ++ +E++ + S +
 Sbjct: 470 MKKSSEEQIAKLQKLHEKELARK-EQELTKKLQTREREFQEQMKVALEKSQSEYLKISQE 528

Query: 57 KKQAAALAFESEVEFGSSKQCHLRQLQQLKKLLVLQOELEFHTTEELQTSYYSLRQYQS 116
 K+Q ++LA EE E++ K+ L + + KL LQOE E + + SL +
 Sbjct: 529 KEQQESLALAELELQ----KKAILTESEN---KLRDLQQAETRYRTRILELESSLEKSLQ 581

Query: 117 ILEKQTSIDLVLHHHCKLKEDE--VILYEE-----EMGNHNENT--GEKLHLAQEQLALA 167
 + Q+ DL + K K ++ ++ E+ E H ++ EKL + ++Q
 Sbjct: 582 ENKNQSKDLAVHLEAEKNKHNKEITVMVEKHKTELESKHOQDALWTEKLOVLKQYQTE 641

Query: 168 GDKIASL--ERSNLNLYRDK---YQSSLS--NIELLECQVKMLQGEKGIMGQEPENKGDH 220
 +K+ + L +DK +Q+ + N + LE ++ + Q EL + + E
 Sbjct: 642 MEKLRKECQEKETLLKDKKEIFQAHIEEMNEKTLE-KLDVKQTELESLSSELSEVLKAR 700

Query: 221 SKVRIYTPCMIQEHQETQKRLSEVWQKVSQDDLIQELRNKLACSNALVLEREKALIKL 280
 K+ S +++++ +T K E+ K+ +Q+ Q+ + + + + +R+ +K
 Sbjct: 701 HKLEELLS--VLKD--QTDKMKQELEAKMDEQKNHHQQQVDSIIKEHEVSIQRTKALKD 756

Query: 281 QADFASCTATHR--YPPSSSEECEDIKKILKHLQEQKDSQCLHVEEYQNLVKDLRVELEA 338
 Q + R + E+++ +K + + ++ +Q+ + +A
 Sbjct: 757 QINQLELLKRDKHLKEHQAHVENLEADIKRSEGELQASAKLDVFSYQSATHEQTKA 816

Query: 339 VSEQNRNIMKDMKLELDLHGLREETSABIERKDKDITILQCRQLQELQLEFTETQKLTILK 398
 EQ + + ++ LE + L ++ A +E + KD+ C EL + Q L +
 Sbjct: 817 YEEQLAQLQKLLDLETERILLTKQV-AEVEAQKQDV----CT--ELDAHKIQVQDLMQ 869

Query: 399 KDKFLQEKDEMLQELEKLTQVQNSLLKK-EKELEKQOCMATELEMTVKEAKQDKSKEAE 457
 +K + EM Q++ K LTQV S L+ KE E+ + + E E + + ++ + KE E
 Sbjct: 870 LEK---QNSEMEQKV-KSLTQVYESKLEDGNKEQEQTQKILVEKENMILQMQREGQKKEIE 925

Query: 458 C--KALQAEVQKLKNSLEEAKQOERLAAQQAQCKEEAALAGCHLEDTORQ--LQKGLLL 513
 + L A+ + EE + + + ++ + K+A ++T +K L + L
 Sbjct: 926 ILTQKLSAKEDSIHILNEEYETKFNQEKMEKVKQKAK---EMQETLKKKLLDQEA 981

Query: 514 DKQKADTIQEL-QRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLENSDKEKRO 572
 K+ +T EL Q+E Q K MA+ V L E + L ++ +R+
 Sbjct: 982 KKELENTALELSQKEKQFNAKMLEMAQANSAGISDAVSLETNQKEQIESL--TEVHRRE 1039

Query: 573 LQKTVAEQDMKMDMLDRIKHQHQREQSGIKCKLEEDLQEATKLEEDKREQLKKS----KE 628
 L ++ + K+N + ++ H Q K + +L++ L ++E++ K KE
 Sbjct: 1040 LNDVISIWEKLNQAAELQEIHEIQLEKEQEVAELKQKILLFGCEKEEMNKEITWLKE 1099

Query: 629 HEKLEMEGELEALRQEFKKDKTLKENSRLKEEENENLRAELQCCSTQLESSLNKYNTSQ 688
 + L L+++ K+K + NS L ++ L+A L+ L SL + Q+
 Sbjct: 1100 EGVKQDITLNLQEQQLKQSAHV--NS--LAQDETCLKAHLEKLEVDLNKSLKENTFLQE 1155

Query: 689 VIQDLNKEIALQKESLMSLQAL---DKALQ--KEKHYLQTTITKEA---YDALSRSKAA 740
 + +L K + L ++L D+ Q K H ++ + LS + A
 Sbjct: 1156 QLVELKMLAEEDKRKVSELTSLKKTDEEFQSLKSSHEKSNSKLEDSLEFKKLSSE-LA 1214

Query: 741 CQDDL----TQAL-----EKLNHVTSETSKSLQSLTQTOEKKAQLEEEIIAYEERMKKL 790
 Q D+ T+AL E +N +S+T ++ ++ Q + +++E ++ + +L
 Sbjct: 1215 IQLDICCKKTEALLEAKTNELINISSKTNAILSRIHQHRTTKVKEALLIKTCTVSEL 1274

Query: 791 NTELRLKRGFHFQSELELVHAFDKKLEEMSCQVLQWQKHQNDLKMLAAKEEQLEFQEEEM 850
 +LR+L + +LEE Q+ K + D++ L ++E L Q+E
 Sbjct: 1275 EAQLROLTEEQNTLNISFQOATHQLEEKENQI---KSMKADIESLVTEKEAL---QKEG 1327

Query: 851 AALKENLLEDDKEPCCLPQWSVPKDCRCLYRGNDQIMTNLEQWAKQKQVANEKLGNLRE 910
 + +KE C + Q + K+ N +T +++ K++KV L QL +
 Sbjct: 1328 G--NQQAASEKESC-ITQ--LKKELSE---NINAVTLMKEELKEKKVEISSLSKQLTD 1378

Query: 911 ---QVNYIAKLSGEKDLHLSVMVHLQENKKLKEIEEKKMAE 951
 Q+ LS ++ + S+ +E+ +L +++ K +
 Sbjct: 1379 LNVQLQNSISLSEKEAAISSLRKQYDEEKCELLDQVQDLSFKVD 1422

Score = 329 (49.4 bits), Expect = 2.9e-25, P = 2.9e-25
 Identities = 226/941 (24%), Positives = 444/941 (47%)

Query: 61 QALAFESEVE--FGSSKQCHLRQLQQLKKLLVLQOELEFHTTEELQTSYYSLRQYQSIL 118
 Q L E+ +++ S+ LR++ +L+++L + QQ + EE S QY S+L
 Sbjct: 165 QMLQREKKKLGILSQSQDKSLRRRIAREELQMDQQAQKHLQEEFDASLEEKDQYISVL 224

Query: 119 EKQTSIDLVLHHHCKLKEDEV-----ILYEEEMGNHNENT---GEKL---HLAQEQLALA 167
 + Q S L + + D + + + E+ EN GE + + + L
 Sbjct: 225 QTQVSLKQRLRNGPMNVDLKPLPQLEPQAEVFTKEENPESDGEPPVEDGTSVKLTETL 284

Query: 168 GDKIASLERSNLNLYRDKYQSSLSNIELLECQVKMLQGEKGIMGQEPENKGDHDKSVRIYT 227

++ E L ++ QS LL + + LQ +L + QE E D + +
 Sbjct: 285 QQRVQRQENLLKRCKETIQSHKEQCTLLTSEKEALQEQLDERL-QELEKIKD---LHMAE 340
 Query: 228 SPCMIQEHQETQKRLSEVWQKVSQQDDLIQELRNKLACSNAVLEREKALIKLQADFASC 287
 +I + ++ + + ++ Q +I E + ++ L ++ E + +L++
 Sbjct: 341 KTKLITQLRDAKNLIEQLEQDKGM---VIAETKROM--HETLEMKEEE-IAQLRSRIKQM 394
 Query: 288 TATH---RYPSSSEEC--EDIKKILKHLQEOKDSQCLHVEEYQNLVKDL-----RVE 335
 T R SE E+++K L Q+ +++ E +K + R+
 Sbjct: 395 TTQGEELREQEKSERAFAEELEKALSTAQKTEEARKKLKAEMDEQIKTIEKTSEEERIS 454
 Query: 336 LEA-VSEQKRNMKDMMKL--ELDLHGLREETSASIERKDKDITILQCRLQELQLEFTET 392
 L+ +S K+ ++ D+MK E + L++ + RK+++T +LQ + EF E
 Sbjct: 455 LQQLSRVKQEVV-DVMKKSSEEQIAKLQKLHEKELARKEQELTK---KLQTREREFQEQ 510
 Query: 393 QKLTLLKDKFLQEKDEMLQELEKLTQVQNSLLKKEKELEKQOCMATELEMTVKEAKQDK 452
 K+ L+K + E ++ QE E+ Q SL +E EL+K+ + TE E +++ +Q+
 Sbjct: 511 MKVALEKSQ--SEYLIKISQEQE---QESLAELELELQKAIL-TESENKLRDLQOE- 561
 Query: 453 SKEAECKALQAEVQKLKNSLEEAKQER-----LAAQAAQCKEEAALAGCHLEDTQR-K 506
 ++ + L+ E L+ SL+E K Q + L A++ KE + H + + K
 Sbjct: 562 AETYRTRILELE-SSLEKSLQENKNQSKDLAVHLEAEKNKHNKEITVMVEKHKTELESK 620
 Query: 507 LQKGLLLDKQKADTIQELQRELQMLQKSSMAEKEQTSNRKRVEELSLELSEALRK-LEN 565
 Q+ L ++ Q+ Q E++ L +E EKE K + + E K LE
 Sbjct: 621 HQQDALWTEKLQVLKQYQTEMEKL-REKCEQEKETLLKDKKEII-FQAHIEEMNEKTLEK 678
 Query: 566 SDKEKRLQKTVAEQDKMNDMLDRIKHQHQREQSI-KCKLEEDLQEA-TKLLDKR--E 621
 D ++ +L+ +E +++++L + +H+ E+ S+ K + ++ QE K+ E K +
 Sbjct: 679 LDVKQTELESLSSE---LSEVL-KARHKEEELSVLKDQTDKMKQELEAKMDEQKNHHQ 733
 Query: 622 QLKKS--KEHEKMEGELEALRQEFKKKDKTLKENSRLKEEN--ENLRAELQCCSTQL 676
 Q S KEHE ++ +AL+ + + LKE + L+E ENL A+++ +L
 Sbjct: 734 QQVDSIIKEHEVSIQRTEKALKDQINQLELLKRDKHLKEHQAHVENLEADIKRSEGEL 793
 Query: 677 ESSLNKYNTSQQVIQDLNKEIALQKESLSLQAQLDKALQKEKHYLQTTITKEAYDALSR 736
 + + K + Q +++ +E L LQ +L L+ E+ L TK+ + ++
 Sbjct: 794 QQASAKLDVFQSYQSATHEQTKAYEEQLAQLQKQL-LDLETERILL----TKQVAEVEAQ 848
 Query: 737 KSAACQD-----DLTQALEKLNHVTSETKSLQQSLSLTQTEKKAQ--LEEEIIAYEE 785
 K C + DL Q LEK N SE + +SLTQ E K + +E+ +
 Sbjct: 849 KKDVTCTELDAHKIQVQDLMQOLEKQN---SEMEQKVKSLSLTQVYESKLEDGNKEQEQTQKI 905
 Query: 786 RMKKLNTELRLRGFHOESELEVHAFDKKLEEMSCQVL--QWQKQHONDLKMLAAKEEQ 843
 ++K N L+ G Q+ E+E+ +E S +L +++ +N K + +++
 Sbjct: 906 LVEKENMILQMREG--QKKEIETLTQKLSAKEDSIHILNEEYETKFKNQEKMEKVKQKA 963
 Query: 844 REFQEEAALKENLLEDDKEPCCLPQWSVPKDTCLRGRNDQIMTNLEQWAKQKQV---- 899
 +E QE LK+ LL+ + + L + + L + Q + + A+
 Sbjct: 964 KEMQE---TLKKLLDQEA---LKK-ELENTALELSQKEKQFNAKMLEMAQANSAGISD 1016
 Query: 900 ANEKLGNLREQVNYIAKLSG-EKDHLHSMVMH-LQENKKLKK--EIEEKKMAENTRL 955
 A +L +EQ+ + ++ E + + S+ L Q+ ++L++ EI+ ++ + E L
 Sbjct: 1017 AVSRLETNQKEQIESLTVHRRRLNDVISIWEKKLNQQAELQEIHEIQLEKEQEVAEL 1076
 Query: 956 CTKALGPSRTESTQREKVCGLTGWKGLPQD 985
 K L E + K L +G+ QD
 Sbjct: 1077 KOKIL-LFGCEKEEMNKEITWLKEEGVKQD 1105
 Score = 326 (48.9 bits), Expect = 6.0e-25, P = 6.0e-25
 Identities = 220/907 (24%), Positives = 444/907 (48%)
 Query: 67 ESEVEFGSSKQCHLRQLQQLKKLLVLQOELEFHTTEELQTSYSLRQYQSILE---KQTS 123
 E+E G+S + QL Q +++ EL T+Y L++ + L+ Q+
 Sbjct: 123 EAEDLVGNSDSLKEQLIQLRRMERSLSSYRGKSELVTAYQMLQREKKLQGILSQSQ 182
 Query: 124 DLVLLHHHCKLKEDEVILYEEEMGNHNTGEKHLHAEQLALAGDKIASLERSLNLYRD 183
 D L +L+E+ + +++ H + E+ +E+ I+ L+ ++L +
 Sbjct: 183 DKSL-RRIAELREE--LQMDQQAQKHLQ---EEFDASLEE---KDQYISVLQTVSLLKQ 233
 Query: 184 KYQSSLSNIELLECQVKMLQGLGGMGQE-PENKG-----DHskVR-IYTSPCMIQEHQ 236
 + ++ N+++L+ + L+ + +E PE+ G D + V+ + T ++ +
 Sbjct: 234 RLRNGPMNVDVLK-PLPQLEPQAEVFTKEENPESDGEPPVEDGTSVKTLETLLQQRVKRQE 292
 Query: 237 ETQKRLSEVWQKVSQQDDLIQELRNKLACSNAVLEREKALIKLQADFASCTATHRYPPS 296
 KR E Q +Q L+ K A L ER + L K++ D T
 Sbjct: 293 NLLKRCKETIQSHKEQCTLLTS--EKEALQEQLD-ERLQELEKIK-DLHMAEKTCLIT-- 346
 Query: 297 SSECEDIKKILKHLQEOKDSQCLHVEEYQNLVKDLRVELEAVSEQKRNMKDMMKLELD 356
 + D K +++ L++ K + E + + + L ++ E ++ Q R+ +K M +
 Sbjct: 347 ---QLRDAKNLIEQLEQDKGM--VIAETKROMHETLEMKEEEIA-QLRSRIKQMTTQGE 400

Query: 357 LHGLREETS-AHIERKDKDITILQCRLOE----LQLEFTTETQKLTLLKKDKFLQEKDEMLQ 411
 L +E++ A E +K ++ Q + +E L+ E E K T++K +E+ + Q
 Sbjet: 401 LREQEKESERAAFEELKALSTAQ-KTEEARRLKAEMDEQIK-TIEKTSE-EERISLQQ 457

Query: 412 ELEKKLTVQVNSLLKK-EKELEKQOCMATELEMTVKEAKQDKSKEAECKALQAEVQKLKN 470
 EL + +V + + K E+++ K Q + E E+ KE Q+ +K+ + + + + Q +K
 Sbjet: 458 ELSRVKQEVVDVMKKSSEEQIAKLQKLH-EKELARKE--QELTKKLQTREREFQEQ-MKV 513

Query: 471 SLEEAQQERLAAQAAQCKEEAALAGCHLEDTORQLQ-KGLLLD-KQKADTIQELQREL 528
 +LE++ Q E L Q + +E AL L+ + + L D +Q+A+T + EL
 Sbjet: 514 ALEKS-QSEYKISQEKQESLALALELELQKKAILTESENKLRDLQQAETRYRTRILEL 572

Query: 529 QMLQKESMAEKEQTSNRKRVEELSLELSEALRKLENS-DKEKRQLOKTVAEQDMKMNDM 587
 + E S+ E + S V L E ++ +++ +K K +L+ +QD +
 Sbjet: 573 ES-SLEKSLQENKNQSKDLAVH-LEAEKNKHNEITVMVEKHKTELESKHHQDQALWTEK 630

Query: 588 LDRIKHQHR-EQGSIKCKLEEDLQEATKLEEDKRE--QLKKSKEHEKLMGELEALRQEF 644
 L +K Q++ E ++ K E QE LL+DK Q + +EK +E +L+ + E
 Sbjet: 631 LQVLKQQYQTEMEKLRKCE---QEKETLLKDKIEIFQAHIEEMNEKTLE-KLDVKQTEL 686

Query: 645 KKKDKTLKE--NSR-KLEENENLRAELQCCSTQLESSLNKY-NTSQQVIQDLNKE--IA 698
 + L E +R KLEEE L+ + +LE+ +++ N QQ + + KE ++
 Sbjet: 687 ESLSELSEVLKARHKLEELSVLKDQTDKMKQELEAKMDEQKNHHQQQVDSIIKEHEVS 746

Query: 699 LQK-ESLMSLQA-QLDKAL-QKEKHYLQTTITKEAYDALSRKS-----AACQDDLTQAL 749
 +Q+ E + Q QL+ L +++KH + E +A ++S A+ + D+ Q+
 Sbjet: 747 IQRTKALKDQINQLELLKERDKHLKEHQAHVENLEADIKRSEGELQQASAKLDVFSY 806

Query: 750 EKLNVHTSETKSLQQSLTQTQEKKAQLEEEI IAYEERMKKLNTLRLRGFHFQSELEVH 809
 + H +TK+ ++ L Q Q+K LE E I +++ ++ + + + + + +V
 Sbjet: 807 QSATH--EQTKAYEEQLAQLQKLLDLETERILLTKQVAEVEAQKQDVCTELDAHKIQQV 864

Query: 810 AFDKLEEMSCQVLQWQKHQ--DLKMLAAKEEQLEFQEEMAALKENLL----EDDK 863
 ++LE+ + ++ Q K + K+ +EQ E +++ KEN++ E K+
 Sbjet: 865 DLMQLEKQNSEMEQKVKSLTQVYESKLEDGNKEQ--EQTKQILVEKENMILQMREGOKK 922

Query: 864 PC-CLPQ-WSVPKDCRLYRGNDQIMTNLE-QWAKQOKVANE--KLGNQLREQV-NYIAK 917
 L Q S +D+ + N++ T + Q K +KV + ++ L++++ + AK
 Sbjet: 923 EIEILTQKLSAKEDSIHIL--NEEYETKFKNQEKMEKVKQAKEMQETLKKKLLDQEA 980

Query: 918 LSGEKDLHLSVMVHLQQENKKLKEIEEKKMKAENTRLCTKALGPSRTESTQREKV 973
 L K L + + L Q+ K+ ++ E M N+ + A+ SR E+ Q+E++
 Sbjet: 981 L---KKELENTALELSQKEKQFNAKMLE--MAQANSAGISDAV--SRLETNQKEQI 1029

Score = 318 (47.7 bits), Expect = 4.4e-24, P = 4.4e-24
 Identities = 184/827 (22%), Positives = 405/827 (48%)

Query: 1 MKDEAGERDREVSSLSKLLSLQLDIKNLHDVCKRQRKTLDQNLQCMEEAMNSSHDKK-Q 59
 ++ E G + + S S + L+ ++ + ++ L++ ++ + D Q
 Sbjet: 1323 LQKEGCGNQQAASEKESCITQLKKELSENINAVTLMKEELKEKKVEISSLSKQLTDLNVQ 1382

Query: 60 AQ-ALAFEESEVEFGSSKQCHLRQLQOLKKLLVLQOELEFTEELQTSYYS-LRQYQS- 116
 Q +++ E E S + +Q + K+LL Q+L F + L S L Q
 Sbjet: 1383 LQNSISLSEKEAAISSLR----KQYDEEKCELLDQVQDLSFKVDLTSKEKISALEQVDDW 1438

Query: 117 ---ILE-KQTSDDLVLHHHCKLKEDEVILYEEEMGNHNENTGEKLHLAQEQLALAGDKIA 172
 E K+ + H +KE ++ L + + ++ E+++L +E+L +
 Sbjet: 1439 SNKFSEWKKKAQSRFTQHONTVKELQILQELKSKEAYEKD--EQINLLKEELDQQNKRF 1496

Query: 173 SLERSLNLYRDKYSSLSNIEL-LECQVKMLQGELEGGIMGQEP-ENKGDHKSVMRIYTSPC 230
 L+ + + K + SN+E L+ Q + EL + Q+ E + + ++ Y
 Sbjet: 1497 CLKGEMEDOKSKMEKKESNLETTELKSQTARIM-ELEDHITQKTIEIESLNEVLKNYNQOK 1555

Query: 231 MIQEHQETQKRLSEVQKVSQDDLIQELRNKLACSNAVLEREKALIKLQADFASCTAT 290
 I EH+E ++L + ++D+ ++E K+ L LE + +K + +
 Sbjet: 1556 DI-EHKELVQKLQHFQELGEEKDNRVKEAEKI-----LTLENQVYSMAELETKKKELE 1609

Query: 291 HRYPPSSSECECEKILKHLQEQKDSQCLHVE-EYQNLVKDLRVELEAVSEQKRNIMKD 349
 H S+E E++K + L+ + ++ ++ + + + ++ +L + E+K ++
 Sbjet: 1610 HVNLSVKSKE-EELKALEDRLSESAKLAELKRKAEQKIAAIKKQLLSQMEEK----EE 1664

Query: 350 MMKLELDLHGLREETS-AHIERKDKDITILQCRLOEQLQLEFTTETQKL--TLKKDKFLQEKD 407
 K + H E + ++ +++++ IL+ +L+ ++ +ET + + K E++
 Sbjet: 1665 QYKKGTESH--LSELNTKLQEREREVHILEEKLSVSESSQSETLIVPRSAKNVAAYTEQE 1722

Query: 408 EM-----LQEL-EKKLTVQVNSLLKKEKEL-----EKQOCMATELEMTVK-EAKQDKSKE 455
 E +Q+ E+K++ +Q +L +KEK L EK++ +++ EM + + + K +
 Sbjet: 1723 EADSQGCYQKTYEEKISVLQRNLTEKEKLLQVRGQKEETVSSHFMERCQYQERLIKLEH 1782

Query: 456 AECKAL--QAEVQKLKNSLEEAQQRERLAAQAAQCK--EEAALAGCHLEDTORQLQKGL 511

AE K Q+ + L+ LEE ++ L Q + + + A +LE+ +QK L
 Sbjct: 1783 AEAQHEDQSMIGHLQEELEEKNNKYSLIVAQHVEKEGGKNNIQAKQNLNVFDDVQKTL 1842

Query: 512 LLDKQKADTIQELQRELQMLQKESMAEKEQTSNRKRVEELS--LELSEALRKLENSDKE 569
 ++K T Q L++++ L +S + ++ +R +EEL+ E +AL++++ +K

Sbjct: 1843 ---QEKELTQCILEQKIKEL--DSCLVQRQEV-HRVEMEELTSKYEKLQALQQMDGRNKP 1896

Query: 570 KRQLQKTVAEQD---MKMNDMLDRIKHQHQREQSGIKCKLEEDLQEATKLEDKREQLKK- 625
 L++ E+ + +L ++ QH + E + Q+ K + ++ L+

Sbjct: 1897 TELLEENTEESKSHLVQPKLLSNMEAQHNDFKLAGAEREKQKLGKEIVRLQKDLRML 1956

Query: 626 SKEHEKLMEGELEALRQEFKKKDKTLKENSRLKEEENENLRAELQCCSTQLESSLNKYNT 685
 KEH++ ELE L++E+ + E K+++E E+L EL+ ST L+ + ++NT

Sbjct: 1957 RKEHQ---ELEILKKEYDQ-----EREKIKQEEDL--ELKHNSL-LKQLMREFNT 2003

Query: 686 S-QQVIQDLNKEIALQKESLSLQAQLDKALQKEKHYLQTTITKEAYDALSRKSAACQDD 744
 Q Q+L I ++A+L ++ Q+E + L I E D L R +A ++

Sbjct: 2004 QLAQKEQELEMTIKETINKAQEVEAEELLESHEQETNQLLKKIA-EKDDDLKR-TAKRYEE 2061

Query: 745 LTQALEKLNHVTSSETKSLQOSLTQTQEKKAQ-LEEEIAYEERMK--KLNTLRLKRGF 801
 + A E+ +T++ + LQ L + Q+K Q LE+E + + +L T+L +

Sbjct: 2062 ILDAREE--EMTAKVRDLQTQLEELQKKYQKLEQEENPGNDNVTIMELQTQLAQKTTLI 2119

Query: 802 QESELEVHAFDKKLEEMSCQVLQWQK 827
 +S+L+ F +++ + ++ ++K

Sbjct: 2120 SDSKLKEQEFREQIHNLEDRLKKYEK 2145

Score = 316 (47.4 bits), Expect = 7.1e-24, P = 7.1e-24
 Identities = 213/977 (21%), Positives = 454/977 (46%)

Query: 4 EAGERD-REVSSLNSKLLSLQLD-IKNLHDVCKRQRKTLQDNQLCMEEAMNSSHDKKQAO 61
 E R+ +V S+ K L+ Q + ++ +H++ + Q K + +L + + ++ +

Sbjct: 1034 EVHRRELNDVISIWEKKLNQQAELQEIHEI-QLQEKEQEVAELKQKILLFGCEKEEMNK 1092

Query: 62 ALAFESEVEFGSSKQCHLRQLQ-QLKKLL---VLQQE--LEFHTTELQTSYYSRLQY 114
 ++ + E G + L +LQ QLK+K + Q E L+ H E+L+ +

Sbjct: 1093 EITWLKEE---GVKQDTLNLQELQKSAHVNSLAQDETCLKAHLEKLEVDLNSLKE 1149

Query: 115 QSILEKQTSDLVLLHHCKLKEDEV---ILYEEEMGNHNENTGEKHLHAEQLALAGDKI 171
 + L++Q +L +L K K E+ + +E +++ EK + + E +L K+

Sbjct: 1150 NTFLEQLVELKMLAEEDKRKVSLETSKLTDEEFQSLKSSHEKSNSKSLKSLK 1209

Query: 172 AS-LERSLNLYRDKYQSSLS--NIELLECQVKMLQELGGIMQEPENKGDHSHKSVRIYTS 228
 + L L++ K ++ L EL+ L I +++ K +

Sbjct: 1210 SEELAIQLDICCKKTEALLEAKTNELINISSKTNAILSRI--SHCQHRTTKVKEALLIK 1267

Query: 229 PCMIQEHQ-----ETQKRLSEVQKVSQ-DDLQELRNKLACSNAVLVLEREKALIKL 280
 + E + E Q L+ +Q+ + Q ++ +++ A +LV E+E L

Sbjct: 1268 TCTVSELEAQLRQLTEQNTLNISFQOATHQLEKENQIKSMKADIESLVTEKEA---L 1323

Query: 281 QADFASCTATHRYPPSSSEECEDIKKILKHLQEQKDSQCLHVEEYQNLVKDLRVELEAVS 340
 Q + + + S E C I ++ K L E ++ L EE +K+ +VE+ ++S

Sbjct: 1324 QKEGGN---QQQAASEKESC--ITQLKKELSENINAVTLMKEE---LKEKKVEISSLS 1373

Query: 341 EQKRNMKDMKLELDLHGLREETSABIERKDKDITILQCRQLQEL--QLEFTETQKLT-L 397
 +Q ++ + + L S+ ++ D++ L ++Q+L +++ +K++ L

Sbjct: 1374 KQLTDLNVQLQN-SISLSEKEAAISSLRKQYDEEKCCELLDQVQDLSFKVDTLSKEKISAL 1432

Query: 398 KK-DKFLQEKDEMLQLEKKLTQVQNSLLKKEKELEKQOCMATELEMTV---KEAQDKS 453
 ++ D + + E ++ + + TQ QN++ + +LE + A E + + KE ++

Sbjct: 1433 EQVDDWSNKFSEWKKKAQSRFTQHQNTVKELQIQLELKSKEAYEKDEQINLLKEELDQON 1492

Query: 454 KEAECKALQAEVOKLKNLSLEAKQERLAAQQAQCKEAAALAGCHLE-DTQRKLQKGLL 512
 K +C + E K K +E+ + L +Q A + E + +E ++ ++ K

Sbjct: 1493 KRFDCLKGEMEDDKSMKESKESNLETLSQTARIMELEDHITQKTIEIESLNEVLKNY- 1551

Query: 513 LDKQKADTIQELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLENSDKEKRQ 572
 ++QK +EL ++LQ Q+ + +++ L ++ +LE KE

Sbjct: 1552 -NQQKDIEHKELVQKLQHFQELGEEKDNVRKEAEEKILTLENQVYSMAELETKKKELEH 1610

Query: 573 LQKTVAEQDMKMNDMLDRIKHQHQREQ-GSIKCKLEEDLQEATKLL---EDKREQLKSKS 627
 + +V ++ + + DR++ + + +K K E+ + K L E+K EQ KK

Sbjct: 1611 VNLSVKSKEELKALDRLESESAAKLAEKRAEKIAAIKKQLLSQMEKEEQYKKG 1670

Query: 628 EHEKLMEGELEALRQEFKKKDKTLKENSRLKEE-ENENL----RAELQCCSTQLESSLNK 682
 E EL QE +++ L+E + +E ++E L A+ T+ E + ++

Sbjct: 1671 ESHL---SELNTKLQEREREVHILEEKLKSVESQSETLIVPRSAKNVAAYTEQEEADSQ 1727

Query: 683 ---YNTSQQVIQDLNKEIALQKESLSLQAQLDKALQKEKHYLQTTITKEAYDALSRKSA 739
 T ++ I L + + +KE L+ Q +K H+ +E L A

Sbjct: 1728 GCVQKTYEEKISVLQRNLT-EKEKLLQRVGQ-EKEETVSSHFMRCQYQERLIKLEHAEA 1785

Query: 740 ACQDDLTQALEKLNHVTSET--KSLOQSLTQTQEKKAQLEEEIIAYEERMKKLNTELRL 797
 +D Q++ + H+ E K+ + SL Q + + + I ++ + + + ++K
 Sbjct: 1786 KQHED--QSM--IGHLQEELEEKNNKYSILVAQHVEKEGGKNNIQAQONLENVFDDVQKT 1841

Query: 798 RGFHQESELEVHAFDCKLEEM-SCQVLQWQKHQNDLKMMLAAKEEQREFQEEMAALKEN 856
 QE EL ++K++E+ SC V Q ++ H+ +++ L +K E+L+ Q+ K
 Sbjct: 1842 L---QEKELTCQILEQKIKELDSCLVRQ-KEVHRVEMEELTSKYEKLOALQOMDGRNKPT 1897

Query: 857 -LLEDDKEPCCLPQWSVPKDTCLRYRGNDQIMTNLEQWAKQKQVANERKLGNLREQVNYI 915
 LLE++ E PK + + + + L A+++K +KLG ++ +
 Sbjct: 1898 ELLEENTEESKSHLVQPKLLSNMEAQHNDLEFKLAG-AEREK---QKLGKEIVRLQKDL 1953

Query: 916 AKLSGE-KDHLHSMVHLQOENK-KLKKEIEEKKMKAENTRLCTKALGPSRTESTQREK 972
 L E + L + QE + K+K+E E+ ++K +T + + T+ Q+E+
 Sbjct: 1954 RMLRKEHQEQELEILKKEYDQEREKIKQEEDLELKHNS--LKQLMREFNTQLAQKEQ 2010

Score = 301 (45.2 bits), Expect = 2.9e-22, P = 2.9e-22
 Identities = 221/952 (23%), Positives = 441/952 (46%)

Query: 1 MKDEAGERDREVSSLSKLLSLQLDIKNLHDVCKRQKTLQDNQL---CMEEAMNSSHD- 56
 +K A E R+VS L SKL + + ++L ++ K+L+D L + E + D
 Sbjct: 1160 LKMLAEEDKRKVSELTSKLTDEEFQSLKSSHEKSNKSLEDKSLFKKLSEELAIQLDI 1219

Query: 57 --KKQAQALAFESE-VEFGSSK-QCHLRQLQQLKKLLVLQOELEFHT---EELQTSYY 109
 KK L + +E + SSK L ++ + + +++ L T EL+
 Sbjct: 1220 CCKKTEALLEAKTNELINISSKTNAILSRISHCQHRTTKVKEALLIKTCTVSELEAQLR 1279

Query: 110 SLRQYQSILEKQTSIDLVLHHHCKLKEDEVILYEEEMGNHNENTGEKLHLAQE---QLAL 166
 L + Q+ L H + KE+++ + ++ EK L +E Q
 Sbjct: 1280 QLTEEQNTLNISFQAT---HQLEEKENQIKSMKADI---ESLVTEKEALQKEGGNQQA 1333

Query: 167 AGDKIASLERSLNLRYDKYQSSLSNIELLECQVKMLQELGGIMGOEPENKGDHSKVRIY 226
 A +K E + + + +++ + L++ +K + E+ + Q + V++
 Sbjct: 1334 ASEK---ESCITQLKELSENINAVTLMKEELKEKKVEISSLSQLTD-----LNVQLQ 1384

Query: 227 TSPCMIQEHQETQKRLSEVWQKVSQDDLIQELRNKLACSNAVLEREKALIKLQADFAS 286
 S + ++ + + + D +Q+L K+ + L E+ AL ++ D+++
 Sbjct: 1385 NSISLSEKEAAISSLRKQYDEEKCELLDQVQDLSFKV---DTLSKEKISALEQVD-DWSN 1440

Query: 287 CTATHRYPPSS---SEECEDIKKILKHLQEOKDSQCLHVEEYQNLVKD-----LRVE-LE 337
 + + S ++ +K++ L E K + +E NL+K+ R + L+
 Sbjct: 1441 KFSEWKKKAQSRFTQHQNTVKELQIQL-ELKSKEAYEKDEQINLLKEELDQQNKRFDCCLK 1499

Query: 338 AVSEQKRNIM-KDMMKLELDLHGLRE---ETSAHIERKDRDITILQCRLOEL-QLEFTET 392
 E ++ M K LE +L E HI +K +I L L+ Q + E
 Sbjct: 1500 GEMEDDCKSMKKESNLETELKSTARIMELEDHITQKTIEIESLNEVLKNYNQKQDIEH 1559

Query: 393 QKLTLLKKDKFLQ---EKDEMLQELEKKLTQVQNSLLKKEKELEKQOCMATELEMTVKEAK 449
 ++L K F + EKD ++E E+K+ ++N + + ELE ++ + ++VK
 Sbjct: 1560 KELVQKLQHFQELGEEKDNRVKEAEKILTLENQVYSMAELETKKKELEHVNLVSK--- 1616

Query: 450 QDKSKEAECKALQAEVQKLKNSLEEAKQERLAAQQAQCKEEAALAGCHLEDTQRLQK 509
 SKE E KAL+ ++ S + + +R A Q+ A K++ +E+ + + +K
 Sbjct: 1617 ---SKEEELKALEDRLS--ESAACKLAELKRAEQKIAAIKKQLL---SQMEEKEEQYKK 1668

Query: 510 GLLLDKQKADT-IQELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLNSDK 568
 G + +T +QE +RE+ +L+++ E Q+ + S + A + E +D
 Sbjct: 1669 GTESHLSELNKLQEREREVHILEKLSVSSQSETL--IVPRSAKNVAAYTEQEEADS 1726

Query: 569 E---KRQLQK-TVAEQDMKMD-MLDRIKHQHREOGSIKCKLEEDLQEATKLEEDKREQ 622
 + K +K +V +++++ + +L R+ Q +E+ ++ E Q +L+ K E
 Sbjct: 1727 QGCVQKTYEEKISVLQRNLTEKEKLLQVRG-QEKEE-TVSSHFMRCQYQERLI--KLEH 1782

Query: 623 LKKSKEHE-KLMGEL-EALRQEFKKKDKTLKENSRLKEEENENLRAELQCCSTQLESSL 680
 + +K+HE + M G L E L ++ KK + ++ K E N++A+ LE
 Sbjct: 1783 AE-AKHEDQSMIGHLQEELEEKNNKYSILVAQHVEK-EGGKNNIQAQ-----QNLE--- 1832

Query: 681 NKYNSTQQVIQDLNKEIALQKESLSLQAQLDKAL--QKEKHYLQTTITKEAYDALSR-K 737
 N ++ Q+ +Q+ KE+ Q L +LD L QKE H ++ Y+ L +
 Sbjct: 1833 NVFDDVQKTLQE--KELTCQ--ILEQKIKELDSCLVRQKEVHRVEMEELTSKYEKLOALQ 1888

Query: 738 SAACQDDLTQALEKLNHVTSETKSLOQSLTQTQEKKAQ-LEEEIIAYEERMKKLNTEL-- 794
 ++ T+ LE+ S++ +Q L E + LE ++ E +KL E+
 Sbjct: 1889 QMDGRNKPTELLEENTEESKSHLVQPKLLSNMEAQHNDLEFKLAGAEREKQKLGKEIVR 1948

Query: 795 --RKLRGFHQESELEVHAFDCKLEEMSCQVLQWQKHQNDLKMMLAAKEEQREFQEEMAA 852
 + LR +E + E+ K+ ++ + ++ Q+Q +LK + ++ +REF ++A
 Sbjct: 1949 LQKDLRMLRKEHQEQELEILKKEYDQEREKIK-QEQEDLELKHNSLTKQLMREFNTQLAQ 2007

Query: 853 LKENLLEDDKEPCCLPQWSVPKDTCLRYRGNDQIMTNLEQWAKQKQVANERKLGNLREQV 912

Sbjct: 2008 ++ L KE Q V + + Q TN Q K K+A EK + R
KEQELEMTIKETINKAQ-EVEAEELLESHE---QEETN--QLLK--KIA-EKDDDLKRTAK 2057

Query: 913 NYIAKLSGEKDLHLSVMVHLQOENKKLKEIEEKKMKAEN 952
Y L ++ + + LQ + ++L+K+ ++K + EN

Sbjct: 2058 RYEEILDAREEEMTAKVRDLQTLEELQKKYQQKLEQEEN 2097

Score = 300 (45.0 bits), Expect = 3.7e-22, P = 3.7e-22
Identities = 195/961 (20%), Positives = 435/961 (45%)

Query: 1 MKDEAGERDREVSSLSKLLSLQLDIKN--LHDVCKRQRKTLQDNQLCMEEAMSSSHDKK 58
+KD+ + +N K L +LD+K L + + L+ +EE ++ D+

Sbjct: 657 LKDKEIIFQAHIEEMNEKTLE-KLDVKQTELESLSSELSEVLKARHK-LEEELSVLKDQT 714

Query: 59 QAQALAFESESEVEFGSSKQCHLRQLQOLKKLLV-LQEELEFHTTEELQTSYYSIRQYQSI 117
+E E + K H +Q+ + K+ V +Q+ + ++ L++

Sbjct: 715 DKMK---QELEAKMDEQKNHHQQVDSIIKEHEVSIQRTEKALKDQINQLELLKERDKH 771

Query: 118 LEKQTSIDLVLHHHCKLKEDEVILYEEEMG--NHNENTGEKLHLAQEQLALAGDKIASL 174
L++ + + L K E E+ ++ ++ T E+ +EQLA K+ L

Sbjct: 772 LKEHQAHVENLEADIKRSEGELQOASAKLDVFSQYSQATHEQTKAYEEQLAQLOQKLLDL 831

Query: 175 ERSNLNLYRDKYQSSLSNIELLECQVKMLQELGGIMQ-EPENKGDHRSKVRIYTSPCMIQ 233
E L + + + + ++ + ++ +M Q E +N KV+ T

Sbjct: 832 ETERILLTKQVAEVEAQKDVCTELDAHKIQVQDLMOQLEKQNSEMEQKVKSLTQ-VYES 890

Query: 234 EHQETQKRLSEVQKVSQQDDLIQELRN---KLACSNALVLEREKALIKLQADFASCTA 289
+ + K + Q + ++++I ++R ++ + +E ++ L ++ +

Sbjct: 891 KLEDGNKEQEQTQKILVEKENMILQMQREGQKKEIILTQKLSAKEDSIHILNEEYET--- 947

Query: 290 THRYPPSSSEECEDIKKILKHLQEQKDSQCLHVEEYQNLVKDLRVELEAVSEQKRNIMKD 349
++ + ++ E +K+ K +QE + L E L K+L +S++++

Sbjct: 948 --KFK-NQEKMEKVKQKAKEMQETLKKLLDQEA--KLKKELENTALELSQKEKQFNAK 1002

Query: 350 MMKL-ELDLHGLREETS-A-HIERKDKDITILQCRQLQELQLEFTETQKLTLLKDKFLQEKD 407
M+++ + + G+ + S +K++ ++ + +EL + +K ++ + LQE

Sbjct: 1003 MLEMAQANSAGISDAVSRLTNQEQIESLTVHRRELNDVISIWEKKLNQQAEEELQEI 1062

Query: 408 EM-LQELEKKLTQVQNSLLK---KEKELEKQCMATE---LEMTVKEAKQD-KSKEAEC 458
E+ LQE E+++ ++ +L +++E+ K+ E + T+ E ++ K K A

Sbjct: 1063 EIQLQEKEQEVAELKQKILLFGCEKEEMNKEITWLKEEGVKQDITLNLQEQELKQKSAHV 1122

Query: 459 KALQAEVQKLNKNSLEAKQOERLAAQQAQCKEEAALAGCHLEDTRKRLQKGLLLDKQKA 518
+L + KKK LE+ + + ++ +E+ E+ +RK+ + L K K

Sbjct: 1123 NSLAQDETLLKAHLEKLEVDLNLKSLKENTFLQEQVLKMLAEEDKRKVSE--LTSKLKT 1180

Query: 519 DTIQELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLKLENSDKEKRQLOKTV 578
T +E Q +K + E + +K EEL+++L +K E + K + +

Sbjct: 1181 -TDEEFQSLKSSHEKSNKSLKEDKSLFKLLSEELAIQLDICCCKTEALLEAKTN--ELIN 1237

Query: 579 EQDMKMNMDLDRIKH-QHREOGSIKCKLEEDLQEQATKLEDKREQLKKSKEHEKLMGEGEL 637
K N +L RI H QHR K++E L T + + QL++ E + +

Sbjct: 1238 ISSSKTNAILSRISHCQHRTT-----KVKEALLIKTCTVSELEAQLRQLTEEQNTLNISF 1292

Query: 638 EALRQEFKKD---KTLKENSRLKEENENLR-----AELQCCSTQLESSL---- 680
+ + ++K+ K++K + L E E L+ +E + C TQL+ L

Sbjct: 1293 QQATHQEEKENQIKSMKADIESLVTEKEALQKEGGNQQQAASEKESCITQLKKELSENI 1352

Query: 681 NKYNTSQVQIQLNKEIALQKESLMSLQALDKALQ-KEKHYLQTTITKEAYDALSRKSA 739
N ++ +++ EI+ + L L QL ++ EK +++ K+ YD +

Sbjct: 1353 NAVTLMKEELKEKKVEISSLSKQLTDLNVQLQNSISLSEKEAAISSLRKQ-YDEEKCELL 1411

Query: 740 ACQDDLTQALEKLN-HVTSETKSLQQLTQTEKKAQLEEEI IAYEERMKKLNTLELRL 797
DL+ ++ L+ S + + + E K + + ++ +K+L +L K

Sbjct: 1412 DQVQDLSFKVDTLSEKISALEQVDDWSNKFSEWKKKAQSRFTQHQNVTVELQIQLELKS 1471

Query: 798 RGFHQESELEVHAFDCKLEEMSCQVLOWQKHQNDLKMALAAKEEQLR-EFQEEAALKEN 856
+ +++ E +++ ++L+++ + + + ++D + KE L E + + A + E

Sbjct: 1472 KEAYEKDE-QINLLKEELDQONKRFDCLEKEMEDDKSKMEKKESNLETELKSTARIME- 1529

Query: 857 LLEDDKEPCCLPQWSPKDTCLRYRGNDQIMTNLEQWAKQKQVANERKLGNLREQVNYIA 916
LED + + T + N+ ++ N Q OK K +L +++ +

Sbjct: 1530 -LEDH-----ITQKTIEIESLNE-VLKNNYQ----QKDIHK---ELVQKLQHFQ 1570

Query: 917 KLSGEKDH----LHSMVHLQOENKKLKEIEEKKMKAENTRLCTKA 959
+L EKD+ ++ L+ + +K E+E KK + E+ L K+

Sbjct: 1571 ELGEEKDNVKEAEKILTLENQVYSMAELETKKKELEHVNLVSVKS 1617

Score = 298 (44.7 bits), Expect = 6.1e-22, P = 6.1e-22
Identities = 207/886 (23%), Positives = 412/886 (46%)

Query: 47 MEEAMNSSHDKKQAALAFESEVEFGSSKQCHLRQLQQLKKLLVLQQLQEFHTEELQ 106
+ E N + + Q EE E + S K ++ L + LQ+E +
Sbjct: 1281 LTEEQNTLNISFQQATHQLEEKENQIKSMKA----DIESLVTEKEALQKEGGNQQAASE 1336

Query: 107 SYSSLRQYQSILEKQTSIDLVLHHHCKLKEDEVILYEEEMGNHNENTGEKHLAQEQAL 166
+ Q + L + + + L+ K K+ E+ +++ + N + L++++ A
Sbjct: 1337 KESCITQLKKELSENINAVTLMKEELKEKKVEISSLSQLTDLNVQLQNSISLSEKEAA- 1395

Query: 167 AGDKIASLERSLNLRYDKYQSSLSNIELLECQVKMLQGEGLGIMGQEPENKGDHSHKVRIY 226
I+SL + Y ++ L ++ L +V L E + Q + S+ +
Sbjct: 1396 ----ISSLRKQ---YDEEKCELLDQVQDLSFKVDTLSEKISALEQVDDWSNKFSEWK-K 1447

Query: 227 TSPCMIQEHQETQKRLS-----EVWQKVSQDDLIQEL--RNK-LACSNALVLE--- 272
+ +HQ T K L E ++K Q + L +EL +NK C + +
Sbjct: 1448 KAQSRFTQHONTVKELQIQLELKSKEAYEKDEQINLLKEELDQONKRFDCCLKGEMEDDKS 1507

Query: 273 -REKALIKLOADFASCTAT----HRYPPSSSEECEDIKKILKHLQEQKDSOCLHVEEYQN 327
EK L+ + S TA + + E E + ++LK+ +QKD E++
Sbjct: 1508 KMEKESNLETTELKSQTARIMELEDHITQKTEIESLNEVLKNYNQKKDI-----EHKE 1561

Query: 328 LVKDLRVELEAVSEQKRNIMKDMMLKLELDLHGLREETSABIERKDKDI--TILQCRLOEL 385
LV+ L+ + + E+K N +K+ + L L A +E K K++ L + +E
Sbjct: 1562 LVQKLQ-HFQELGEEKDNRVKEAEKILTLENQVYSMAELETKKKELEHVNLSVKSKEE 1620

Query: 386 QLEFTETQKLTLLKDKFLQEKDEMLQELEKLTQVQNSLLKKEKELEKQOCMATELEMTV 445
+L+ E + L+ + + E+ ++ E+K+ ++ LL + +E E+Q TE ++
Sbjct: 1621 ELKALEDL--LESES-AAKLAELKRKAEQKIAAIKKQLLSQMEKEEQYKKGTESHLSE 1676

Query: 446 KEAQDKSKEAECKALQAEVQKLKNSLEEAKQERLAAQQAACK-EEAALAGCHLEDTQ 504
K + +E E L+ +++ ++S E R A AA + EEA GC + +
Sbjct: 1677 LNTKLQE-REREVHILEEKLKSVESQSETLIVPRSAKNVAAYTEQEEADSQGCQVQKTYE 1735

Query: 505 RKLQKGLLLDKQKADTIQELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLE 564
K+ +L + + + LQR Q +KE +++ + R + +E ++L A K
Sbjct: 1736 EKIS---VLQRNLTEKEKLLQVRVG--EKEETVSSHFEM--RCQYQERLIKLEHAEAKQH 1788

Query: 565 NSDKEKRQLQKTVAEQDMKMNMDLDRKHQHREOG--SIKCK--LE---EDLQ-----E 611
LQ+ + E++ K + ++ +H +E G +I+ K LE +D+Q E
Sbjct: 1789 EDQSMIGHLQEELEEKNNKYSILV--AQHVEKEGGKNNIQAQONLENVDDVQKTLQKEKE 1846

Query: 612 AT-KLLEDKREQLKKSKEHEKLMEG-ELEALRQEFKKDKTLKENS---KLEENENL 665
T ++LE K ++L +K + E+E L +++K + + R +L EEN
Sbjct: 1847 LTCQILEQKIKELDSCLVRQKEVHRVEMEELTSKYELQALQMDGRNKPTELEENTEE 1906

Query: 666 RAELOCCSTOLESSLN-KYNTSQQVIQDLNKEIALQKESLSLQALQDLKALQKEKHYLOT 724
+++ +L S++ ++N + + +E + ++ LQ L + L+KE H +
Sbjct: 1907 KSKSHLVQPKLLSNMEAQHNDLEFKLAGAEREKQKLGKEIVRLQKDL-RMLRKE-HQEL 1964

Query: 725 TITKEAYDALSRKSAACQDDLTQALEKLNHVTSETKSLOQSLTQTEKKAQLEEEIAYE 784
I K+ YD R+ Q+ + LE L H ++ + +++ TQ +K+ +LE I +
Sbjct: 1965 EILKKEYDQ-EREKIKQEQ--EDLE-LKHNSTLKQLMREFNTQLAQKEQELEMTI---K 2017

Query: 785 ERMKKLNTLRLKRGFHOESELEVHAFDKKLEEMSCQVLQWQKHQNDLKLAAKEEQLR 844
E + K +L HQE E + KK+ E + + K+++ ++L A+EE++
Sbjct: 2018 ETINKAQEVAEELLESHE---ETNQLKKIAEKDDDLKRTAKRYE---EILDAREEEMT 2071

Query: 845 EFQEEMAALKENLLEDDKEPCCLPQWVSP-KDTCRLYRGNDQIMTNLEQWAKQKQVANER 903
++ E L + ++ L Q P D + ++ T L Q K +++ K
Sbjct: 2072 AKVRDLQTLQLEELQKQYQK--LEQEENPGNDNVTIM----ELQTLAQ--KTTLISDSK 2123

Query: 904 LGNQ-LREQVNYIA-KLSGEKDLHLSVMV-HL 932
L Q REQ++ + +L + +++ V HL
Sbjct: 2124 LKEQEFREQIHNLEDRLKKYKENVYATTVGHL 2155

Score = 280 (42.0 bits), Expect = 5.2e-20, P = 5.2e-20
Identities = 209/938 (22%), Positives = 432/938 (46%)

Query: 3 DEAGERDREVS-SLNSKLLSLQLDIKN-LHDVC-KRQRKTLQDNQLCMEEAM-NSSHDKK 58
++ ++ +E+ +L KLL + +K L + + +K Q N +E A NS+
Sbjct: 957 EKVQKAKEMQETLKKKLLDQEAKLKKELENTALELSQKEKQFNAMLEMAQANSAGISD 1016

Query: 59 QAALAFESEVEFGSSKQCHLRQLQQLKKLLVLQQLQEFHTEELQTSYSSLRQYQSIL 118
L + E + S + H R+L + + + ++L EELQ + ++ +
Sbjct: 1017 AVSRLETNQKE-QIESLTEVHRRLENDV---ISIWKKLNQQAELQ-EIHEIQLQEK-- 1069

Query: 119 EKQTSIDL--LLHHHCKLKE-DEVILYEEEMGNHNENTGEKHLAQEQALAGDKIASLE 175
E++ ++L +L C+ +E ++ I + +E G +T +L +Q + + +A E
Sbjct: 1070 EQEVAELKQKILLFGCEKEEMNKEITWLKEEGVKQDITLNLQEQKQKSAHVNSLAQDE 1129

Query: 176 RSLNLRYDKYQSSLSNIELLECQVKMLQGEGLGI--MGQEPENKGDHSHKVRIYTSPCMIQ 233
L + +K + L N L E LQ +L + + +E + K ++ T+ Q

Sbjct: 1130 TKLKAHLEKLEVDL-NKSLKENT--FLQEQVLKMLAEEDKRKVSELTSKLKTTDEEFQ 1186

Query: 234 E---HQETQKRLSEVWQKVSQQDDLIQELRNKL--AC--SNALVLEREKALIKLQADFA 285
H+++ K L + K + L +EL +L C + AL+ + LI + +

Sbjct: 1187 SLKSSHEKSNKSLD---KSLEFKLSEELAIQLDICCKKTEALLEAKTNELINISSSKT 1243

Query: 286 SCTATH-RYPPSSSEECEDIKKILKHLQEOKDSQCLHVEEYQNLVKDLRVELEAVSEQKR 344
+ + + + + I + ++Q + E QN + + E+K

Sbjct: 1244 NAILSRISHCQHRTTKVKEALLIKTCTVSELEAQLRQLTEEQNTLNISFQQATHQLEEKE 1303

Query: 345 NIMKDMMKLELD-LHGLREETSABIERKDKDITILQCRLQELQLEFTET-QKLTLLKKDKF 402
N +K M K +++ L +E + + + + + +L+ E +E +TL K++

Sbjct: 1304 NQIKSM-KADIESLVTEKEALQKEGNGQQQAASEKESCITQLKKELSENINAVTLMKEE- 1361

Query: 403 LQEKDEMLQELEKKLTVQNSLLKKEKELEKQCCMATELEMTVKEAKQDKSKEAECKALQ 462
L+EK + L K+LT + N L+ L +++ + L E K + + + + L

Sbjct: 1362 LKEKKVEISSLSKQLTDL-NVQLQNSISLSEKEAAISSLRKQYDEEKCELLOQVQ--DLS 1418

Query: 463 AEVOKLKNLSLEEAKQOERLAAQQAACKEEAALAGCHLEDTQRKLQKGLLLDKQKA---- 518
+V L A +Q + + ++ K++A ++T ++LQ L L ++A

Sbjct: 1419 FKVDTLSEKISALEQVDDWSNKFSEWKKKAQSRFTQHONTVKELQIQLELKSKEAYEKD 1478

Query: 519 DTIQELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLENSDKERQLOKTVA 578
+ I L+ EL K +E ++ ++E+ L +L++ +L+ +

Sbjct: 1479 EQINLLKEELDQONKRFDCLEGGEDDKSMEKKESNLET---ELKSQTARIMELEDHIT 1535

Query: 579 EQDMKMNDMLDRIKHQHREQGSICK-LEEDLQEATKLEDKREQLKKSKEHEKLMEGEL 637
++ +++ + + +K+ + +Q I+ K L + LQ +L E+K ++K+++E +E ++

Sbjct: 1536 QKTIEIESLNEVLKN-YNQOKDIEHKELVQKLQHFQELGEEKDNRVKEAEKILTLENQV 1594

Query: 638 EALRQEFKKDKTLKENSRLKEEENENLRAELQCCSTQLES-SLNKYNTSQQVIQDLNKE 696
+++ E + K K L+ + ++ + E L+A L+ +LES S K ++ + ++

Sbjct: 1595 YSMKAELETKKKELEHVNLVSVKSKEELKA-LE---DRLESESAKL---AELKRKAEOK 1647

Query: 697 IALQKESLMSLQALQDLKALQEKHYLQTTITKEAYDALSRKSAACODDLTQALEKLNHVT 756
IA K+ L+S Q++ +KE+ Y + T + L+ K + ++ EKL V

Sbjct: 1648 IAAIKQLLS---QME---EKEEQYKKG--ESHLSELNTKLQEREREVHILEEKLKSVE 1699

Query: 757 S---ET---KSLQSLTQTOEKKAQLEEEII-AYEERMKKLNTLRLRGFQHESELEV 808
S ET +S + T++++A + + YEE++ L L E E +

Sbjct: 1700 SSQSETLIVPRSAKNVAAYTEQEEADSQGCQVQKTYEEKISVLQRNLT-----EKEKLL 1752

Query: 809 HAFDKKLEEMSCQVLQWQKHQNDLKMLAAKEEQLEFQEEAALKENLLEDDKEPCCLP 868
++ EE + + Q+Q L L E + E Q + + L+E L E +K+ +

Sbjct: 1753 QRVGQKEETVSSHFMRCQYQERLIKLEHAEAKQHEDQSMIGHLQEELEEKNNKYSLV 1812

Query: 869 QWSVPKDTCLRYRGNDQIMTNLEQ-WAKQKQVANKE-LGNQLREQ-VNYIAKLSGEKDH 925
V K+ + N Q NLE + QK EK L Q+ EQ + + + + +

Sbjct: 1813 AQHVEKEGGK---NNIQAKQNLNENFDDVQKTLQEKELTCQILEQKIKELDSCLVRQKEV 1869

Query: 926 HSV-MVHLQQENKKLK 940
H V M L + +KL+

Sbjct: 1870 HRVEMEELTSKYEKLO 1885

Score = 227 (34.1 bits), Expect = 2.5e-14, P = 2.5e-14
Identities = 160/716 (22%), Positives = 318/716 (44%)

Query: 233 QEHQETQKRLSEVWQKVSQQDDLIQE-LRNKLACSNALV-LEREKALIKL-QADFASCTA 289
+E +TQ ++ +V + L + + + L S++ L R + L + D S TA

Sbjct: 53 RESGDTQSFAQKLQLRVPSVESLFRSPIKESLFRSSSKESLVRTSSRESLNRLDLDSSTA 112

Query: 290 THRYPPSSSEECEDIKKILKHLQEOKDSQCLHVEEYQNLVKDLRVELEAVSEQKRNIMKD 349
+ P E ED+ L +++ Q L + + R + + + + +

Sbjct: 113 SFDPPSDMOSEAEDLVGNSDSLNEQLIQRLR--RMERSLSSYRGKYSLVTAQMLQRE 170

Query: 350 MMKLELDLHGLREETSABIERKDKDIT-ILQCRLQELQLEFTETQKLTLLKKDKFLQEKDE 408
KL+ G+ ++ +DK + I + R +ELQ++ + L + D L+EKD+

Sbjct: 171 KKKLQ----GILSQS-----QDKSLRRIAELR-EELQMDQQAKKHLQEEFDASLEEKDQ 219

Query: 409 MLQELEKKLTVQVNSLLKKEKELEKQCCMATELEMTVKEAKQDKSKEAECKALQAE---V 465
+ L + ++ ++ L ++ + + +LE + + +++ E++ + + + V

Sbjct: 220 YISVLQTVSLLKQRLRNGPMNVDLKPLP-QLEPQAEVFTKEENPESOGEPVVEDGTSV 278

Query: 466 QKLKNSLEEAKQOERLAAQQAACKEEAALAGCHLEDTQRKLQKGLL-LDKQKADTI 521
+ L+ + K+QE L ++ Q KE+ L E Q +L + L L+K K +

Sbjct: 279 KTLETQQRVKRQENLLKRCKETIQSHKEQCTLLTSEKEALQEQLDERLQELEKIKDLHM 338

Query: 522 QELQRELQMLQKESMAEKEQTSNRKRVEELSLELSEALRKLENSDKERQLOKTVAEQD 581
E + + L+ ++ E+ + + E ++EL E + R K + Q

Sbjct: 339 AEKTKLITQLRDAKNLIEQLEQDKGMVIAETKQRMHETLEMKEEIEAQLRSRIKQMTTQG 398

Query: 582 MKMNDMLDRIKHQHREQGSICKLEEDLQEAT-KLLEDKREQLK---KSKEHEKL-MEGE 636
 ++ + ++ + E+ + +EA KL + EQ+K K+ E E++ ++ E
 Sbjct: 399 EELREQKEKSERAAFELEKALSTAQKTEEARRLKAEMDEQIKTIEKTSEEERISLQQE 458

Query: 637 LEALRQEFKK-KDKTLKENSRLKEEENENLRAELQCCSTQLESSLNKYNTSQQVIQDLNK 695
 L ++QE K+ +E KL++ +E EL +L L T ++ Q+ K
 Sbjct: 459 LSRVKQEVVDMKKSSEEQIAKLQKLHEK---ELARKEQELTKKLQ---TREREFQEQMK 512

Query: 696 EIALQKESLMSLQAQLDKALQKEKHLYLQTTITKEAYDALSRKSAACQDDLTQALEKLN-H 754
 +AL+K L+ +K Q+ + + K+A S DL Q E
 Sbjct: 513 -VALEKSQSEYLLKISQEKEQESLAELELQKKAILTESENKLR---DLQQAETYRTR 568

Query: 755 VTSETKSLQQSLTQTEKKAQLEEEIAYEERMKKLNTLRLRGFHOESELEV--HAFD 812
 + SL++SL QE K Q ++ + E K N E+ + H+ +ELE H D
 Sbjct: 569 ILELESSLEKSL---QENKNQSKDLAVHLEAKNKHKEITVMVEKHK-TELESKHQD 624

Query: 813 KKLEEMSCQVLQWQKHQNDLKMMLAAKEEQLRE-----FQEEMAALKENLLED-DK 862
 E QVL+ +Q+Q +++ L K EQ +E FQ + + E LE D
 Sbjct: 625 ALWTE-KLQVLK--QQYQTEMEKLEKCEQEKETLLKDKEIIFQAHIEEMNEKTLEKLDV 681

Query: 863 EPCCLPQWSPKDTCLRYRGNDQIMTNLEQWAKQKQVANKEKLGNLREQVNYIAKLSGEK 922
 + L S+ + + + ++ L Q ++L ++ EQ N+ +
 Sbjct: 682 KQTELE--SLSELSEVLKARHKLEELSVLKDQTDKMKQELEAKMDEQKNHHQQVDSI 739

Query: 923 DHLHSMVHLQENKKLKEIEEKKM 948
 H V + Q+ K LK +I + ++
 Sbjct: 740 IKEHEVSI--QRTEKALKDQINQLEL 763

Score = 183 (27.5 bits), Expect = 1.3e-09, P = 1.3e-09
 Identities = 132/584 (22%), Positives = 251/584 (42%)

Query: 409 MLQELEKKLTQVQNSLLKKEKELEKQCMATELEMTVKEAK-QDKSKEAECKALQAEVQK 467
 M ++L++K+++ Q L + + +T M + + ++ E + Q
 Sbjct: 1 MFKKLKQKISEEQQLQALAPAQASSNSSTPTRMSRTSSFTEQLDEGTPNRESGDTQS 60

Query: 468 LKNSLE-EAKQQRERLAAQQAQCKEEAALAGCHLEDTQKRLQKGLLLDKQKA--DTIQEL 524
 L+ E L + ++ + + R+ L LD A D ++
 Sbjct: 61 FAQKLQLRVPSVESLFRSPIKESLFRSSSKESLVRTSSRESLNRDLDSSTASFDPPSDM 120

Query: 525 QRELQMLQKESSMAEKEQTSNRKRVEELSL-----ELSEALRKLNSDKEKRLQKTVAE 579
 E + L S KEQ R R E SL + SE + + +EK++LQ +++
 Sbjct: 121 DSEAEDLVGNSDSLNEQLIQLRLRMERSLSSYRGKYSSELVTAYQMLQREKKKLQGISLQ 180

Query: 580 -QDMKNDMLDRIKHQHREQGSICKLEE---DLQEATK---LLEDKREQLKKSKEHEKL 632
 QD + + + + +Q + K EE L+E + +L+ + LK+ + +
 Sbjct: 181 SQDKSLRRIAELREELQMDQAKKHLQEEFDASLEEKDQYISVLQTVSLLKQRLRNGPM 240

Query: 633 MEGELEALRQ-EFKKDKTLKENSRLKEE---ENENLRAELQCCSTQLESSLNKYNTSQ 688
 L+ L Q E + + T +EN E E+ L+ +++ N ++
 Sbjct: 241 NVDVLKPLPQLEPQAEVFTKEENPESDGEPVVEDGTSVKTLETQQRVVRQENLLKRCKE 300

Query: 689 VIQDLNKEIALQKESLMSLQAQLDKALQKEKHLYLQTTITKEAYDALSRKSAACQDDLTQA 748
 IQ ++ L +LQ QLD+ LQ E ++ E +++ A +L +
 Sbjct: 301 TIQSHKEQCTLLTSEKEALQEQLDERLQ-ELEKIKDLHMAEKTCLITQLRDA--KNLIEQ 357

Query: 749 LEK-LNHVTSETKSLQQSLTQTEKKAQLEEEIAYEERMKKLNTLRLRGFHOESELE 807
 LE+ V +ETK + + +T E K EEEI R+K++ T+ +LR Q+ + E
 Sbjct: 358 LEQDKGMVIAETK---RQMHELTLEMK---EEIEAQLRSRIKQMTTQGEELR--EQKEKSE 409

Query: 808 VHAFDKKLEEMSCQVLQWQKHQNDLKMMLAAKEEQLREFQ---EEMAALKENLLEDDKE 863
 AF EE+ + QK + K+ A +EQ++ + EE +L++ L +E
 Sbjct: 410 RAAF---EELEKALSTAQKTEEARRLKAEMDEQIKTIEKTSEEERISLQQELSRVKQE 465

Query: 864 PCCLPQWSPKDTCLRYRGNDQIMTNLEQ-WAKQKQVANKEKLGNLRL-----EQVNYIAK 917
 + + S + +L + +++ + EQ K+ + + Q++ Q Y+ K
 Sbjct: 466 VVDVMKKSSEEQIAKLQKLHEKELARKEQELTKKLQTREREFQEQMKVALEKSQSEYL-K 524

Query: 918 LSGEKDHLHSMVHL-QQENKKLKEIEEK---KMAENTRLCTKALGPSRTSTQREK 972
 +S EK+ S+ + L+ + K+ E E K + +AE R L S +S Q K
 Sbjct: 525 ISQEKEQEQESLAELELQKKAILTESENKLRDLQQAETYRTRILELESSLEKSLQENK 584

Pedant information for DKF2phtes3_lg13, frame 1

Report for DKFZphtes3_lg13.1

[LENGTH] 1007
 [MW] 117480.77
 [PI] 5.90

[HOMOL] TREMBL:AF092090_1 product: "cpl151"; Rattus norvegicus cpl151 mRNA, partial cds.
0.0

[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 5e-15
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w]
5e-15

[FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 1e-11
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YDR356w] 1e-11
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR356w] 1e-11
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w] 1e-08
[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision
repair) [S. cerevisiae, YKR095w] 1e-08
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR309c] 1e-08
[FUNCAT] 1 genome replication, transcription, recombination and repair [M.
jannaschii, MJ1322] 4e-06

[FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YLR086w] 9e-06
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YHR023w
MYO1 - myosin-1 isoform] 3e-04
[FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 -
myosin-1 isoform] 3e-04

[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-04
[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR134c] 5e-04
[EC] 3.6.1.32 Myosin ATPase 1e-16

[PIRKW] nucleus 3e-10
[PIRKW] phosphotransferase 6e-09
[PIRKW] duplication 2e-06
[PIRKW] citrulline 2e-12
[PIRKW] tandem repeat 1e-16
[PIRKW] endocytosis 2e-13
[PIRKW] heart 8e-13
[PIRKW] transmembrane protein 1e-13
[PIRKW] serine/threonine-specific protein kinase 6e-09
[PIRKW] zinc finger 2e-13
[PIRKW] metal binding 2e-13
[PIRKW] DNA binding 4e-12
[PIRKW] muscle contraction 1e-16
[PIRKW] acetylated amino end 1e-11
[PIRKW] actin binding 1e-16
[PIRKW] mitosis 5e-15
[PIRKW] microtubule binding 5e-15
[PIRKW] ATP 1e-16
[PIRKW] thick filament 1e-16
[PIRKW] phosphoprotein 4e-16
[PIRKW] skeletal muscle 2e-14
[PIRKW] calcium binding 2e-12
[PIRKW] alternative splicing 1e-16
[PIRKW] coiled coil 1e-16
[PIRKW] P-loop 1e-16
[PIRKW] heptad repeat 3e-10
[PIRKW] methylated amino acid 1e-16
[PIRKW] immunoglobulin receptor 2e-06
[PIRKW] peripheral membrane protein 2e-13
[PIRKW] cardiac muscle 8e-13
[PIRKW] hydrolase 1e-16
[PIRKW] microtubule 3e-10
[PIRKW] muscle 8e-13
[PIRKW] EF hand 2e-12
[PIRKW] cytoskeleton 2e-15
[PIRKW] hair 2e-12
[PIRKW] calmodulin binding 2e-13
[PIRKW] Golgi apparatus 3e-10
[SUPFAM] myosin heavy chain 1e-16
[SUPFAM] conserved hypothetical P115 protein 1e-07
[SUPFAM] centromere protein E 5e-15
[SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 6e-09
[SUPFAM] calmodulin repeat homology 2e-12
[SUPFAM] myosin motor domain homology 1e-16
[SUPFAM] alpha-actinin actin-binding domain homology 2e-07
[SUPFAM] plectin 2e-07
[SUPFAM] trichohyalin 2e-12
[SUPFAM] pleckstrin repeat homology 8e-08
[SUPFAM] ribosomal protein S10 homology 2e-07
[SUPFAM] giantin 3e-13
[SUPFAM] protein kinase homology 6e-09
[SUPFAM] protein kinase C zinc-binding repeat homology 8e-08
[SUPFAM] kinesin motor domain homology 5e-15
[SUPFAM] human early endosome antigen 1 2e-13
[SUPFAM] M5 protein 1e-07
[PROSITE] LEUCINE ZIPPER 7
[PROSITE] MYRISTYL 2
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] CK2_PHOSPHO_SITE 20

Prosites for DKFZphtes3 1q13.1

(No Pfam data available for DKFZphtes3 lgl3.1)

group: cell structure and motility

DKFZphtes3_1k11 encodes a novel 589 amino acid protein with strong similarity to *Mus musculus* actin-binding protein (ENC-1).

Ectoderm-neural cortex-1 protein (ENC-1) is an early and highly specific marker of neural induction in vertebrates. The protein is related to the kelch family proteins and is expressed during early gastrulation in the prospective neuroectodermal region of the epiblast and later in development throughout the nervous system (NS). ENC-1 functions as an actin-binding protein organising the actin cytoskeleton during neural differentiation and development of the NS. The novel protein is highly similar to ENC-1.

The new protein can find application in modulation of cyto skeleton organisation in human testicular cells.

strong similarity to mouse ENC-1

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 3525 bp

Poly A stretch at pos. 3515, polyadenylation signal at pos. 3499

```

1 GGTGGAGAGC CGGCCGACGG GAGCCGCGGC GGAGCCTGTT GAGCTCGCGC
51 GGGCTGCCGG GAGTGGTCTC TGAGGCGGCG GCGGCGGCGG GGATCGTCTC
101 CGGCACGTGGC GCACCATGTC GGTCAGTGTC CATGAGACCC GCAAGTCGCG
151 GAGCAGCAGC GGGTCCATGA ACGTCACCCT CTTCCACAAG GCCTCCACCC
201 CGGACTGTGT GCTGGCCAC CTCAACACGC TTCGCAAGCA CTGCATGTTC
251 ACCGACGTCA CACTCTGGGC GGGCGACCGT GCCTTCCCCT GTCAACGTGC
301 CGTGTGGGCC GCCTCTAGCC GCTATTTTGA GGCCATGTTT AGCCATGGCC
351 TTCGGGAGAG CCGGGATGAC ACTGTCAACT TCCAGGACAA CCTGCACCCG
401 GAGGTGCTGG AGCTGCTGCT GGACTTTGCC TACTCCTCAC GCATCGCCAT
451 CAACGAGGAG AACGCTGAGT CACTGCTGGA GGCAGGCGAC ATGCTGCAGT
501 TCCACGATGT GCGGGATGCT GCCGCGGAGT TCCTGGAGAA GAACCTTTTC
551 CCTCCCAACT GCCTGGGCAT GATGCTGCTC TCGGACGCCC ACCAGTGCCG
601 CCGGCTGTAT GAGTTCTCCT GGCGCATGTG CCTGGTGCAC TTTGAGACGG
651 TGAGGCAGAG CGAGGACTTC AACAGCCTGT CCAAGGACAC ACTGCTGGAC
701 CTCATCTCGA GCTGTAGCT GGAGACCGAG GACGAGCGGG TGGTCTTCGA
751 GGCCATCCTC CAGTGGGTGA AGCAGGACCT GGAGCCACGG AAGGTCCACT
801 TGCCCGAGCT CCTCCGCAGC GTGCGTCTGG CCTTGCTGCC GTCCGACTGC
851 CTGCAGGAGG CCGTCTCCAG CGAGGCCCTC CTCATGGCAG ACGAGCGCAC
901 CAAGCTTATC ATGGATGAGG CCCTGCGCTG CAAGACCAGG ATCTGCAGA
951 ATGATGGCGT GGTCACCAGC CCCTGTGCCC GGCCACGCAA GCGGGGCCAC
1001 ACGCTACTCA TCCTGGGGGG CCAGACCTTC ATGTGTGACA AGATCTACCA
1051 GGTGGACCAC AAGCCCAAGG AGATCATCCC CAAGCCGAC CTGCCCAGCC
1101 CCCGGAAGGA GTTCAGCGCC TCAGCGATCG GCTGCAAGGT CTATGTGACG
1151 GGGGGCAGGG GCTCCGAGAA CGGGGTCTCC AAGGATGTCT GGGTGTACGA
1201 CACCGTACAT GAGGAATGGT CCAAGGCGGC GCCATGCTG ATTGCCCGCT
1251 TTGGCCATGG CTCAGCTGAG CTGGAGAAT GCCTCTATGT GGTGGGGGGA
1301 CACACATCCC TGGCAGGGGT CTTCCCGGCC TCGCCTTCTG TCTCCCTGAA
1351 ACAAGTGGAG AAATACGACC CTGGGGCCAA CAAGTGGATG ATGGTGGCCC
1401 CTTTGGCGGA TGGCGTCAGC AATGCCGCG TGGTGAGTGC CAAGCTGAAG
1451 CTCTTTTGTG TGGAGGAAC CAGCATCCAC CGGGACATGG TGTCCAAGGT
1501 CCAGTGCTAT GACCCCTCGG AGAACAGGTG GACGATCAAG GCCGAGTGCC
1551 CCCAGCCTTG GCGGTACACA GCCGCTGCCG TCCTGGGCAG CCAGATCTTC
1601 ATCATGGGAG GTGACACGGA ATTCACAGCC GCCTCGCCCT ACCGCTTTGA
1651 CTGTGAGACC AACCAGTGGA CGCGGATTGG GGACATGACT GCCAAGCGCA
1701 TGTCTTGCCA TGCCCTGGCT TCCGGCAACA AGCTCTATGT GGTGCGGGGC
1751 TACTTTGGGA CCCAGAGGTG TAAGACTCTG GACTGTATG ACCCACTTC
1801 AGATACATGG AACTGCATCA CCACAGTGCC CTACTCACTT ATCCCCACGG
1851 CCTTTGTGAG CACCTGGAAG CACCTGCCCG CGTGAGGAGC ACCTGCTGAG
1901 CCGGCCAGA GCGCGGCCCT CAGTGTACA GCGTGGCCTT GCTTGTCTGC
1951 CACAGCGGGA GCTAAGCCGG CCCTGGGCCA GCACTCCGAG AGGTGGAAGG
2001 GGCCCTTGCA GCTCTGGGGA GCAGCAGCCT TGGGCTGTTG TGAGCTTTAG
2051 GCAAGAGAGG AGAAGCATCT CTTGCATCCG TGCCCTTGGG GGCTCTTCA
2101 GCTTTGCACT GGTTTGTGGG AAGACATACC TCCCAGAGGG GCATGGACTG
2151 CCACCAAGAG TGACCCCTGGC GTCGGGGAGA AGGACACTTG CAGAGCCTTG
2201 AGATCACTGT TTTGGCAGGT CCTGGACTGG GCGCGGCGAG GCAGGGGCG
2251 GGAGGCGCCC CGGGTGGGCT TTGGGGCTGC GGCATGCCA CACATCCTTT
2301 CCTCTCTGGC CTGCCCTGCT GGGGCTCTAC TGCCATCTAT AGATGGTGTG
2351 CTGGGCTGGG GAACTAGGT TCCCAGGGGT TGAGACCAGA AAGGTGACCA
2401 AGACAGATTT TTTAAGGTGC AGAACTGCA GGGGGGCTC AGTGACATCC
2451 ATGAGGCTTT ATTAGCAAAG GACACCCAGA CCTCCAAGGT TTGTGGGCCC
2501 CTTCCACAAA GCTGTAAGTC CCAGCCACCC TACTCAGGGC CTTGCTCAGT
2551 GCTGTGGCCC GGTGGGGACA CAGTTGCTCG TGGCCACTCA GTGGAGCTGG
2601 GCCTGCAGCA GACTCAAGGC TCCGAGTGCC CTGGGGGTCA CCCCTCCCCT
2651 CCCTCTCTCA GAGCCACCC TGAGAGGCAG CAGTGACCCC CATGGCACAC
2701 ACCTGCCAAC AGCACTGGGG GCTTCTCCCC AGGAGACCAC GCTGCCCTCC

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2751 AAGACCAGGA GCAGCTGTGA GCTGGAGACA GCAGAGGGAC CCCAGGGTGT
2801 CCCCTGCAGA TCCCACCAGG GCCGCATCCA TCTCAGTGTG GAGGACAGTG
2851 ACGGGACCCT CACCATCCTC TTGCGTTTTG GCCCCCATTT GCTCCCTGAG
2901 CTCCAAGATA AGAATGGCCC CGAGAGAACT GCTGAACATT TGTTTCATTGC
2951 TGTACCTCC TGAGTCACTG GGGTCCCTCA CCAGCACCTC CCTGACACCT
3001 GGGCTATGGA GAGGTTGGCG CCTGTCACTG ACCATCCTAA TGCCTCTCGC
3051 TCACTCCCAA GCCACCATT GAGAGGGAGG GGTGTTGGTG CCCTGACAGG
3101 GACTGGGCAG GGTGTCCAAA CTTGGGGCTT CCCAGGCACC TGCAGTGTGA
3151 ACACTGCTTG GCTGGCTCAA GATTAGGGCC GCGGAGGGGG CTGTGCACAT
3201 ACCAGTTACT TAAGCAGCCA CGAGTGTCCC CCATGCCTTG GTGCGGGTCC
3251 TGGAGGCCCTC TTGGGGGTGG GACCTTTGGG CAGGGTTTGC CCACTGACGC
3301 GCCCGCCATG GGGCACTGGC TGCATGGGGC TCCTTGGACC CTGTAGAGCC
3351 AGCAGGAGCC TGGCCCGGGG GACTGCAGGG AGGGTGCCTG GACCCGTGGG
3401 GTTGCTTCAT TGAGATAAAG CACACTTATC ACATAGCACA AAGGACGTGC
3451 CATGGTGTCT TCCCAAAAAG TTGTGTTGCT TTTATCAGTT TTCTAACTTA
3501 ATAAAAAGAG TTGAGAAAAA AAAAA

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BLAST Results

No BLAST result

Medline entries

98350113:

Cloning of human ENC-1 and evaluation of its expression and regulation in nervous system tumors.

97252647:

ENC-1: a novel mammalian kelch-related gene specifically expressed in the nervous system encodes an actin-binding protein.

98234394:

NRP/B, a novel nuclear matrix protein, associates with p110(RB) and is involved in neuronal differentiation

Peptide information for frame 2

ORF from 116 bp to 1882 bp; peptide length: 589

Category: strong similarity to known protein

Classification: Cell structure/motility

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1 MSVSVHETRK SRSSTGSMNV TLFHKASHPD CVLAHLNLT R KHCMTDVT L
51 WAGDRAFPCH RAVLAASSRY FEAMFSHGLR ESRDDTVNFQ DNLHPEVLEL
101 LLDFAYSRI AINEENAESL LEAGDMLQFH DVRDAAAEFL EKNLFPSNCL
151 GMLLSDAHQ CRRLYEFSWR MCLVHFETVR QSEDFNSLSK DTLLDLISSD
201 ELETEDERVV FEAILQWVKH DLEPRKVHLP ELLRSVRLAL LPSDCLQEAV
251 SSEALLMADE RTKLIMDEAL RCKTRILQND GVVTPCARP RKAGHTLLIL
301 GGQTFMCDKI YQVDHKAKEI IPKAOLPSPR KEFSASAIGC KVVYVTGGRGS
351 ENGVS KD VVY YDTVHEEWSK AAPMLIARFG HGSAELENC L YVVGGH TSLA
401 GVFPASPSVS LKQVEKYDPG ANKWMVAPL RDGVSNAAVV SAKLKL FVFG
451 GTSIHRDMVS KVQCYDPSEN RWTIKAECPO PWRYTAAAVL GSQIFIMGGD
501 TEFTAASAYR FDCETNQWTR IGDMTAKRMS CHALASGNKL YVVGGYFGTQ
551 RCKTLDCYDP TSDTWCNITT VPYSLIPTAF VSTWKHLPA

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BLASTP hits

Entry MMU65079_1 from database TREMBL:

gene: "ENC-1"; product: "actin-binding protein"; Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.

Score = 2402, P = 1.9e-249, identities = 440/589, positives = 513/589

Entry AF059611_1 from database TREMBLNEW:

gene: "NRPB"; product: "nuclear matrix protein NRP/B"; Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds.

Score = 2400, P = 3.0e-249, identities = 440/589, positives = 512/589

Entry AF010314_1 from database TREMBL:

gene: "PIG10"; product: "Pig10"; Homo sapiens Pig10 (PIG10) mRNA, complete cds.

Score = 1745, P = 7.8e-180, identities = 335/507, positives = 403/507

Entry KELC_DROME from database SWISSPROT:
RING CANAL PROTEIN (KELCH PROTEIN). >TREMBL:DMRCPA_1 product: "ring canal protein"; Drosophila melanogaster ring canal protein and ORF2 mRNA, complete cds.
Score = 672, P = 3.9e-66, identities = 168/536, positives = 257/536

Alert BLASTP hits for DKFZphtes3_1k11, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3_1k11, frame 2

Report for DKFZphtes3_1k11.2

[LENGTH] 589
[MW] 65923.45
[pI] 6.10
[HOMOL] TREMBL:MMU65079_1 gene: "ENC-1"; product: "actin-binding protein"; Mus musculus
actin-binding protein (ENC-1) mRNA, complete cds. 0.0
[FUNCAT] 10.05.99 other pheromone response activities (S. cerevisiae, YHR158c)
2e-09
[BLOCKS] BL01016D Glycoprotease family proteins
[PIRKW] zinc finger 1e-08
[PIRKW] DNA binding 1e-08
[PIRKW] transcription factor 1e-08
[SUPFAM] POZ domain homology 3e-68
[SUPFAM] vaccinia virus 59K HindIII-C protein 1e-15
[SUPFAM] A55R protein 5e-29
[SUPFAM] hypothetical protein YHR158c 4e-08
[SUPFAM] A55R protein middle region homology 5e-29
[SUPFAM] myxoma virus M9-R protein 1e-14
[SUPFAM] A55R protein carboxyl-terminal homology 5e-29
[KW] Alpha_Beta

SEQ MSVSVHETKRSRSTGSMNVTLFHKASHPCVLAHLNLTLRKHCMTDVTWAGDRAFPCH
PRD ccc

SEQ RAVLAASSRYFEAMFSGHGLRESRDDTVNFQDNLHPEVLELLLDFAYSRIAINEENAESL
PRD hcc

SEQ LEAGDMLQFHDVDRDAAAEFLEKNLFPSNCLGMMLLSDAHQCRRLYEFWRMCLVHFETVR
PRD hhh

SEQ QSEDFNSLSKDTLLDLISSDELETEDERVVFEAILQWVKHOLEPRKVHLPELLRSVRLAL
PRD hhh

SEQ LPSDCLQEAVSSEALLMADERTKLIMDEALRCKTRILQNDGVVTSPCARPRKAGHTLLIL
PRD ccc

SEQ GGQTFMCDKIYQVDHKAKEIIPKADLPSPRKEFSASAIGCKVYVTGGRGSENGVSKDVWV
PRD ccc

SEQ YDTVHEEWSKAAPMLIARFGHGSAELENCYLVVGHTSLAGVFPASPSVSLKQVEKYDPG
PRD ccc

SEQ ANKWMVMVAPLRDGVSNAAVVSALKLKFVFGGTSIHRDMVSKVQCYDPSENRTIKAECPO
PRD ccc

SEQ PWRYTAAAVLGSQIFIMGGDTEFTAASAYRFDCEINQWTRIGDMTAKRMSCHALASGNKL
PRD ccc

SEQ YVVGGYFGTQRCKTLDCYDPTSDTWNCITVTPYSLIPTAFVSTWKHLPA
PRD eee

(No Prosite data available for DKFZphtes3_1k11.2)

(No Pfam data available for DKFZphtes3_1k11.2)

DKF2phtes3_ln3

group: signal transduction

DKF2phtes3_ln3 encodes a novel 1196 amino acid protein with similarity to *S. pombe* Tup1 protein.

The protein contains 1 WD-40 repeat, which is typical for the beta-transducin subunit of G-proteins. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. In addition, a RGD site is present.

The new protein can find application in modulating/blocking G-protein-dependent pathways.

similarity to Tup1p

complete cDNA, complete cds, EST hits

Sequenced by DKF2

Locus: /map="6q24"

Insert length: 5277 bp

Poly A stretch at pos. 5267, polyadenylation signal at pos. 5244

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1 GCTGCATAAA GCTGAGAGAT GCCTACAGCT GAGAGTGAAG CAAAAGTAAA
51 AACCAAAGTT CGCTTTGAAA AATTGCTTAA GACCCACAGT GATCTAATGC
101 GTGAAAAGAA AAAAAGTGAAG AAAAAAAGTTG TCAGGTCTGA AGAAAACATC
151 TCACCTGACA CTATTAGAAG CAATCTTCAC TATATGAAAG AAACATACAAG
201 TGATGATCCC GACACTATTA GAAGCAATCT TCCCCATATT AAAGAAACTA
251 CAAGTGATGA TGTAAAGTGCT GCTAACACTA ACAACCTGAA GAAGAGCAGC
301 AGAGTCACCT AAAACAAATT GAGGAACACA CAGTTAGCAA CTGAAAATCC
351 TAATGGTGTG GCTAGTGTAG AGGAAGACAA ACAAGGAAAG CCAAATAAAA
401 AGGTGATAAA GACGGTGCCC CAGTTGACTA CACAAGACCT GAAACCGGAA
451 ACTCCTGAGA ATAAGGTTGA TTCTACACAC CAGAAAACAC ATACAAAGCC
501 ACAGCCAGGC GTTGATCATC AGAAAAGTGA GAAGGCAAAT GAGGGAAGAG
551 AAGAGACTGA TTTAGAAGAG GATGAAGAAT TGATGCAAGC ATATCAGTGC
601 CATGTAACCT AAGAAATGGC AAAGGAGATT AAGAGGAAAA TAAGAAAGAA
651 ACTGAAAGAA CAGTTGACTT ACTTTCCCTC AGATACTTTA TTCCATGATG
701 ACAAACTAAG CAGTGAAAAA AGGAAAAAGA AAAAGGAAGT TCCAGTCTTC
751 TCTAAAGCTG AAACAAGTAC ATTGACCATC TCTGGTGACA CAGTTGAAGG
801 TGAACAAAAG AAAGAATCTT CAGTTAGATC AGTTTCTTCA GATTCTCATC
851 AAGATGATGA AATAAGCTCA ATGGAACAAA GCACAGAAGA CAGCATGCAA
901 GATGATACAA AACCTAAACC AAAAAAACA AAAAAGAAGA CTAAGGCAGT
951 TGCAGATAAT AATGAAGATG TTGATGGTGA TGGTGTTCAT GAAATAACAA
1001 GCCGAGATGA CCGGTTTAT CCCAAATGTT TGCTTGATGA TGACCTTGTC
1051 TTGGGAGTTT ACATTCACCG AACTGATAGA CTTAAGTCAG ATTTTATGAT
1101 TTCTCACCCA ATGGTAAAAA TTCATGTGGT TGATGAGCAT ACTGGTCAAT
1151 ATGTCAAGAA AGATGATAGT GGACGGCCTG TTTTCTTTA CTATGAAAAA
1201 GAGAATGTGG ATTAATATTCT TCCTATTATG ACCCAGCCAT ATGATTTTAA
1251 ACAGTTAAAA TCAAGACTTC CAGAGTGGA AGAACAAATT GTATTTAATG
1301 AAAATTTTCC CTATTTGCTT CGAGGCTCTG ATGAGAGTCC TAAAGTCATC
1351 CTGTTCTTTG AGATTTCTGA TTTCTTAAAG GTGGATGAAA TTAAGAATAA
1401 TTCTGAGGTT CAAACCAAG AATGTGGCTT TCGGAAAATT CCCTGGGCAT
1451 TTCTTAAGCT TCTGGGAGCC AATGGAAATG CAAACATCAA CTCAAAACCTT
1501 CGCTTGCAGC TATATTACCC ACCTACTAAG CCTCGATCCC CATTAAAGTGT
1551 TGTTGAGGCA TTTGAATGCT GGTCAAATG TCCAAGAAAT CATTACCCAT
1601 CAACACTGTA CGTAACTGTA AGAGGACTGA AAGTTCCAGA CTGTATAAAG
1651 CCATCTTACC GCTCTATGAT GGCTCTTCAG GAGGAAAAAG GTAAACCAAGT
1701 GCATTGTGAA CGTCACCATG AGTCAAGCTC AGTAGACACA GAACCTGGAT
1751 TAGAAGAGTC AAAGGAAGTA ATAAAGTGGG AACGACTCCC TGGGCAGGCT
1801 TGCCGTATCC CAAACAAACA CCTCTTCTCA CTAAATGCAG GAGAACGAGG
1851 ATGTTTTTTT CTTGATTTCT CCCACAATGG AAGAATATTA GCAGCAGCTT
1901 GTGCCAGCCG GGATGGATAT CCAATTATTT TATATGAAAT TCCTTCTGGA
1951 CGTTTTCATG GAGAATTGTG TGGCCACCTC AATATCATTT ATGATCTTTC
2001 CTGGTCAAAA GATGATCACT ACATCCTTAC TTCATCATCT GTGGCACTG
2051 CCAGGATATG GAAAAATGAA ATAAACAATA CAAATACTTT CAGAGTTTTA
2101 CCTCATCTTT CTTTGTGTTA CACGGCTAAA TTCCATCCAG CTGTAAGAGA
2151 GCTAGTAGTT ACAGGATGCT ATGATTCCAT GATACGGATA TGGAAAGTTG
2201 AGATGAGAGA AGATTCTGCC ATATTGGTCC GACAGTTTGA TGTTCAACAA
2251 AGTTTTATCA ACTCACTTTG TTTTGATACT GAAGGTCATC ATATGTATTTC
2301 AGGAGATTGT ACAGGGGTGA TTGTTGTTTG GAATACCTAT GTCAGATTAA
2351 ATGATTGGA ACATTCAGTG CACCACTGGA CTATAAATAA GGAAATTAAA
2401 GAAACTGAGT TTAAGGGAAT TCCAATAAGT TATTGGAGA TTCATCCCAA
2451 TGGAAAACGT TTGTTAATCC ATACCAAGA CAGTACTTTG AGAATTATGG
2501 ATCTCCGGAT ATTAGTAGCA AGGAAGTTTG TAGGAGCAGC AAATTATCGG
2551 GAGAAGATTC ATAGTACTTT GACTCCATGT GGGACTTTTC TGTTTGCTGG
2601 AAGTGAGGAT GGTATAGTGT ATGTTTGGA CCCAGAAACA GGAGAACAAG
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2651 TAGCCATGTA TTCTGACTTG CCATTCAAGT CACCCATTTC AGACATTTCT
2701 TATCATCCAT TTGAAAATAT GGTTCGATTC TGTGCATTTG GGCAAAATGA
2751 GCCAATTCTT CTGTATATT ACGATTTCCTA TGTTGCCAG CAGGAGGCTG
2801 AAATGTTCAA ACCTACAAT GGAACATTTT CATTACCTGG AATACACCAA
2851 AGTCAAGATG CCTATGTAC CTGTCCAAAA CTACCCATC AAGGCTCTTT
2901 TCAGATTGAT GAATTTGTCC ACACGTAAAG TTCTTCAACG AAGATGCAGC
2951 TAGTAAACA GAGGCTTGAA ACTGTCACAG AGGTGATACG TTCCTGTGCT
3001 GCAAAAGTCA ACAAATCT CTCATTTACT TCACCACCAG CAGTTTCCTC
3051 ACAACAGTCT AAGTTAAAGC AGTCAAACAT GCTGACCGCT CAAGAGATTC
3101 TACATCAGTT TGGTTTCACT CAGACCGGGA TTATCAGCAT AGAAAGAAAG
3151 CCTGTAACTC ATCAGGTAGA TACAGCACCA ACGGTAGTGG CTCTTTATGA
3201 CTACACAGCG AATCGATCAG ATGAACTAAC CATCCATCGG GGAGACATTA
3251 TCCGAGTGTT TTTCAAAGAT AATGAAGACT GGTGGTATGG CAGCATAGGA
3301 AAGGGACAGG AAGGTTATTT TCCAGCTAAT CATGTGGCTA GTGAAACACT
3351 GTATCAAGAA CTGCTCCTG AGATAAAGGA GCGATCCCCT CCTTTAAGCC
3401 CTGAGGAAAA AACTAAATA GAAAAATCTC CAGCTCCTCA AAAGCAATCA
3451 ATCAATAAGA ACAAGTCCCA GGACTTCAGA CTAGGCTCAG AATCTATGAC
3501 ACATTCTGAA TAGGAAAAAG AACAGAGCCA TGAGGACCAA GGACACATAA
3551 TGGATACACG GATGAGGAAG AACAAGCAAG CAGGCAGAAA AGTCACTCTA
3601 ATAGAGTAAA GAATTGAAGA AAAGTTAAGA GCTGCCGAAA TGCACAGAGG
3651 TGAAATGAGT AAACCAAATG GAATTTCTCT TCAGAGTTCA GAATTTTCAG
3701 ATACTAAGGA GGAAGAAAGG ATCCACTACT TCTTGTCTT ATGAATGACT
3751 CTAGAAAAAT CAGAATCAAG TTGTGGGTGG AAAAATCAAC GTGGCCTTTG
3801 AGTTCAGTTG TTATAAACCA TTGTGACTAT TGTTGGTCAA AGTATTGGTA
3851 CTTATATTGT TAGTAATTGC ATCATAATTA CATTACCAGT GTTGGAAAAC
3901 TAATGAAGAA AACACTGTAA TTGCTACTCA GCAATGTGA ATAAAGGTG
3951 TTTGCGTTAT TAGGATGTCT GTTAAGTAAT CATTTAATAT TATTATATTG
4001 GTAATGGTTG TATGTGTGAT GCTATGCCCA GAATATGAAG TATCTGTTTT
4051 TGAAATTCAC TTTATTTAAA AGATAAGCAG CTGACTGGGC ACGGTGCCTC
4101 ATGCCTGTAA TCCTAGCACC TTGGGAGGCT GAGGCAGGTG GATCACCTAA
4151 GGTCAAGAGT TCAACAACAC CAGCTGACC AACATGGTGA AACCCCATCT
4201 CTACTAAAAA TACAAAAATC AGCCGGGTCT CATGGCAGGC ACCTGTAATC
4251 CCATCTACTG AGGCAGGAGA ATTGCTTGAC CCAGGAGGCA GAGGTTCAG
4301 TGAGCCAAGA TCACGCCATT GCACTCCAGC CTGGGGGACA GAGCAAGACT
4351 CTATCTCCAA AAAACAAAAA AGATAAGCAG CTTTAGAATA TGGCGCATTC
4401 AAAACAGTCT CAGTAACAAA GACATTAAAA GAAACAAAT TACTTTCTAA
4451 TTAATATTTT GTGTTCTTA AGATCAAATC ATATAGGTAA CTTATAGAC
4501 CTAAATTTAA AGTGATTTT GGCTGGACTG GCAACAATGT TCCCAATGTC
4551 TTTACTTTTT AAAAAGGCTT TTTTATTTT AAGCACATAC CTATTTTGTA
4601 GACTTACATT GTTAAATATT TATTTAATC TTAATATTTT TACATTATTA
4651 TATTGCATTA TTTATTTTTT CTAAGTTCCA GAATAATAGT GTCATTATTA
4701 TAGACTATAT GTTTTGAAGT TTGATATTAT AATGGGATAT TCATTTTTTG
4751 TTCTTTTCTT GACTCCTTTC TCAAGTGTGT GATAAGGTCT GCTGATAAAA
4801 TATTTAACCC CAAGAAAGTG AAACTAATA TAAATTAGA AAGACCTATC
4851 CAAATTAGAC AGTCAATTCC ATTAATAATA GAAGTGAGAA AAACAATGTT
4901 GGGCATTGAG GTGTAAATTT TGCCAGATG TATACCCAGT GTGAAATATC
4951 TTCTAATAAA AATATATTTG GCTCTTATCC CTGCACATGT AGAGGCATAA
5001 AAATTGGTAA ACATGTCCCG CTGTGTAGAA CTTTAAAAA AAGGCATTTT
5051 TGAAAGTGTT GAGTGGCACT GATAACTGGT GAAGCCTACA GCCATCCGCC
5101 CAAAGTCTG TTCTGATGGC ACTGAGTTT CATTGTTCTG GATGTATAAG
5151 TCTGTGTGTC AGGTACAGCT GGGCCAGCC AGCTTGAGTC ACTCTGTAC
5201 AAGCTTGTGTT TTTTCTGTCT TGTGAATGCA CTTGATAATT TAAAAATAAA
5251 AATATCTGTT TCTCTGCAA AAAAAA

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BLAST Results

Entry HS32B1 from database EMBL:
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1
 Score = 4445, P = 0.0e+00, identities = 889/889

Entry U93816 from database EMBL:
 Human exon-trapped sequence from 6q24.
 Score = 965, P = 4.0e-35, identities = 193/193

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 19 bp to 3606 bp; peptide length: 1196
 Category: similarity to known protein

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1 MPTAESEAKV KTKVRFKELL KTHSDLMREK KKLKKKLVRSEENISPDITR
51 SNLHYMKETT SDDPDTIRSN LPHIKETTSDDVSAANTNNL KKSTRVTKNK
101 LRNTQLATEN PNGDASVEED KQKPNKKVI KTVPQLTTQD LKPETPENKV
151 DSTHQKTHTK PQPGVDHQKS EKANEGREET DLEEDEELMQ AYQCHVTEEM
201 AKEIKRRIK KLKEQLTYFP SOTLFHDDKL SSEKRRKKKE VPVFSKAETS
251 TLTISGDTVE GEQKKESSVR SVSSDSHQDD EISSMEQSTE DSMQDDTKPK
301 PKKTKKKTKA VADNNEDVDG DGVHEITSRD SPVYPKCLLD DDLVLGVYIH
351 RTDRLKSDFM ISHPMVKIHV VDEHTGQYVK KDDSGRPVSS YYEKENVDYI
401 LPIMTQPYDF KQLKSRLPEW EEQIVFNENF PYLLRGSDS PKVILFFEIL
451 DFLSVDEIKN NSEVQNQECG FRKIAWAFK LLGANGNANI NSKLRLQLYY
501 PPTKPRSPLS VVEAFEWWSK CPRNHYPSTL YVTVRGLKVP DCIKPSYRSM
551 MALQEEKGKP VHCERHHESS SVDTEPGLLE SKEVIKWKRL PGQACRIPNK
601 HLFSLNAGER GCFCCLDFSHN GRILAAACAS RDGYPIILYE IPSGRFMREL
651 CGHLNIIYDL SWSKDDHYIL TSSSDGTARI WKNEINNTNT FRVLPHPSFV
701 YTAKFHPAVR ELVVTGCVDS MIRIWKVEMR EDSAILVRQF DVHKSFINSL
751 CFDTEGHHMY SGDCTGVIVV WNTYVKINDL EHSVHHWTIN KEIKETEFKG
801 IPISYLEIHP NGKRLLIHTK DSTLRIMDLR ILVARKFVGA ANYREKIHST
851 LTPCGTFLFA GSEDGIVYVW NPETGEQVAM YSDFPFKSPI RDISYHPFEN
901 MVAFCAFGQN EPILLYIYDF HVAQQAEMF KRYNGTFPLP GIHQSQDALC
951 TCPKLPHQGS FQDEFVHTE SSSTKMQLVK QRLETVTEVI RSCAAKVNKN
1001 LSFTSPPAVS SQQSKLKQSN MLTAQEILHQ FGFTQTGIIS IERKPCNHQV
1051 DTAPTVALY DYTANRSEDL TIHRGDIIRV FFKDNEDWWY GSIGKGQEGY
1101 FPANHVASET LYQELPPEIK ERSPLSPPEE KTKIEKSPAP QKQSINKNKS
1151 QDFRLGSESM THSEMRKEQS HEDQGHIMDT RMRKNKQAGR KVTLIE

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_1n3, frame 1

TREMBL:U92792_1 gene: "tup1"; product: "Tup1"; Schizosaccharomyces pombe general transcriptional repressor Tup1 (tup1) mRNA, complete cds., N = 1, Score = 186, P = 1e-10

TREMBL:AF104258_1 gene: "Pmc733"; product: "putative copper-inducible 35.6 kDa protein"; Festuca rubra putative copper-inducible 35.6 kDa protein (Pmc733) mRNA, complete cds., N = 1, Score = 235, P = 4.6e-18

TREMBL:SPAC3H5_8 gene: "SPAC3H5.08c"; product: "beta-transducin"; S.pombe chromosome I cosmid c3H5., N = 2, Score = 231, P = 2e-14

PIR:T02533 hypothetical protein F13M22.17 - Arabidopsis thaliana, N = 2, Score = 228, P = 1e-13

TREMBL:AF104258_1 gene: "Pmc733"; product: "putative copper-inducible 35.6 kDa protein"; Festuca rubra putative copper-inducible 35.6 kDa protein (Pmc733) mRNA, complete cds., N = 1, Score = 235, P = 4.6e-18

TREMBL:SPAC3H5_8 gene: "SPAC3H5.08c"; product: "beta-transducin"; S.pombe chromosome I cosmid c3H5., N = 2, Score = 231, P = 2e-14

TREMBL:CER03E1_1 gene: "R03E1.1"; Caenorhabditis elegans cosmid R03E1, N = 1, Score = 215, P = 2.3e-13

SWISSPROT:YZLL_CAEEL HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTAINING PROTEIN K04G11.4 IN CHROMOSOME X., N = 1, Score = 203, P = 7.1e-13

>TREMBL:AF104258_1 gene: "Pmc733"; product: "putative copper-inducible 35.6 kDa protein"; Festuca rubra putative copper-inducible 35.6 kDa protein (Pmc733) mRNA, complete cds.
Length = 321

HSPs:

Score = 235 (35.3 bits), Expect = 4.6e-18, P = 4.6e-18
Identities = 59/225 (26%), Positives = 111/225 (49%)

Query: 647 MRELCSHLNIIYDLSWSKDDHYILTSSSDGTARIWKNEINNTNTFRVLPHPSFVYTAKFH 706
+ E GH + I DLSWSK+ +L++S D T R+W ++ + +V H ++V +F+

Sbjct: 63 VHEFYGHGDAILDLSWSKNGD-LLSASMDKTVRWL--QVGRDSCLKVFESHTNYVTCVQFN 119

Query: 707 PAVRELVTGCVDSMIRIWKVEMREDSAILVRQFDVHKSFINSLCFDTEGHHMYSGDCTG 766

P +TGC D ++RIW V LV + K + ++C+ +G +G TG

Sbjct: 120 PTNGNYFITGCDGLVRIWDVRK----CLVVDWANSKEIVTAVCYRPDGKGAVAGTIT 174

Query: 767 VIVVWNTYVKINDLEHSVHHWTINKEIKETEFKGIPISYLEIHPNGKRLLIHTKDSTLRI 826

++ +LE V ++N K + + Y P K+L++ + D+ +RI

Sbjct: 175 NCRYYDASENRLELESQV---SLNGRKKSLHKRIVGFQYCPSPD--KKLMVTSGDAQVRI 229

Query: 827 MDLRILVARKFVGAANYREIKHSTLTFCGTFLFAGSEDGIVYVWN 871
 +D +++ + G + ++ + TP G + + S+D +Y+WN

Sbjct: 230 LDGAHVISN-YKGLQS-SSQVARSFPTPDGDHIVSASDDSRIMWN 272

Pedant information for DKFZphtes3_ln3, frame 1

Report for DKFZphtes3_ln3.1

[LENGTH] 1196
 [MW] 137114.70
 [pI] 6.79
 [HOMOL] SWISSPROT:YKY4_CAEEL HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
 C14B1.4 IN CHROMOSOME III. 8e-21
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YKL121w] 2e-11
 [FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YBR198c
 TAF90 - TFIID subunit] 4e-10
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YBR198c TAF90 - TFIID subunit]
 4e-10
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR178w] 1e-08
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPR178w] 1e-08
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR364c] 4e-08
 [FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YDR364c] 4e-08
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL145c]
 9e-08
 [FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae,
 YDL145c] 9e-08
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YCR084c] 2e-07
 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YHL002w] 7e-07
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YFR024c-a] 2e-06
 [FUNCAT] 02.16 fermentation [S. cerevisiae, YMR116c] 4e-06
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YMR116c] 4e-06
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae,
 YMR116c] 4e-06
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YFL009w] 4e-05
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL009w]
 4e-05
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YFL009w] 4e-05
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YCR088w] 6e-05
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YCR057c] 7e-05
 [BLOCKS] BL00024H
 [SCOP] dltbgsd_ 2.46.3.1.1 betal-subunit of the signal-transducing 3e-91
 [SCOP] dlqfc_ 2.21.2.1.9 Growth factor receptor-bound protein 2 (GRB2), N 4e-14
 [SCOP] dlqfm_ 2.21.2.1.8 (1-64) c-src tyrosine kinase [human (Hom 5e-15
 [SCOP] dlad5b1_ 2.21.2.1.7 (1-63) Hemopoietic cell kinase Hck [human (Hom 3e-15
 [SCOP] dlckal_ 2.21.2.1.16 (1-54) p56-lck tyrosine kinase, SH3 domain [huma 1e-13
 [SCOP] dlqwea_ 2.21.2.1.15 Src kinase, SH3 domain [Avian sarcoma virus 2e-15
 [SCOP] dlshg_ 2.21.2.1.6 alpha-Spectrin, SH3 domain [chicken (Gallu 2e-13
 [SCOP] dlprmc_ 2.21.2.1.13 Src kinase, SH3 domain [chicken (Gallus gallus) 2e-15
 [SCOP] dlhsq_ 2.21.2.1.12 Phospholipase C, SH3 domain [human (Hom 2e-13
 [SCOP] dlboa_ 2.21.2.1.3 Abl tyrosine kinase, SH3 domain [Mouse (Mu 3e-13
 [SCOP] dlafna_ 2.21.2.1.2 Fyn, SH3 domain [human (Homo sapiens) 2e-15
 [SCOP] dlsema_ 2.21.2.1.11 Growth factor receptor-bound protein 2 (GRB2), N 1e-13
 [SCOP] dlgbqa_ 2.21.2.1.10 Growth factor receptor-bound protein 2 (GRB2), N 3e-16
 [SCOP] dlckaa_ 2.21.2.1.1 C-Crk, N-terminal SH3 domain [mouse (Mu 3e-15
 [EC] 3.1.4.3 Phospholipase C 2e-07
 [EC] 3.1.4.11 1-Phosphatidylinositol-4,5-bisphosphate phosphodiesterase 7e-07
 [EC] 3.6.1.32 Myosin ATPase 7e-07
 [EC] 2.7.1.112 Protein-tyrosine kinase 8e-06
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 [PIRKW] P-loop 7e-07
 [PIRKW] hydrolase 7e-07
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 [SUPFAM] SH2 homology 2e-07
 [SUPFAM] protozoan myosin heavy chain IB 7e-07
 [SUPFAM] myosin motor domain homology 7e-07
 [SUPFAM] pleckstrin repeat homology 2e-07
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 [SUPFAM] WD repeat homology 3e-12
 [SUPFAM] 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homology 2e-07
 [SUPFAM] protein kinase homology 8e-06
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 [SUPFAM] GTP-binding regulatory protein beta chain 7e-09
 [SUPFAM] yeast coatomer complex alpha chain 4e-07
 [PROSITE] RGD 1
 [PROSITE] MYRISTYL 6
 [PROSITE] AMIDATION 2
 [PROSITE] CAMP_PHOSPHO_SITE 4
 [PROSITE] CK2_PHOSPHO_SITE 25
 [PROSITE] TYR_PHOSPHO_SITE 4
 [PROSITE] PKC_PHOSPHO_SITE 19
 [PROSITE] ASN_GLYCOSYLATION 6
 [PFAM] Src homology domain 3
 [PFAM] WD domain, G-beta repeats
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 5.77 %
 [KW] COILED_COIL 2.42 %

SEQ MPTAESEAKVTKVRFEKLLKTHSDLMREKKKKLKKLVSEENISPDITIRSNLHYMKETT
 SEGxxxxxxxxx.....
 COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....
 lgotB

SEQ SDDPDTIRSNLPHIKETTSDVSAANTNNLKKSTRVTKNKLRLNTQLATENPNGDASVEED
 SEG
 COILS
 lgotB

SEQ KQGKPNKKVIKTVPLTQDLKPETPENKVDSTHQKTHTKPQPGVDHQKSEKANEGREET
 SEGxxx
 COILS
 lgotB

SEQ DLEEDDELMQAYQCHVTEEMAKEIKRKIRKKLKEQLTYFPSDTLFHDDKLSSEKRRKKKE
 SEG xxxxxxxx.....xxxxxxxxxxxxxxxxxxxxxxxxxxxx
 COILS
 lgotB

SEQ VPVFSKAETSTLTISGDTVEGEQKKESSVRSVSSDSHQDDEISSMEQSTEDSMQDDTKPK
 SEGxxxxx
 COILS
 lgotB

SEQ PKKTKKKTKAVADNEDVDGDGVHEITSRDSVPVYPKCLLDDDLVLGVYIHRTDRLKSDFM
 SEG xxxxxxxx.....
 COILS
 lgotB

SEQ ISHPMVKIHHVDEHTGQYVKKDDSGRPVSSYYEKENVDYILPIMTQPYDFKQLKSRLPEW
 SEG
 COILS
 lgotB

SEQ EEQIVFNENFPYLLRGSDSPKVLFFEILDFLSVDEIKNNSEVQNQECGFRKIAWAFK
 SEG
 COILS
 lgotB

SEQ LLGANGNANINSKLRLQLYYPPTKPRSPLSVVEAFEWWSKCPRNHYPSTLYVTVRGLKVP
 SEG
 COILS
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SEQ DCIKPSYRSMALQEEKGKPVHCERHHSSSVDTPEGLEESKEVIKWKRLPGQACRIPNK
 SEG
 COILS
 lgotB

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SEG      .....
COILS    .....
lgotB    .....CEEEEECCCCCEEE

SEQ      SWSKDDHYILTSSSDGTARIWKNEINNTNTFRVLPHPSFVYAKFHPAVRELVVTCYDS
SEG      .....
COILS    .....
lgotB    EETTTTTEEEETTTEEEETT--TTCEEEETTTCEEEEETTT-TCEEEETT

SEQ      MIRIWKVEMREDSAILVRQFDVHKSFINSCLFDTEGHHMYSGDCTGVIVVWNTYVKINDL
SEG      .....
COILS    .....
lgotB    EEEEEETTTTBTTEEEEEECCCCCE-EEEEETTEEEETTTEEEEEE.....

SEQ      EHSVHHWTINKETEFKGIPIISYLEIHPNGKRLLIHTKDSTLRIMDLRILVARKFVGA
SEG      .....
COILS    .....
lgotB    .....

SEQ      ANYREKIHSTLTPCGTFLFAGSEGDIVYVWNPETGEQVAMYSDLFPKSPIRDISYHPFEN
SEG      .....
COILS    .....
lgotB    .....

SEQ      MVAFCAFGQNEPILLYIDFHVAAQEAEMFKRYNGTFPLPGIHQSQDALCTCPKLPHQGS
SEG      .....
COILS    .....
lgotB    .....

SEQ      FQIDEFVHTESSSTKMQLVKQRLETVTEVIRSCAAKVNKNLSFTSPPAVSSQQSKLKQSN
SEG      .....
COILS    .....
lgotB    .....

SEQ      MLTAQEILHQFGFTQTGIISIERKPCNHQVDTAPTVVALYDYTANRSEDLTIHRGDIIRV
SEG      .....
COILS    .....
lgotB    .....

SEQ      FFKDNEDWYWSIGKGQEGYFPANHVASETLYQELPPEIKERSPPLSPEEKTKEKSPAP
SEG      .....
COILS    .....
lgotB    .....

SEQ      QKQSINKNKSQDFRLGSESMTHSEMRKEQSHEDQGHIMDTRMRKNKQAGRKVTLIE
SEG      .....
COILS    .....
lgotB    .....

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Prosites for DKFZphtes3_in3.1

PS00001	460->464	ASN_GLYCOSYLATION	PDOC00001
PS00001	686->690	ASN_GLYCOSYLATION	PDOC00001
PS00001	934->938	ASN_GLYCOSYLATION	PDOC00001
PS00001	1000->1004	ASN_GLYCOSYLATION	PDOC00001
PS00001	1065->1069	ASN_GLYCOSYLATION	PDOC00001
PS00001	1148->1152	ASN_GLYCOSYLATION	PDOC00001
PS00004	91->95	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	264->268	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	305->309	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	1190->1194	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	48->51	PKC_PHOSPHO_SITE	PDOC00005
PS00005	66->69	PKC_PHOSPHO_SITE	PDOC00005
PS00005	93->96	PKC_PHOSPHO_SITE	PDOC00005
PS00005	170->173	PKC_PHOSPHO_SITE	PDOC00005
PS00005	232->235	PKC_PHOSPHO_SITE	PDOC00005
PS00005	268->271	PKC_PHOSPHO_SITE	PDOC00005
PS00005	304->307	PKC_PHOSPHO_SITE	PDOC00005
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PS00005	352->355	PKC_PHOSPHO_SITE	PDOC00005
PS00005	384->387	PKC_PHOSPHO_SITE	PDOC00005
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PS00005	533->536	PKC_PHOSPHO_SITE	PDOC00005
PS00005	546->549	PKC_PHOSPHO_SITE	PDOC00005
PS00005	643->646	PKC_PHOSPHO_SITE	PDOC00005
PS00005	677->680	PKC_PHOSPHO_SITE	PDOC00005
PS00005	690->693	PKC_PHOSPHO_SITE	PDOC00005
PS00005	702->705	PKC_PHOSPHO_SITE	PDOC00005

PS00005	823->826	PKC_PHOSPHO_SITE	PDOC00005
PS00005	973->976	PKC_PHOSPHO_SITE	PDOC00005
PS00006	22->26	CK2_PHOSPHO_SITE	PDOC00006
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PS00006	116->120	CK2_PHOSPHO_SITE	PDOC00006
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PS00006	288->292	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
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PS00006	663->667	CK2_PHOSPHO_SITE	PDOC00006
PS00006	672->676	CK2_PHOSPHO_SITE	PDOC00006
PS00006	804->808	CK2_PHOSPHO_SITE	PDOC00006
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PS00007	1083->1091	TYR_PHOSPHO_SITE	PDOC00007
PS00007	211->219	TYR_PHOSPHO_SITE	PDOC00007
PS00007	1083->1091	TYR_PHOSPHO_SITE	PDOC00007
PS00007	210->219	TYR_PHOSPHO_SITE	PDOC00007
PS00008	483->489	MYRISTYL	PDOC00008
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PS00008	941->947	MYRISTYL	PDOC00008
PS00009	811->815	AMIDATION	PDOC00009
PS00009	1188->1192	AMIDATION	PDOC00009
PS00016	1074->1077	RGD	PDOC00016

Pfam for DKF2phtes3_ln3.1

HMM_NAME WD domain, G-beta repeats

HMM *MrCHnnWVVCVaFSPDGrWFIvSGSWDgTCRLWD*

Query 650 LCGHLNIIYDLWSKDDHY-ILTSSSDGTARIWK 682

HMM_NAME Src homology domain 3

HMM *pyVIALYDYqAqdpDELSFkEGDIIiIIEdsDD.WWrgRnnnTNGQEGW

Query 1054 PTVVALYDYTANRSDELTIHRGDIIRVFFKDNDWWYGSIGK--GQEGY 1100

HMM IPSNYVEPi*

Query 1101 FPANHVASE 1109

DKFZphtes3_20c21

group: testes derived

DKFZphtes3_20c21 encodes a novel 708 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

Sequenced by MediGenomix

Locus: /map="22q11.2-12.2"

Insert length: 3997 bp

Poly A stretch at pos. 3877, polyadenylation signal at pos. 3853

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1 GGTAGGCGGG GCGGCGCGTG ACCTAAGGCC TCTCTGCCGC GCGCGCAGGT
51 ACGGGGCGAGA AGTCGCGAGGT ACCCAGCTGC TGCCACGTT TCTGGTCCAG
101 AGTCCCGAAC CCCGAGCACT GGGATGCCTG GCTACTCCGA GCCAAGGCAC
151 TGATGTTTGA ACTGGAACT TCAAAACGTT TAATAAGAGT CTTCAGGATG
201 GGGTTGAACT AGACAAGCTA GAAATTTCTT TAGAACACCA GCTCTAGCAT
251 GCATCTCCCA CTTTGGCTT TCCTGGAGAG GAGCTTGAAG AGGTGGTTCT
301 GCAGACAGCC ACAGTGATAC TCAGGAAACC AGAGGAATGG ATTTGACTTT
351 TCTGCTAGGA TTCTTTGTTA TAGTTTCTCC CTGAGTTGTA AGAGGCATGG
401 AAATATACAT GAACTGAAG AACCTGCAAG GAAGGGAAGT GGAACCTTCC
451 ATGCTGAGTG AAAACTAACC AAGTGGCAGT TGTGACTGAA AACACTGAAA
501 CCTACCAAGT CCAGATTAC TGGATTGGGG GATAGAGGAA CGGTCACAGC
551 TAGGGAGAAA GAAGTGATAC CGGAAAAGAA AACCTAAATG AAGAGAATGA
601 GGATGACTGC ACAGTAGATG GCCACCTCTA CCTCCACAGA GGCAAAGTCA
651 GCCTCGTGGT GGAATTATTT TTTCTTTAT GATGGTTCCA AGGTAAAGGA
701 AGAAGGCGAT CCAACAAGAG CTGGCATTG TTACTTTTAT CCTTCCAGA
751 CCCTGCTAGA CCAACAGGAG TTGCTTTGTG GACAGATTGC TGGAGTTGTC
801 CGCTGTGTTT CTGACATTTC TGACTCTCCT CCTACTCTTG TCCGCTGAG
851 AAAACTGAAG TTTGCCATAA AAGTTGATGG AGATTACCTT TGGGTGCTGG
901 GCTGTGCTGT GGAGCTCCCT GATGTCAGCT GCAAGCGGTT TCTGGATCAG
951 CTAGTTGGAT GTTTAATTT TTACAATGGA CCTGTTTCCC TAGCTTATGA
1001 GAACTGTTCT CAGGAAGAAC TGAGCACGGA GTGGGACACC TTCATCGAGC
1051 AAATTCTGAA AAACACCACT GATCTGCATA AGATTTTCAA TTCCCTCTGG
1101 AACTTGGACC AAACATAAGT GGAGCCCCTG TTGTTGCTGA AGGCAGCCCCG
1151 CATTCTGCAG ACCTGCCAGC GCTCGCCTCA CATTCTCGCT GGCTGCATCC
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1251 AAGGTCCCTG TTCACCGAAC AGCACCTCAG GAGCAGAGAG TCCCTACGGG
1301 AGGGGATGCC CCGCAGGAAC ATGGAGCGGC ATTGCCCCCG AATGTCCAGA
1351 TTATCCCTGT TTTTGTGACC AAAGAGGAAG CCATTAGTCT CCACGAGTTC
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1451 TGTTTCAGCC CAGCACCATC CAAAGGGTGG GAGCACATCT GCCCTGAAAG
1501 AAAACGCCAC TGCCATGTG GAATCCATGG CCTGGACCAC CCCAGATCCC
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1601 GTCTGGCCAT GATCTGGAGA GCATCAGGCC CGCAGGACTG CACAACCTCTG
1651 CCAGGGGTGA GGTCTTTGGC CTCAGCTCCT CCCTGGGGAA GGAAGTAGTC
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1751 GGAAGTGGA ATGGCCTCAG GTCATTTTGC ETTCTACAT GTGCCTGTTT
1801 CAGATGGCAG GGCTCCTTAC TGCAAGGCAT CTCTCAGCGC CTCACGAGC
1851 CTGGAACCCA CGCCTCCTGA GGACACAGCC ATCAGCAGCT TGCGCCCTCC
1901 CTCTGCTCCT GAGATGCTGA CCCAGCATGG AGCCCAAGAG CAGGTGGAAG
1951 ACCATCCTGG CCATAGCAGC CAAGCCCCCA TTCCAGAGC AGACCTCTC
2001 CCCAGAAGGA CCCGCAAGGC CTTGTTATTG CCTCGCTTAG ATCCAGGACA
2051 GAGAGGAAC AAGCTTCCCA CGGGGAACA AGGCCTGGAT GAGGATGTTG
2101 ATGGGGTCTG TGAAGCCAC GCAGCCCCCTG GTCTGGAATG CAGTTCAGGC
2151 TCAAGAACTG TCGAGGGTGC TGGCCCCCTC GCAGATGGAA TCAGCTCCAG
2201 GCTGACACCA GCAGAGTCTT GCATGGGGCT CGTGAGGATG AATCTCTACA
2251 CTCCTGCGT CAAAGGGCTG ATGCTGTCCC TGCTGGCTGA GGAGCCGCTG
2301 CTGGGAGACA CGCAGCCAT AGAGGAAGTG TACCACAGCA GCCTGGCTTC
2351 ACTGAATGGG CTGGAAGTCC ACCTGAAAGA GACGCTGCCC AGGGATGAGG
2401 CAGCCTCCAC GAGCAGCACC TACAACCTCA CATATTACGA CCGCATTGAG
2451 AGCTTGCTGA TGGCAAACTT GCCGAGGTG GCCACCCCGC ATGATCGCCG
2501 CTTCTCCAG GCGTCTAGC TGATGCATAG CGAATTTGCC CAGCTGCCCC
2551 CGCTTTATGA AATGACTGTC AGAAATGCCT CCACGGCTGT GTACGCTGTG
2601 TGCAACCCCA TCCAGGAGAC ATATTTCCAG CAGCTGGCAC CTGCAGCAG
2651 GAGCTCCGGC TTCCCAAACC CTCAGGATGG CGCCTTCAGC CTCTCCGGCA
2701 AAGCAAAGCA GAAGCTGCTG AAGCAGGGG TGAACCTGCT CTGAAGTCA
2751 CCCAGGAGGT GACTGGGAAG GAGAAAACCA GCAAAGGAAG CTCTGCTTTT
2801 TATAATTGAA AAGGCCCTC TATTTTATTT TTCTTGAAAA CATTCCCTTT
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2851 TTTAGGAACC AAATGATATT TGAGTTTTTG TTATTCCTTT TGCAGATTGG
2901 GATGTGTTTT GGGGGCAGGG GTTAGTTCTT CAGGTCGGCA GACCCAGAGC
2951 ACTTGATAAA GAACTGTATT TAATCGGTAG TGTGGGGGCC GGGACGGGCT
3001 TGGCTCCCTC TCTGCCATAC TGAGCCTGAG GTATTTCATA TCTCCTGCTG
3051 TTCCATCCCA GCTTGAATTG GTGCCACAAG CTTCCAAGTT GGCATTTTTT
3101 CTAGAACCTG ATCGTCCACT AGCCCAGAGT GTGTGTGTTC AACCCCCACA
3151 CCAGGTGGTG GTAGGCGGTG TGAAGTCACA GCGAGGTGCC GGATCTGTGA
3201 GCAGGCCGAC TCCACTCCCA CGCGCGAGGT AGGTTTCTCC AGTGCCTCT
3251 TGCTGGGAGG TCCGGATCGT TCCTGCAGGG AAGCGGCAGC ACACGGAGAC
3301 CACTTGTTTG AATTCTGTTG GAACTCTACT CAAATCTAGG GCGCTCTTCT
3351 TTGGACCCAC AATGGGGGCA AGCCTTAATA ATATGGAAGG GAGTTTGGGC
3401 TTTAGAGATC CCTTTATAAA AGCTCTGGGG GCTGAGCCCT GAGAATTCAG
3451 TGACAACAGG ACCAACCTGC GCTGCCTTTG ACTACAAGTG GGCCGTGCAG
3501 CTGGTTCCTC TCGAGCGAGT GTCCCTAAAT AGGAGTTTAC AAGATGTCTG
3551 GGGGTAAAG CACTGTGCTT TTCAGTGGTG GCTGCGTGAA AGGGAGCGAC
3601 ACTCAGCTGT GTGTTCTCTG GCTTGTGTGG TACTTAGAAC CTCAGTTCTA
3651 TTACGTTATA GTCAGACATT TTTTGTACAG TATGAGACAG ACTGCAGGAT
3701 GAAAAATATT GTCAAAATCT TAACTGAATG TTTACTGGAA GTACTTGAGA
3751 TTCCATTTGA GAGTTGTATT GTTAATAATT TCATGTCAGT GAACTGATAT
3801 CTGATGTTTA TGATATGGTG TCTTTTCTT GAAACAAGCT TCCAAGGGCT
3851 AGAAATAAAA TAGCCAAAAA ATGCTGGAAA AAAAAAAAAA AAAAAAAAAA
3901 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3951 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

```

BLAST Results

Entry HS1048E9 from database EMBLNEW:
 Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2
 Contains pseudogene similar to ribosomal protein S3A and part of a gene
 similar to C.elegans protein CE02118, ESTs, STS, GSS.
 Score = 6540, P = 0.0e+00, identities = 1308/1308
 -14 exons

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 618 bp to 2741 bp; peptide length: 708
 Category: putative protein
 Classification: no clue

```

1 MATSTSTEAK SASWWNYFFL YDGSKVKEEG DPTRAGICYF YPSQTLLDQO
51 ELLCGQIAGV VRCVSDISDS PPTLVRLRKL KFAIKVDGDY LWVLGCVEL
101 PDVSKRFLD QLVGFNFYFN GPVSLAYENC SQEELSTEDW TFIEQILKNT
151 SDLHKIFNSL WNLDQTKVEP LLLKKAARIL QTCQSPHIL AGCILYKGLI
201 VSTQLPPSLT AKVLLHRTAP QEORLPTGGD APQEHGAALP PNVQIIPVFE
251 TKEEAISLHE FPVEQMTRSL ASPAGLQDGS AQHHPKGGST SALKENATGH
301 VESMAWTPPD PTSPDEACPD GRKENGCLSG HDLESIRPAG LHNSARGEVL
351 GLSSSLGKEL VFLQEELDLS EIHIPEAQEV EMASGHFAFL HVPVPDGRAP
401 YCKASLSASS SLEPTPPEDT AISSLRPPSA PEMLTQHGAQ EQVEDHPGHS
451 SQAPIPRADP LPRRRRRLPL LPRLDPGQRG NKLPTGEQGL DEDVDGVCES
501 HAAPGLECSS GSANCQGAGP SADGISSRLT PAESCMLVR MNLYTHCVKG
551 LMLSLLAEPP LLGDSAAIEE VYHSSLASLN GLEVHLKETL PRDEAASTSS
601 TYNFTYYDRI QSLLMANLPQ VATPHDRRFL QAVSLMHSEF AQLPALYEMT
651 VRNASTAVYA CCNPIQETYP QQLAPAAARS GFNPQDQAF SLSGKAKQKL
701 LKHGVNLL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_20c21, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_20c21, frame 3

Report for DKFZphtes3_20c21.3

[LENGTH] 708
[MW] 76900.23
[pI] 5.30
[KW] Alpha_Beta
[KW] LOW_COMPLEXITY 6.36 %

SEQ MATSTSTEAKSASWWNYFFLYDGSKVKEEGDPTRAGICYFYPSQTLLDQQELLCCGQIAGV
SEG .xxxxxxxxxxxxx.....
PRD ccc

SEQ VRCVSDISDSPPTLVRLRLKFAIKVDGDLWVLGCVELPDVSCRFLDQLVGFFNFYN
SEG
PRD eeeeecc

SEQ GPVSLAYENCSEQEELSTEWDTFIEQILKNTSLHKLIFNSLWNLDTQKVEPLLLLKAARIL
SEG
PRD ccc

SEQ QTCQRSFILAGCILYKGLIVSTQLPPSLTAKVLLHRTAPQEQLPTGGDAPQEHGAALP
SEG
PRD hhhcc

SEQ PNQIIPVFTVKEEATSLHEFPVEQMTSLASPAQLQDGSQAHHKGGSTSALKENATGH
SEG
PRD ccc

SEQ VESMAWTTDPDTPSDEACPDGRKENGCLSGHDLESIRPAGLHNSARGEVLGLSSSLGKEL
SEG
PRD ccc

SEQ VFLQEELDLSEIHIPEAQEVEMASGHFAFLHVPVDPGRAPYCKASLSASSSLEPTPPEDT
SEG
PRD hhhhhhhcc

SEQ AISSLRPPSAPEMLTQHGAEQVEDHPGHSSQAPIPRADPLPRRTRRPLLLPRLDPGQRG
SEGxxxxxxxxxxxxxxxxxxxxxxxx.....
PRD ccc

SEQ NKLPTGEQGLDEDVGVCESHAAPGLECSSGSANCQAGPSADGISSRLTPAESCMGLVR
SEG
PRD ccc

SEQ MNLYTHCVKGLMSLLAEPLLGDSAAIEEVYHSSLASLNGLEVHLKETLPRDEAASTSS
SEGxxxxxxxxxxxxx.....
PRD ceeeeeehh

SEQ TYNFTYYDRIQSLLMANLPQVATPHDRRFLQAVSLMHSEFAQLPALYEMTVRNASTAVYA
SEG
PRD ccccccehh

SEQ CCNPIQETYFQQLAPARSSGFPNPQDGAFLSGKAKQKLLKHGVNLL
SEG
PRD eccchhh

(No Prosite data available for DKFZphtes3_20c21.3)

(No Pfam data available for DKFZphtes3_20c21.3).

DKFZphtes3_20k2

group: signal transduction

DKFZphtes3_20k2 encodes a novel 839 amino acid protein with strong similarity to rat vanilloid receptor subtype 1.

VR1 seems to play an important role in the activation and sensitization of nociceptors. It is the receptor for e.g. capsaicin, a selective activator of nociceptors, a natural product of capsicum peppers. The novel protein is the human orthologue of rat VR1.

The new protein can find application as a target for the development of new nociception-modulating drugs.

strong similarity to rat vanilloid receptor subtype 1

Sequenced by MediGenomix

Locus: unknown

Insert length: 4187 bp

Poly A stretch at pos. 4154, polyadenylation signal at pos. 4135

```

1 GGCTCAGGCA GGCCTGGCCC AGAGTCACGC TGGCAACCAC GAGTTTGGGA
51 AGCAGTCGTA TTCTCTCTCT CTCTCTCTCT CTCTCAGTAT CCATGACAGT
101 GTGATGGAGA GTCTCTGCCG TGCCATCTGG GATGCAAACC GTCCCTGTGT
151 CCCCCACGTC CAGGCCGTAG ATGCTCCCCG CCGGTCAGTC ACTTAGTCGT
201 CAGATCGCCC GTCCTGGTAT CACAGTGCTT CTGTTCAAGT TGCACACTGG
251 GCCACAGAGG ATCCAGCAAG GATGAAGAAA TGGAGCAGCA CAGACTTGGG
301 GGCAGCTGCG GACCCACTCC AAAAGGACAC CTGCCCAGAC CCCCTGGATG
351 GAGACCCATA CTCCAGGCCA CCTCCAGCCA AGCCCCAGCT CTCCACGGCC
401 AAGAGCCGCA CCCGGCTCTT TGGGAAGGGT GACTCGGAGG AGGCTTTCCC
451 GGTGGATTGC CCTCACGAGG AAGGTGAGCT GGACTCCTGC CCGACCATCA
501 CAGTCAGCCC TGTTATCACC ATCCAGAGGC CAGGAGACGG CCCCACCGGT
551 GCCAGGCTGC TGTCCAGGGA CTCTGTCTGC GCCAGCACCG AGAAGACCCCT
601 CAGGCTCTAT GATCGCAGGA GTATCTTTGA AGCCGTTGCT CAGAATAACT
651 GCCAGGATCT GGAGAGCCTG CTGCTCTTCC TGCAGAAGAG CAAGAAGCAC
701 CTCACAGACA ACGAGTTCAA AGACCCCTGAG ACAGGGAAGA CCTGTCTGCT
751 GAAAGCCATG CTCAACCTGC ATGACGGACA GAACACCACC ATCCCCCTGC
801 TCCTGGAGAT CGCGCGGCAA ACGGACAGCC TGAAGGAGCT TGTCACGCC
851 AGCTACACGG ACAGCTACTA CAAGGGCCAG ACAGCACTGC ACATCGCCAT
901 CGAGAGACGC AACATGGCCC TGGTGACCCCT CTGGTGGAG AACGGAGCAG
951 ACGTCCAGGC TCGCGCCCAT GGGGACTTCT TTAAGAAAAC CAAAGGGCGG
1001 CCTGGATTCT ACTTCGGTGA ACTGCCCTGT TCCCTGGCCG CGTGACCAA
1051 CCAGCTGGGC ATCGTGAAGT TCCTGCTGCA GAACTCCTGG CAGACGGCCG
1101 ACATCAGCGC CAGGGACTCG GTGGGCAACA CCGTGCTGCA CGCCCTGGTG
1151 GAGGTGGCCG ACAACACGGC CGACAACACG AAGTTTGTGA CGAGCATGTA
1201 CAATGAGATT GTATCCTTGG GGGCCAAACT GCACCCGACG CTGAAGCTGG
1251 AGGAGCTCAC CAACAAGAAG GGAATGACGC CGCTGGCTCT GGCAGCTGGG
1301 ACCGGGAAGA TCGGGGTCTT GGCCTATATT CTCCAGCGGG AGATCCAGGA
1351 GCCCGAGTGC AGGCACCTGT CCAGGAAGTT CACCGAGTGG GCCTACGGGC
1401 CCGTGCACTC CTCGCTGTAC GACCTGTCTT GCATCGACAC CTGCGAGAAG
1451 AACTCGGTGC TGGAGGTGAT CGCCTACAGC AGCAGCGAGA CCCCTAATCG
1501 CCACGACATG CTCTTGGTGG AGCCGCTGAA CCGACTCCTG CAGGACAAGT
1551 GGGACAGATT CGTCAAGCGC ATCTTCTACT TCAACTTCCT GGTCTACTGC
1601 CTGTACATGA TCATCTTCAC CATGGCTGCC TACTACAGGC CCGTGGATGG
1651 CTTGCCTCCC TTAAAGATGG AAAAAATTGG AGACTATTTC CGAGTTACTG
1701 GAGAGATCCT GTCTGTGTTA GGAGGAGTCT ACTTCTTTT CCGAGGGATT
1751 CAGTATTTCC TGCAGAGGCG GCCGTGATG AAGACCCGTG TTGTGGACAG
1801 CTACAGTGAG ATGCTTTTCT TTCTGCAGTC ACTGTTTCATG CTGGCCACCG
1851 TGGTGCTGTA CTTACGCCAC CTCAAGGAGT ATGTGGCTTC CATGGTATTC
1901 TCCCTGGCCT TGGGCTGGAC CAACATGCTC TACTACACCG GCGGTTTCCA
1951 GCAGATGGGC ATCTATGCCG TCATGATAGA GAAGATGATC CTGAGAGACC
2001 TGTGCCGTTT CATGTTTGTG TACATCGTCT TCTTGTTCGG GTTTTCCACA
2051 CCGGTGGTGA CGCTGATTGA AGACGGGAAG AATGACTCCC TGCCGTCTGA
2101 GTCCACGTCG CACAGGTGGC GGGGGCCTGC CTGCAGGCCC CCGGATAGCT
2151 CCTACAACAG CCTGTACTCC ACCTGCCTGG AGCTGTCAA GTTCACCATC
2201 GGCATGGGCG ACCTGGAGTT CACTGAGAAC TATGACTTCA AGGCTGTCTT
2251 CATCATCCTG CTGCTGGCCT ATGTAATTCT CACCTACATC CTCCTGCTCA
2301 ACATGCTCAT CGCCCTCATG GGTGAGACTG TCAACAAGAT CGCACAGGAG
2351 AGCAAGAACA TCTGGAAGCT GCAGAGAGCC ATCACCATCC TGGACACGGA
2401 GAAGAGCTTC CTTAAGTGCA TGAGGAAGGC CTTCCGCTCA GGCAAGCTGC
2451 TGGAGTGGGG GTACACACCT GATGGCAAGG ACGACTACCG GTGGTGCTTC
2501 AGGTGGAGCG AGGTGAACCT GACCACCTGG AACACCAACG TGGGCATCAT
2551 CAACGAAGAC CCGGCAACT GTGAGGCGT CAAGCGCACC CTGAGCTTCT
2601 CCCTGCGGTC AAGCAGAGTT TCAGGCAGAC ACTGGAAGAA CTTTGCCCTG
2651 GTCCCCCTTT TAAGAGAGGC AAGTGCTCGA GATAGGCAGT CTGCTCAGCC

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2701 CGAGGAAGTT TATCTGCGAC AGTTTTCAGG GTCTCTGAAG CCAGAGGACG
2751 CTGAGGTCTT CAAGAGTCCT GCCGCTTCCG GGGAGAAGTG AGGACGTCAC
2801 GCAGACAGCA CTGTCAACAC TGGGCCCTTAG GAGACCCCGT TGCCACGGGG
2851 GGCTGCTGAG GGAACACCAG TGCTCTGTCA GCAGCCTGGC CTGGTCTGTG
2901 CCTGCCCAGC ATGTTCCCAA ATCTGTGCTG GACAAGCTGT GGAAGCGTT
2951 CTTGGAAGCA TGGGGAGTGA TGTACATCCA ACCGTCAGTG TCCCCAAGTG
3001 AATCTCCTAA CAGACTTTCA GGTTTTTACT CACTTTACTA AACAGTTTGG
3051 ATGGTCAGTC TCTACTGGGA CATGTTAGGC CCTTGTTTTT TTTGATTTTA
3101 TTCTTTTTTT TGAGACAGAA TTTCACCTCT CTCACCCAGG CTGGAATGCA
3151 GTGGCACAAT TTTGGCTCCC TGCAACCTCC GCCTCCTGGA TTCCAGCAAT
3201 TCTCCTGCCT CGGCTTCCCA AGTAGCTGGG ATTACAGGCA CGTGCCACCA
3251 TGTCTGGCTA ATTTTTTGTA TTTTTTTAAT AGATATGGGG TTTCCGCCATG
3301 TTGGCCAGGC TGGTCTCGAA CTCCTGACCT CAGGTGATCC GCCCACCTCG
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3401 TTCTTTGATT TTATTCTTTT TTTTTTTTCT GTGAGACAGA GTTTCACCTC
3451 TGTTGCCAGG GCTGGAGTGC AGTGGGTGTA TCTTGCTCCT CTGCAACCTC
3501 TGCCTCCCGG GTTCAAGCGA TTCTTCTGCT TCAGTCTCCC AAGTAGCTTG
3551 GATTACAGGT GAGCACTACC ACGCCCGGCT AATTTTTGTA TTTTTAATAG
3601 AGACGGGGTT TCACCATGTT GGCCAGGCTG GTCTCGAACT CTTGACCTCA
3651 GGTGATCTGC CCGCCTTGGC CTCCCAAAGT GCTGGGATTA CAGGTGTGAG
3701 CCGCTGCGCT CGGCCTTCTT TGATTTTATA TTATTAGGAG CAAAAGTAAA
3751 TGAAGCCAGG GAAAACACCT TTGGGAACAA ACTCTTCCTT TGATGGAAAA
3801 TGCAGAGGCC CTTCCTCTCT GTGCCGTGCT TGCTCCTCTT ACCTGCCCGG
3851 GTGGTTTGGG GGTGTTGGTG TTCTCTCCCT GGAGAAGATG GGGGAGGCTG
3901 TCCCACTCCC AGCTCTGGCA GAATCAAGCT GTTGCAAGCAG TGCCTCTTTC
3951 ATCCTTCTCT ACGATCAATC ACAGTCTCCA GAAGATCAGC TCAATGCTG
4001 TGCAGGTTAA AACTACAGAA CCACATCCCA AAGGTACCTG GTAAGAATGT
4051 TTGAAAGATC TTCCATTCTT AGGAACCCCA GTCCTGCTTC TCCGCAATGG
4101 CACATGCTTC CACTCCATCC ATACTGGCAT CCTCAAATAA ACAGATATGT
4151 ATACATATAA AAAAAAAAAA AAAAAAAAAA AAAAAAA

```

BLAST Results

No BLAST result

Medline entries

99288727:

Recent advances in neuropharmacology of cutaneous nociceptors.

99231880:

A non-pungent triphenyl phenol of fungal origin, scutigeral, stimulates rat dorsal root ganglion neurons via interaction at vanilloid receptors.

Peptide information for frame 2

ORF from 272 bp to 2788 bp; peptide length: 839
 Category: strong similarity to known protein
 Classification: Cell signaling/communication

```

1 MKKWSSTDLG AAADPLQKDT CPDPLDGDPN SRPPPAKPQL STAKSRTLRF
51 GKGDSSEAFP VDCPHEEGEL DSCPTITVSP VITIQRPGDG PTGARLLSQD
101 SVAASTEKTL RLYDRRSIFE AVAQNQCQDL ESLLLFLQKS KKHLLTDNEFK
151 DPETGKTCLL KAMLNLDHGO NTIPLLLEI ARQTDLSKEL VNASYTDSYY
201 KGQTAHIAI ERRNMAVLTL LVENGADVQA AAHGDFFKKT KGRPGFYFGE
251 LPLSLAECTN QLGIVKFLQ NSWQTADISA RDSVGNVLH ALVEVADNTA
301 DNTKFVTSY NEILILGAKL HPTLKLEEL NKKGMTPLAL AAGTGKIGVL
351 AYILQREIQE PECRHLRKE TEWAYGPVHS SLYDLSCIDT CEKNSVLEVI
401 AYSSSETPNR HDMLLVEPLN RLLQDKWDRF VKRIFYNFEL VYCLYMIIFT
451 MAAYYRPVDG LPPFKMEKIG DYFRVTGEIL SVLGGVYFFF RGIQYFLQRR
501 PSMKTLFVDS YSEMLFFLQS LFMLATVVLY FSHLKEYVAS MVFSLALGWT
551 NMLYYTRGFQ QMGIYAVMIE KMILRDLCRF MFVYIVFLFG FSTAVVTLIE
601 DGKNDLPSSE STSHRWGPA CRPPDSSYNS LYSTCLELFK FTIGMGDLF
651 TENYDFKAVF IILLAYVIL TYILLNMLI ALMGETVNKI AQESKNIWKL
701 QRAITLDTE KSFLKMRKA FRSGKLLQVG YTPDGKDDYR WCFRVDENVW
751 TTWNTNVGII NEDPGNCEGV KRTLSFSLRS SRVSGRHWN FALVPLLREA
801 SARDRQSAQP EEVYLRFQSG SLKPDAEVE KSPAASGEK

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_20k2, frame 2

TREMBL:AF029310_1 product: "vanilloid receptor subtype 1"; Rattus norvegicus vanilloid receptor subtype 1 mRNA, complete cds., N = 1, Score = 3760, P = 0

TREMBLNEW:AB015231_1 product: "stretch-inhibitable nonselective channel (SIC)"; Rattus norvegicus mRNA for stretch-inhibitable nonselective channel (SIC), complete cds., N = 2, Score = 2090, P = 2e-219

>TREMBL:AF029310_1 product: "vanilloid receptor subtype 1"; Rattus norvegicus vanilloid receptor subtype 1 mRNA, complete cds.
Length = 838

HSPs:

Score = 3760 (564.1 bits), Expect = 0.0e+00, P = 0.0e+00
Identities = 721/839 (85%), Positives = 773/839 (92%)

```
Query:      1 MKKWSSTD LGAAADPLQKDTCPDPLDGD PNSRPPPAKPQLSTAKSRTRLFGKGDSEEAFF 60
             M++ +S D + P Q+++C DP D DPN +PPP KP + T +SRTLFGKGDSEEA P
Sbjct:      1 MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVPKPHIFTTRSRTLFGKGDSEEAFF 60

Query:      61 VDCPHEEGELDSCPTITVSPVITIQRPDGPPTGARLLSQDSVAASTEKTLRLYDRRSIFE 120
             +DCP+EEG L SCP ITVS V+TIQRPDGP R SQDSV+A EK RLYDRRSIF+
Sbjct:      61 LDCPYEEGLASCPITVSSVLTIQRPDGPASVRPSSQDSVSAG-EKPPRLYDRRSIFD 119

Query:     121 AVAQNNCQDLESLLLFLQSKKHLTDNEFKDPETGKTCLLKAMLNLDHGQNTTIPLLLEI 180
             AVAQ+NCQ+LESLL FLQ+SKK LTD+EFKDPETGKTCLLKAMLNLDHGQNTTIPLLLEI
Sbjct:     120 AVAQSNQCQELLESLLPFLQSKKRLTDSEFKDPETGKTCLLKAMLNLDHGQNTTIALLLDV 179

Query:     181 ARQTDLSKELVNASYTDSYKQGTALHIAIERRNMALVTLVLENGADVQAAAHGDFEFKKT 240
             AR+TDSLK+ VNASYTDSYKQGTALHIAIERRNM LVTLLVLENGADVQAAA+GDFEFKKT
Sbjct:     180 ARKTDLSKQFVNASYTDSYKQGTALHIAIERRNMTLVTLVLENGADVQAAANGDFEFKKT 239

Query:     241 KGRPGFYFGEPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNTVLHALVEVADNTA 300
             KGRPGFYFGEPLSLAACTNQL IVKFLQNSWQ ADISARDSVGNTVLHALVEVADNT
Sbjct:     240 KGRPGFYFGEPLSLAACTNQLAIVKFLQNSWQPADISARDSVGNTVLHALVEVADNTV 299

Query:     301 DNTKFVTSMYNEILILGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAYILQREIQE 360
             DNTKFVTSMYNEILILGAKLHPTLKLEE+TN+KG+TPLALAA +GKIGVLAYILQREI E
Sbjct:     300 DNTKFVTSMYNEILILGAKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQREIHE 359

Query:     361 PECRHLRSRKFTWAYGPHVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLN 420
             PECRHLRSRKFTWAYGPHVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLN
Sbjct:     360 PECRHLRSRKFTWAYGPHVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLN 419

Query:     421 RLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYYRPVDGLPPFKMEK-IGDYFRVTGEI 479
             RLLQDKWDRFVKRIFYFNFLVYCLYMIIFT AAYYRPV+GLPP+K++ +GDYFRVTGEI
Sbjct:     420 RLLQDKWDRFVKRIFYFNFLVYCLYMIIFTAAAYYRPVEGLPPYKLNKNTVGDYFRVTGEI 479

Query:     480 LSVLGGVYFFFRGIQYFLQRRPSMKTLEFVDSYSEMLFFLQSLFMLATVVLYFSLKEYVA 539
             LSV GGVYFFFRGIQYFLQRRPS+K+LFVDSYSE+LFF+QSLFML +VVLYFS KEYVA
Sbjct:     480 LSVSGGVYFFFRGIQYFLQRRPSLKSLEFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVA 539

Query:     540 SMVFSLALGWTNMLYYTRGFQOMGIYAVMIEKMILRDLRCRFMEVYIVFLFGFSTAVVTLI 599
             SMVFSLA+GWTNMLYYTRGFQOMGIYAVMIEKMILRDLRCRFMEVY+VFLFGFSTAVVTLI
Sbjct:     540 SMVFSLAMGWTNMLYYTRGFQOMGIYAVMIEKMILRDLRCRFMEVYLVFLFGFSTAVVTLI 599

Query:     600 EDGKNDLSPSESTSHRWGPACRPDPSSYNSLYSTCCLFELFKFTIGMGDLEFTENYDFKAV 659
             EDGKN+SLP EST H+ RG AC+P +SYNSLYSTCCLFELFKFTIGMGDLEFTENYDFKAV
Sbjct:     600 EDGKNNSLPSESTPHKCRGSACKP-GNSYNSLYSTCCLFELFKFTIGMGDLEFTENYDFKAV 658

Query:     660 FIILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTEKSFLKCMRK 719
             FIILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTEKSFLKCMRK
Sbjct:     659 FIILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTEKSFLKCMRK 718

Query:     720 AFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWTWNTNNGIINEDPGNCEGVKRTLSFSLR 779
             AFRSGKLLQVG+TPDGKDDYRWCFRVDEVNWTWNTNNGIINEDPGNCEGVKRTLSFSLR
Sbjct:     719 AFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTWNTNNGIINEDPGNCEGVKRTLSFSLR 778

Query:     780 SSRVSGRHWKNFALVPLLRASARDRQSAQPEEVYLRQFSGSLKPDAEVFKSPAASGEK 839
             S RVSGR+WKNFALVPLLR+AS RDR + Q EEV L+ ++GSLKPDAEVFK GEK
Sbjct:     779 SGRVSGRNWKNFALVPLLRDASTRDRHATQEEVQLKHYTGSLKPDAEVFKDSMVPGEK 838
```

Pedant information for DKFZphtes3_20k2, frame 2

Report for DKFZphtes3_20k2.2

[LENGTH] 839
[MW] 94950.75
[pI] 6.90
[HOMOL] TREMBL:AF029310_1 product: "vanilloid receptor subtype 1"; Rattus norvegicus
vanilloid receptor subtype 1 mRNA, complete cds. 0.0
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YIL112w] 4e-05
[PIRKW] alternative splicing 3e-06
[PIRKW] peripheral membrane protein 3e-06
[SUPFAM] ankyrin repeat homology 3e-06
[SUPFAM] unassigned ankyrin repeat proteins 3e-06
[PFAM] Ank repeat
[KW] TRANSMEMBRANE 4

SEQ MKKWSSTDLGAAADPLQKDTCPDPLDGDPNRPPPAKQLSTAKSRTLFGKGDSEEAFF
PRD ccc
MEM
SEQ VDCPHEEGELDSCPTITVSPVITIQRPDGTGARLLSQDSVAASTEKTLRLYDRRSIFE
PRD cchhhhhhhhhhhhh
MEM
SEQ AVAQNNQDLESLLLFLQSKKHLTDNEFKDPETGKTCLLKAMNLNLDGQNTTIPLLLEI
PRD hhhhchhhhhhhhhhhhhhhcc
MEM
SEQ ARQDLSKELVNASYTDSSYKQGTALHIAIERRNMALVTLVENGADVQAAAHGDFFKKT
PRD hhhcc
MEM
SEQ KGRPGFYFGLPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNTVLHALVEVADNTA
PRD cccccccccccccchhhhhhhcc
MEM
SEQ DNTKFVTSMYNEILILGAKLHPTLKLEELTNKKGMTPLALAAAGTGKIGVLAYILQREIQE
PRD chhhhhhhhhhhhhhhcc
MEM
SEQ PECRHLRSRKFTWAYGPVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLN
PRD cccccchhhhhheeecc
MEM
SEQ RLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYRVPDGLPPFKMEKIGDYFRVTGEIL
PRD hhh
MEMMMMMMMMMMMMMMMMM.....
SEQ SVLGGVYFFFRGIQYFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYFSLKEYVAS
PRD cccccccccccccchhhhhhhheeecccccccccccccccccccccccccccccccccccc
MEMMMMMMMMMMMMMMMMMMMMM.....
SEQ MVFSLALGWTNMLYYTRGFQOMGIYAVMIEKMIILDLRFMFVYIVFLFGFSTAVVTLIE
PRD hhhhhhhhhhhhhheeecc
MEMMMMMMMMMMMMMMMMMMMMM.....
SEQ DGKNDLPSESTSHRWGPACRPPDSSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVF
PRD ccc
MEMMM
SEQ IILLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLRITILDEKSFLLKCMRKA
PRD hhh
MEMMMMMMMMMMMMMMMMM.....
SEQ FRSGKLLQVGYPDGKDDYRWCFRVDEVNWTWNTNVTGIIINEDPGNCEGVKRTLSFSLRS
PRD hhcc
MEM
SEQ SRVSGRHWKNFALVPLLREASARDQSAQPEEVYLRQFSGSLKPDAEVFKSPAASGEK
PRD cccccccccchhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccc
MEM

(No Prosite data available for DKFZphtes3_20k2.2)

Pfam for DKFZphtes3_20k2.2

HMM_NAME	Ank repeat	
HMM	*GyTPLHIAARYNNvEMVrLLQHGADIN*	
	G+T+LHIA +++N+ +V LL+++GAD+	
Query	202 GQTALHIAIERRNMALVTLLVENGADVQ	229

DKFZphtes3_2013

group: transmembrane protein

DKFZphtes3_2013 encodes a novel 595 amino acid protein with partial similarity to the IL-17 receptor.

The novel protein contains one transmembrane region.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

similarity to IL-17 receptor

Sequenced by MediGenomix

Locus: unknown

Insert length: 2406 bp

Poly A stretch at pos. 2345, no polyadenylation signal found

```
1 GCCTCAGGTG TTCCTGCGTT GTTTGTCAGT GGAGAGCAGG GAGTGGGGCC
51 AGCCAGCAGA AACAGTGGGC TGTACAACAT CACCTTCAAA TATGACAATT
101 GTACCACCTA CTTGAATCCA GTGGGGGAGC ATGTGATTGC TGACGCCCAG
151 AATATCACCA TCAGCCAGTA TGCTTGCCAT GACCAAGTGG CAGTCACCAT
201 TCTTTGGTCC CCAGGGGCCC TCGGCATCGA ATTCCTGAAA GGATTTCGGG
251 TAATACTGGA GGAGCTGAA GCGGAGGGAA GACAGTGCCA ACAACTGATT
301 CTAAAGGATC CGAAGCAGCT CAACAGTAGC TTCAAAAGAA CTGGAATGGA
351 ATCTCAACCT TTCCTGAATA TGAATTTGA AACGGATTAT TTCGTAAAGG
401 TTGTCCCTTT TCCTTCCATT AAAAACGAAA GCAATTACCA CCCTTTCTTC
451 TTTAGAACCC GAGCCTGTGA CCTGTTGTTA CAGCCGGACA ATCTAGCTTG
501 TAAACCCTTC TGGAAGCCTC GGAACCTGAA CATCAGCCAG CATGGCTCGG
551 ACATGCAGGT GTCCTTCGAC CACGCACCGC ACAACTTCGG CTTCCGTTTC
601 TTCTATCTTC ACTACAAGCT CAAGCACGAA GGACCTTTCA AGCGAAAGAC
651 CTGTAAGCAG GAGCAAACTA CAGAGATGAC CAGCTGCCTC CTTCAAAATG
701 TTTCTCCAGG GGATTATATA ATTGAGCTGG TGGATGACAC TAACACAACA
751 AGAAAAGTGA TGCATTATGC CTTAAAGCCA GTGCACTCCC CGTGGGCCGG
801 GCCCATCAGA GCCGTGGCCA TCACAGTGCC ACTGGTAGTC ATATCGGCAT
851 TCGCGACGCT CTTCACTGTG ATGTGCCGCA AGAAGCAACA AGAAAATATA
901 TATTCACATT TAGATGAAGA GAGCTCTGAG TCTTCCACAT ACATGCAGC
951 ACTCCAAGA GAGAGGCTCC GGCGCGGCC GAAGGTCTTT CTCTGCTATT
1001 CCAGTAAAGA TGGCCAGAA CACATGAATG TCGTCCAGTG TTTCCGCTAC
1051 TTCCTCCAGG ACTTCTGTGG CTGTGAGGTG GCTCTGGACC TGTGGGAAGA
1101 CTTCAGCCTC TGTAAGAAAG GGCAGAGAGA ATGGGTCATC CAGAAGATCC
1151 ACGAGTCCCA GTTCATCATT GTGGTTTGTT CCAAAGCTAT GAAGTACTTT
1201 GTGGACAAGA AGAACTACAA ACACAAAGGA GGTGGCCGAG GCTCGGGGAA
1251 AGGAGAGCTC TTCCTGGTGG CCGTGTACAG CATTGCCGAA AAGCTCCGCC
1301 AGGCCAAGCA GAGTTCGTCC GCGGCGCTCA GCAAGTTTAT CGCCGTCTAC
1351 TTTGATTATT CCTGCGAGGG AGACGTCCCC GGTATCCTAG ACCTGAGTAC
1401 CAAGTACAGA CTCATGGACA ATCTTCTCCA GCTCTGTTCC CACCTGCACT
1451 CCCGAGACCA CGGCCTCCAG GAGCCGGGGC AGCACACGCG ACAGGGCAGC
1501 AGAAGGAAGT ACTTCCGGAG CAAGTCAGGC CCGTCCCTAT ACGTCGCCAT
1551 TTGCAACATG CACCAAGTTA TTGACGAGGA GCCCGACTGG TTCGAAAAGC
1601 AGTTCGTTCC CTTCCATCCT CCTCCACTGC GCTACCGGGA GCCAGTCTTG
1651 GAGAAATTTG ATTCGGGCTT GGTTTTAAAT GATGTCATGT GCAAACCAGG
1701 GCCTGAGAGT GACTTCTGCC TAAAGGTAGA GCGGCTGTT CTTGGGGCAA
1751 CCGGACCAGC CGACTCCCAG CACGAGAGTC AGCATGGGGG CCTGGACCAA
1801 GACGGGGAGG CCCGGCCTGC CCTTGACGGT AGCGCCGCCC TGCAACCCCT
1851 GCTGCACACG GTGAAAGCCG GCAGCCCCTC GGACATGCCG CGGGACTCAG
1901 GCATCTATGA CTCGTCTGTG CCCTCATCCG AGCTGTCTCT GCCACTGATG
1951 GAAGGACTCT CGACGGACCA GACAGAAACG TCTTCCCTGA CGGAGAGCGT
2001 GTCCTCCTCT TCAGGCCTGG GTGAGGAGGA ACCTCCTGCC CTTCTTCCA
2051 AGCTCCTCTC TCTGGGTCA TGCAAAGCAG ATCTTGTTG CCGCAGCTAC
2101 ACTGATGAAC TTACACGCGT CGCCCCCTTG TAACAAACG AAAGAGTCTA
2151 AGCATTGCCA CTTTAGCTGC TGCCCTCCCTC TGATTCCCCA GCTCATCTCC
2201 CTGGTTGCAT GGCCCACTTG GAGCTGAGGT CTCATACAAG GATATTTGGA
2251 GTGAAATGCT GGCCAGTACT TGTCTCCCT TGCCCCAACC CTTTACCGGA
2301 TATCTTGACA AACTCTCAA TTTCTAAAA TGATATGGAG CTCTGAAAAA
2351 AAAAAA AAAA AAAA AAAA AAAA
2401 AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 346 bp to 2130 bp; peptide length: 595
 Category: similarity to known protein
 Classification: unclassified

```

1 MESQPFLNMK FETDYFVKV PFPSIKNESN YHPFFFRTRA COLLQPDNL
51 ACKPFWKPRN LNISOHGSDM QVSFDHAPHN FGFRFFYLHY KLKHEGPFKR
101 KTCKQEQTTE MTSCLLQNVS PGDYIIEVD DTNTRKVMH YALKPVHSPW
151 AGPIRAVAIT VPLVVISAFA TLFTVMCRKK QQENIYSHLD EESSESSTYT
201 AALPRERLRP RPKVFLCYSS KDGQNHMNVV QCFAYFLQDF CGCEVALDLW
251 EDFSLCREGO REWVIQKIHE SQFIIVVCSK GMKYFVDKKN YKHKGGRGS
301 GKGLFLVAV SAIAEKLRA QSSSAALSK FIAVYFDYSC EGDVPGILD
351 STKYRLMDNL POLCSHLHSR DHGLQEPGQH TRQGSRRNYF RSKSGRSLYV
401 AICNMHQFID EEPDWFEKQF VPFHPPPLRY REPVLEKFD GLVLNDVMCK
451 PGPESDFCLK VEA AVL GATG PADSQHSQH GGLDQDGEAR PALDGSAAQ
501 PLLHTVKAGS PSDMPDSCI YDSSVPSSSL SLPLMEGLST DQTETSSLTE
551 SVSSSSGLGE EEPALPSKL LSSGCKADL GCRSYTDELH AVAPL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2013, frame 1

TREMBL:U58917_1 product: "IL-17 receptor"; Homo sapiens IL-17 receptor mRNA, complete cds., N = 1, Score = 215, P = 4.7e-14

TREMBL:MM31993_1 product: "interleukin 17 receptor"; Mus musculus interleukin 17 receptor mRNA, complete cds., N = 2, Score = 152, P = 1.1e-13

>TREMBL:U58917_1 product: "IL-17 receptor"; Homo sapiens IL-17 receptor mRNA, complete cds.
 Length = 866

HSPs:

Score = 215 (32.3 bits), Expect = 4.7e-14, P = 4.7e-14
 Identities = 85/284 (29%), Positives = 131/284 (46%)

```

Query: 213 KVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV-IQK---I 268
      KV++ YS+ D +++VV FA FL CG EVALDL E+ ++ G WV QK +
Sbjct: 379 KVVIIYS A-DHPLYVDVVLKFAQFLITACGTEVALDLLEEQAISEAGVMTWVGRQKQEMV 437

Query: 269 HESQFIIVVCSKGMKY----FVDKKNXXXXXXXXXXXXXELFLVAVSAIAEXXXXXXXXXX 324
      + IIV+CS+G + + + +LF A++ I
Sbjct: 438 ESNSKIIIVLC SRGTRAKWQALLGRGAPVRLRCDHGKPVGD LFTAAMNMILPDKRPACFG 497

Query: 325 XXXXXXFIAYF-DYSCGEGDVP GILDSTKYRIMDNLPQLCSHLHSR DHGLQEPGQHTRQ 383
      ++ YF + SC+GDVP + + +Y LMD ++ + +D + +PG+ R
Sbjct: 498 T-----YVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEV--YFRIQDLEMFPQGRMHRV 550

Query: 384 G--SRRNYFRSKSGRSLYVAICNMHQFIDEEDWFEKQFV----PFHPPPLR---YREP 434
      G S NY RS GR L A+ + PDWFE + + P L + EP+
Sbjct: 551 GELSGDNYLRSPGGRQLRAALDRFRDQVRCPDWFECEENLYSADDQDAPSLDEEVFEEPL 610

Query: 435 LEKFD SGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQH GGLDQDGEAR 491
      L +G+V + + P S CL ++ V G G A H L G+ P
Sbjct: 611 LPP-GTGI VKRAPLVRE-PGSQACLAIDPLV-GEEGAAVAKLEPH--LQPRGQPAP 662

```

Pedant information for DKFZphtes3_2013, frame 1

Report for DKFZphtes3_2013.1

[LENGTH] 595
[MW] 66847.05
[PI] 6.27
[HOMOL] TREMBL:MM31993_1 product: "interleukin 17 receptor"; Mus musculus interleukin
17 receptor mRNA, complete cds. 2e-14
[BLOCKS] BL00740A MAM domain proteins
[BLOCKS] BL01224B N-acetyl-gamma-glutamyl-phosphate reductase proteins
[KW] TRANSMEMBRANE 1
[KW] LOW_COMPLEXITY 13.61 %

SEQ MESQPFLLNMKFETDYFVKVVPFSPKSNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRN
SEG
PRD ccc
MEM

SEQ LNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNV
SEG
PRD eeeeecc
MEM

SEQ PGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK
SEG
PRD ccc
MEMMMMMMMMMMMMMMMMM.....

SEQ QQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFLQDF
SEGxxxxxxx.....xxxxxxxxxx.....
PRD hhhhhhhhhcc
MEM

SEQ CGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCCKGMYFVDKKNYKHKGGGRGS
SEGxx
PRD ccchhhhhhhhhcc
MEM

SEQ GKGELFLVAVSAIAEKLQAKQSSAALSFKFIAVYFDYSCGDVPGILDSTKYRLMDNL
SEG xxx.....xx
PRD ccc
MEM

SEQ PQLCSHLHSRDHGLQEPQHQTRQGSRRNYFRSKSCRSLYVAICNMHQFIDEEDWFEKQF
SEG
PRD cchhhhhhhcc
MEM

SEQ VPFHPPLRYREPVLKFDGSLVLDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQH
SEG
PRD ecc
MEM

SEQ GGLDQDGEARPALDGSAAQLPLHTVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLST
SEGxx
PRD ccc
MEM

SEQ DQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSKADLGCRSYTDELHAVAPL
SEGxx
PRD hhhhhhhhhhecc
MEM

(No Prosite data available for DKFZphtes3_2013.1)

(No Pfam data available for DKFZphtes3_2013.1)

DKFZphtes3_20m18

group: nucleic acid management

DKFZphtes3_20m18 encodes a novel 132 amino acid protein with similarity to the *S. cerevisiae* mitochondrial carrier protein RIM2.

The novel protein contains a leucine zipper and a Prosite mitochondrial energy transfer proteins signature. It is member of a family of substrate carrier proteins which are found in the inner mitochondrial membrane and are involved in energy transfer. The RIM2/MRS12 gene encodes a predicted protein of 377 amino acids that is essential for mitochondrial DNA metabolism and proper cell growth. Inactivation of this gene causes the total loss of mitochondrial DNA and, compared to wild-type rho⁰ controls, a slow-growth phenotype on media containing glucose. The novel protein seems to be the human orthologue of this protein.

The new protein can find application in modulation of mitochondrial DNA replication and maintenance.

similarity to carrier protein RIM2

Sequenced by MediGenomix

Locus: unknown

Insert length: 3572 bp

Poly A stretch at pos. 3530, polyadenylation signal at pos. 3510

```
1  GCCGCGGGGA GGGCTGTGCC GGTGCTTTC TGCAGCCGCA TCTCGGCCAG
51 CTCTCCTCGC CGTCCCGGG GCGCTGTGCG TCTCCAGTCC GGGACCGAAG
101 CCGCCTGCCG TAGCGGGCGG CCAGATCCGC GTCCCGCCTC AGCGGCCGGA
151 GGACATCGCG GAGAGAGAAT GAGCCAGAGG GACACGCTGG TGCATCTGTT
201 TGCCGGAGGA TGTGGTGGTA CAGTGGGAGC TATTCTGACA TGCCCACTGG
251 AAGTTGTAAA AACACGACTG CAGTCATCTT CTGTGACGCT TTATATTTCT
301 GAAGTTTCAAG TGAACACCAT GGCTGGAGCC AGTGTCAACC GAGTAGTGTC
351 TCCCGGACCT CTTCAATTGCC TAAAGGTGAT CTGGGAAAAA GAAGGGCCTC
401 GTTCCTTTGT TAGAGGACTA GGCCCAATT TAGTGGGGGT AGCCCCTTCC
451 AGAGCAATAT ACTTTGCTGC TTATTCAAAC TGCAAGGAAA AGTTGAATGA
501 TGTATTTGAT CCGTATTCTA CCCAAGTACA TATGATTTCA GCTGCAATGG
551 CAGGTATGAA TGTATAATAT TAAAAAATAA AAAAAGTTTC TGAACCTAG
601 AGGCTTAATA TTGAATTATA AGTTTGTAGT GAAAAGTTGA TGATTAATGT
651 GCTTTTCTAT GATTAGATGA TTTTACGTT TATCGATATA AACCAAAATA
701 GGTATATGTA AATCTGTGTA TCAGTTGACA TTTTGTAGT CAGGAGTTTA
751 CATGCTAGGG TACAAGTAAT ATATTTATAT TGCCTTGTGT AGTCCACTGA
801 ATGTTTAGTG ATCATTGTGA ACAGTTTTAA GAATCCAACC ATAATTACAC
851 TATAAATAAG TTATGGAGCT GTAATTTACT CTCTCTCTCT CAATTTCTGT
901 TAGTGCCTTT TCCCTTTTGT CTGCATGTTT TGGCTTCTGT CTGAAATGTG
951 TCGGCAATTC TTGGTAAAGT ATTCATTTTG TCCTGTGCTC AAATGCTGAA
1001 ATTTTGTGTA GTGATGTATT ATTATTGACA ATTCAGTTAC TATGTGTATT
1051 TTTTAAATTT GTTTATTATT CTACATAATT CACACTAGAC AGCACCTGAA
1101 ATTTAGACAC TGCTATGTG TACATGCTTA CTATAGAAAT GTTCCAGGA
1151 ACTCTCTGTT TCTGTCATCA CTGATAAGTA TATATGATTC TGAATTAATA
1201 TAACTAGTTT TAGGTCTTTA CCCTGCCATA AAGATAAACA GTTGGTTTGA
1251 CCAATCTGGT TCTGGAATCA TTTGCTGCTA TGCATGTTAG ACAAGGCCAC
1301 GAACCTTTGAT TTTCCATTGA AAATTCTCCC TAATATCTGA GATTTATTGT
1351 ATATTTACTC ATATCTCACA TTTCAAATT ATGCTGTAAC TTTATAAACT
1401 GTAGCTGCTT TCATCAGCTA TTGATCAATA AATTGAATGT CAATTATGTG
1451 CTTAATAATG AGTGCCTTAA ACTGTTAAAC ACTTTTGGTT TAGAAATAAA
1501 GTGAATCAAT TTGACCTATA TACTTCATGA AGTAAGTAAG TTTGAAATAC
1551 AAATTTCTGA AAGGTCAATA GCCCTTATCG TATTACAAAT TGTTTTTAAG
1601 GCTTTTTGTA TTTATTAATT GTCAGTTGAT TCACTGAAGC TTTAAAACTG
1651 GAAGGGACAA TCCAAAGGTC AAAAGAGTGA AATACAATCA TTTACCAATA
1701 AGGAAACCTT GGGCAAATTA TGTAAATTTAT GTGAACCTCT CTTAGCTTAC
1751 CCATGGGAATG AGTCAAGTGG TCTACATAGA TTTGGATTTT GAGAATTAGT
1801 TCTTTTCATT AGTGTTATAG AGATTATCTT GTTACAACCT GAATTATTTT
1851 TAATGTAATT TTTACAGATG TTGAATATTA GTAGATAGGA TTTTCCCTT
1901 CCACTTTTGG ATCTAAGGTA AAGGTTGGTG GCCAGTGACA AACCTTATAA
1951 CCACTTTTATC AGGTTCTTTA AAAATATATT TGTGAATTAC CAGTGATTAT
2001 GTTTTTGGCT TATAACCTCA GATAATTATA AAGAAATGTT AATCTTATTT
2051 GAAAGAATTG GAATCTAGAA AGTTAGATGA GCAGTCATTT TATATTGATA
2101 TTTGTTATAT CAGTATAGCA AATGCAGAGG TTCAGAATAT CTTTATTTCC
2151 ACTGGAACAT CTTATTTTCT TAGAGTATCT CATCAGAATT TATTACTGTA
2201 TTTGTATCAC ATTGCAAAGA ATTTCACTAG AATTGTCAGT TTGCACTTTT
2251 TTCTCAAATG TGTACAAATG TTAACATATA GTTCATTTT ATCTGTACAT
2301 TGATGCCATT TCCCAACTTG AATTCCTCAA GTTTTGGTAA ACTTACAATC
2351 TCATCACTGT TCAGAGGTTA TTGCACTGTA CACTTACTGT GTAGAAAATA
2401 CTGTTTGAAT TTGTTTGAG TTACATTGTT CTGAGAACTG TGCTCTCAGA
2451 GCTTCTGTGC ACTATTCATG AGCATTAACA CTTAGCCTTG CAGTTTATA
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2501 CATAACTATA TGGTTAGTAA AACTGAATGG TCCAATGCAG ACTCATTAAA
2551 GTAGGCTTTT GCCCCCTTTG TTCTTGAAAT AATCTAGACC AGATTACTCG
2601 GGGTTTTTTT TAGGATTATT TTTATAGGTC TAAATATGAA TGATTGGGG
2651 GTATGAAGTA CTAAAGATA GTTCTGTCAA AAATCATTTT CAGCTGTCTA
2701 TTCAAGGGAA AAAATGCTAA CCTGTGCACT TTACTACACA AAACCACACT
2751 AAAATAAACC ATTAATGATA CTGCCTGCAA GATTTTAAAC CACCAGATAG
2801 CACACACATT AAGGATTTAT AAGGCACTGT ACGTAATTTT TATTCCAAGT
2851 GACCTCTCAA TTCATTTTCA TTTTGCATT TATCCATATG AACTCATGTT
2901 TAATTTAGAT AATAAAAATT TATTTTATTA AAAGGACAGT TTATTTAAAG
2951 TGGGTCTTTT TATTTGTTGT AGTGCATACT ATAAGAATTT GTAAGCCTCT
3001 AAAGTTGAGC TATAAATTT CATGCATTAA AAATTTGTTT CAGTTGTGAG
3051 GATATTTAAT CAGATTAAAT AATGTTGACT CTTAATATTT TGCCTGCCTT
3101 TTTTTCCTCC TACACATGAC CTTTGACAGA CTAAGTATAT CTCAGCTATT
3151 GAGGGTATCT GTTTTGTGTC CTGTATATT TGTTTAAATT AACTTGTATA
3201 TTCCTTTGTA TACACCTAGG CACAGATGTA TGCAAAAAAA ATTTGTTAAA
3251 TTAATTCCTT CTTTATACTA ATTCTCAATT TTTAAAAGAT TTTATCTGGC
3301 ATGTATATAC TTTTATATAG AACATTATAA ATGTAAAGGA AATGAATTCT
3351 AATTTTAATT GGATTATGTA TTCATACAGT TATCTCAAT TTTTAAATA
3401 CTAATAATGT AATCATTGAA TGTTCCTAC ATACGTAGTG GGTTTTATT
3451 GCTCACAGCA TACAGTTATT TTCAATTTA TGTTTTTCTA TTAGACTTAA
3501 ATTTTCATTAT AATAAAGGCT TTTACTCATT AAATACAAAA AAAAAAATAA
3551 AAAAAAATAA AAAAAAATAA AA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

95198680:

Overexpression of a novel member of the mitochondrial carrier family rescues defects in both DNA and RNA metabolism in yeast mitochondria.

Peptide information for frame 1

ORF from 169 bp to 564 bp; peptide length: 132
 Category: similarity to known protein
 Classification: Intracellular transport and traffic
 Prosite motifs: LEUCINE_ZIPPER (27-49)
 MITOCH_CARRIER (26-36)

```

1 MSQRDTLVHL FAGGCGGTVG AILTCPLEVV KTRLOSSSVT LYISEVCLNT
51 MAGASVNRVV SPGPLHCLKV ILEKEGPRSL FRGLGPNLVG VAPSRAYFA
101 AYSNCKEKLN DVFDPDSTQV HMISAAMAGM NV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_20m18, frame 1

PIR:S44092 probable carrier protein c2 - *Caenorhabditis elegans*, N = 2,
 Score = 147, P = 1.5e-19

PIR:S36081 probable carrier protein RIM2, mitochondrial - yeast
 (*Saccharomyces cerevisiae*), N = 1, Score = 230, P = 6.2e-19

>PIR:S36081 probable carrier protein RIM2, mitochondrial - yeast
 (*Saccharomyces cerevisiae*)
 Length = 377

HSPs:

Score = 230 (34.5 bits), Expect = 6.2e-19, P = 6.2e-19
 Identities = 55/133 (41%), Positives = 80/133 (60%)

```

Query:      8 VHLFAGGCGGTVGAILTCPLEVVKTRLOSSV-VTLYISEVQLNTMAGA----SVNRVVSP 62
            VH AGG GG GA++TCP ++VKTRLQS + Y S+ +N G+ S+N V+
Sbjct:     54 VHFVAGGIGMGAGAVVTCFPLVVKTRLOSDIFLKAYKSOA-VNISKGSTRPKSINYVIA 112

```

Query: 63 GP-----LHCLKVILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKEKLNDVFD--P 115
 G L + ++EG RSLF+GLGPNLVGV P+R+I F Y K+ F+
 Sbjct: 113 GTHFKETLGIIGNVYKQEGFRSLFKGLGPNLVGVIPARSINFFTYGTTKDMYAKAFNNGQ 172

Query: 116 DSTQVHMISAAMAG 129

++ +H+++AA AG
 Sbjct: 173 ETPMIHLMAAATAG 186

Score = 77 (11.6 bits), Expect = 1.1e+00, P = 6.8e-01
 Identities = 25/88 (28%), Positives = 39/88 (44%)

Query: 3 QRDTLVHLFAGGCGGTGAILTCPLEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVSP 62
 Q ++HL A G A T P+ ++KTR VQL+ SV + +
 Sbjct: 172 QETPMIHLMAAATAGWATATATNPILIKTR-----VQLDKAGKTSVRQYKNS 219

Query: 63 GPLHCLKVILEKEGPRSLFRGLGPNLVG 90

CLK ++ EG L++GL + +G
 Sbjct: 220 WD--CLKSVIRNEGFTGLYKGLSASYLG 245

Score = 71 (10.7 bits), Expect = 6.6e+00, P = 1.0e+00
 Identities = 28/91 (30%), Positives = 45/91 (49%)

Query: 12 AGGCGGTGAILTCPLEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVSPGPLHCLKVI 71
 + G V +I T P EVV+TRL+ + + N G R + G + KVI
 Sbjct: 294 SAGLAKFVASIATYPHEVVRTLRQTP-----KEN---G---KRKYT-GLVQSFKVI 338

Query: 72 LEKEGPRSLFRGLGPNLVGVAPSRAIYFAAY 102

+++EG S++ GL P+L+ P+ I F +
 Sbjct: 339 IKEEGLFSMYSGLTPHLMRTVPNSIIMFGTW 369

Pedant information for DKFZphtes3_20ml8, frame 1

Report for DKFZphtes3_20ml8.1

[LENGTH] 132
 [MW] 13993.36
 [pI] 8.42
 [HOMOL] PIR:S36081 probable carrier protein RIM2, mitochondrial - yeast (Saccharomyces cerevisiae) 7e-19
 [FUNCAT] 07.16 purine and pyrimidine transporters [S. cerevisiae, YBR192w] 3e-20
 [FUNCAT] 08.04 mitochondrial transport [S. cerevisiae, YBR192w] 3e-20
 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YBR192w] 3e-20
 [FUNCAT] 02.13 respiration [S. cerevisiae, YBR192w] 3e-20
 [FUNCAT] 01.05.07 carbohydrate transport [S. cerevisiae, YPR021c] 3e-10
 [FUNCAT] 07.07 sugar and carbohydrate transporters [S. cerevisiae, YPR021c] 3e-10
 [FUNCAT] 07.99 other transport facilitators [S. cerevisiae, YEL006w] 1e-09
 [FUNCAT] 01.07.10 transport of vitamins, cofactors, and prosthetic groups [S. cerevisiae, YIL006w] 3e-09
 [FUNCAT] 07.04.07 anion transporters (cl, so4, po4, etc.) [S. cerevisiae, YKL120w] 2e-08
 [FUNCAT] 01.03.19 nucleotide transport [S. cerevisiae, YPR011c] 3e-08
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YKR052c] 4e-08
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YJR095w] 2e-07
 [FUNCAT] 01.01.07 amino-acid transport [S. cerevisiae, YOR130c] 5e-05
 [FUNCAT] 07.10 amino-acid transporters [S. cerevisiae, YOR130c] 5e-05
 [FUNCAT] 01.04.07 phosphate transport [S. cerevisiae, YJR077c] 7e-05
 [FUNCAT] 13.04 homeostasis of other ions [S. cerevisiae, YJR077c] 7e-05
 [BLOCKS] BL00215B Mitochondrial energy transfer proteins
 [BLOCKS] BL00215A Mitochondrial energy transfer proteins
 [PIRKW] duplication 6e-09
 [PIRKW] transmembrane protein 6e-09
 [PIRKW] mitochondrial inner membrane 4e-07
 [PIRKW] transport protein 5e-06
 [PIRKW] mitochondrion 7e-08
 [PIRKW] chloroplast 3e-08
 [SUPFAM] Bt1 protein 3e-08
 [SUPFAM] ADP,ATP carrier protein repeat homology 4e-09
 [SUPFAM] Caenorhabditis probable carrier protein c2 4e-09
 [SUPFAM] probable carrier protein YPR021c 6e-09
 [PROSITE] LEUCINE ZIPPER 1
 [PROSITE] MITOCH_CARRIER 1
 [PFAM] Mitochondrial carrier proteins
 [KW] Alpha_Beta

SEQ MSQRDTLVHLFAGGCGGTGAILTCPLEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVV

```

PRD      cccccceeeccccccccccccccccccchhhhhhhhhhhcccccccccccccccccccccc
SEQ      SPGPLHCLKVILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVDFDPDSTQV
PRD      cccchhhhhhhhhhhccccceeeccccceeeccccceeeehhhhhhhhhcccccccccc
SEQ      HMISAAMAGMNV
PRD      chhhhhhcccc
    
```

Prosite for DKFZphtes3_20ml8.1

```

PS00029      27->49      LEUCINE_ZIPPER      PDOC00029
PS00215      26->36      MITOCH_CARRIER      PDOC00189
    
```

Pfam for DKFZphtes3_20ml8.1

```

HMM_NAME      Mitochondrial carrier proteins
HMM      *pFwkdfLAGGIAGmMeHTvMFPIDtIKTRMQlQgEMpM..ahpR.....
          ++++++AGG +G + +++++P++++KTR+Q++ ++ + ++
Query      5      DTLVHLFAGGCGGTVGAILTCPLVVKTRLQSS-SVTLYISEVQLNTMA      52
HMM      .....YkGMIdCFRwiwkNEGWRGLWRGLgANvIRYIPqWaIRFGFY
          G+++C++ I+++EG+R+L+RGLG+N+++++P +AI+F+ Y
Query      53      GASVNRVSPGPLHCLKVILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAY      102
HMM      EFMKeMFiDyfgeddnYWmWFwmnYMaGs*
          +KE ++D F++ D+++++ + +MAG+
Query      103      SNCKEKLNDVDFDP-DSTQVHMISAAMAGM      130
    
```

DKFZphtes3_21d4

group: signal transduction

DKFZphtes3_21d4 encodes a novel 464 amino acid putative GTP exchanging factor related to RCC1.

RCC1 (regulator of chromosome condensation) is a eukaryotic protein which binds to chromatin and interacts with ran, a nuclear GTP-binding protein. RCC1 promotes the exchange of bound GDP with GTP, acting as a guanine-nucleotide dissociation stimulator.

The new protein can find application in the regulation of gene expression by activation of nuclear GTP-binding proteins. The X-linked retinitis pigmentosa is a result of a defect GTPase regulator, which contains a RCC1-type repeat.

similarity to RCC1-like G exchanging factor RLG

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="20"

Insert length: 2321 bp

Poly A stretch at pos. 2293, polyadenylation signal at pos. 2262

```
1 GGGTCACGCA AGATGGCGGC GCCCAGAGGC TGCTGAGGCG CGGAACGGAG
51 GATGGCGCTG GTGGCGTTGG TGGCTGGGGC TCGGCTGGGG CGGCGGCTGA
101 GCGGGCCGGG GCTGGGGCGA GGGCACTGGA CGGCGCCAG GCGCTCCCGG
151 AGCCGGCGCG AAGCGGCAGA AGCCGAGGCG GAGGTGCCCG TGGTCCAGTA
201 CGTGGGCGAG CGCGCTGCCC GCGCCGATCG CGTCTCGTG TGGGGCTTCA
251 GCTTCTCGGG GCGCTGGGC GTGCCTTCCT TTGTGGTGCC CAGCTCCGGG
301 CCCGGGCCCC GCGCCGGCGC CCGACCGCGC CGCAGGATCC AGCCCCGTGCC
351 CTATCGCCTG GAGCTGGACC AAAAGATTTC ATCTGCTGCT TCGGGCTATG
401 GATTCACACT GCTGCTCTCT AAGACTGCGG ATGTTACGAA AGTCTGGGGG
451 ATGGGACTCA ACAAAGATTC TCAGCTTGGA TTTACAGGA GCCGGAAGA
501 TAAACGAGG GGCTACGAGT ATGTGTTGGA GCCCTCACCC GTCTCCCTGC
551 CTCTGGACAG ACCTCAGGAG ACACGGGTGC TGCAGGTCTC CTGCGGCCGA
601 GCTCACTCTC TTGTGTTGAC TGACAGGGAA GGAGTCTTCA GCATGGGAAA
651 CAATTCTTAT TGTGGAATGTG GAAGAAAGGT GGTGAAAAAT GAAATTTACA
701 GTGAAAGTCA CAGAGTCCAC AGGATGCAGG ACTTCGATGG CCAGGTGGTC
751 CAGGTCGCCT GTGGTCAGGA TCATAGTCTG TTCCTGACGG ATAAAGGAGA
801 AGTCTATTCT TGTGGATGGG GTGCTGATGG GCAAACAGGT CTGGGTCAC
851 ACAATATCAC CAGCTCGCCC ACCAAGCTGG GTGGAGACCT GGCGGGAGTG
901 AACGTTATCC AAGTTGCCAC CTACGGTGAT TGCTGCCTGG CCGTGTCCGC
951 CGACGGAGGA CTTTTTGGTT GGGGAAACTC GGAGTACCTG CAGCTGGCCT
1001 CTGTCACTGA CTCACACAG GTGAATGTGC CCCGCTGCTT ACACTTCTCA
1051 GGAGTGGGGA AGGTGCGACA GGCTGCATGC GGTGGCACGG GCTGTGCAGT
1101 GTTAAACGGA GAAGGACATG TTTTGTCTG GGGCTATGGA ATTCTTGGGA
1151 AAGGTCCAAA CCTAGTGGAA AGTGCCGTC CTGAAATGAT TCCACCCACT
1201 CTCTTTGGCT TGACGGAGTT CAACCCAGAA ATCCAGTTT CCCGCATCCG
1251 ATCTGCACTC AGCCACTTTG CTGCACTGAC CAACAAAGGA GAGCTGTTTG
1301 TATGGGGCAA GAACATCCGA GGGTGCCTGG GAATCGGTG CCTGGAGGAC
1351 CAGTATTTCC CATGGAGGTT GACGATGCCT GGGGAGCCTG TGGACGTGGC
1401 ATGTGGCGTG GACCACATGG TGACCCTGGC CAAGTCATTC ATCTAAACCT
1451 CCTCACCTG CTGGGGCGGC CCGTCCCGG GAACCACTGG CACTCCTTGG
1501 CAGAGGCCAG CGCGTGGCCA GCGCCCGGG GTTCTTGGAT GGTGGTGGCG
1551 GAGGACCCTG CGTGCAGTGT GACGCTCTGT CCTGAATCCC TTAGCGGGTA
1601 CCTACCAGGA GGATCAGGGC AAGGTCCCTC TCCAGCTGCA GGTGAGGCCT
1651 GCGGAACCTA GCTTGGATGG CAGCCTTTGG TGGGCCGCTG TGGCCGCGAC
1701 GTCTCTGTTC TCTCCAAGTA ACATGCGACG GTGTCTGGTG TCACGTCTCG
1751 CCTGAGAAGC CCGTCTTAGG AAAGCTTAGC TTGAACACAG TGCTCGGGAG
1801 GTTCTGCTC TGTCTGTCAT GGCAGTCTCT TGGTTTGTGT CTGGCCAAGG
1851 CCATGCGTGT GCCTCGGACC GAGCCCCAGC TTAGGCGAGG GAGTCAGGCT
1901 GGCTTCGGCC CTCGGTTTTT ATTCAGGCCA CCTGTCTCAT GGCCCTTCTT
1951 GCGCGGCTGC CACACCGCAA GCTCGCTGGG GGGACACTAG AAGCACCGTG
2001 GCCTGGGATT CCATCTGGAG CTGTCCGCAG GCACCAGCCC CAGCCTCCCA
2051 CCACGCTCAC TGCCTGGCTT GGAAAAGTTA AGAAGCCCTT CAGGAAGAGA
2101 ATCGAGGCTA AGTTCTCTG CCGCAGGGC CCGGACATA TCCGCCAAGG
2151 CTCAGCTGCA GTGCCAGGCG GAGGAGGAAG ATCCAGAAAT TGTGAACAAT
2201 GTTTGATTTA GTAGCGTGAC TTGCCTTTCC CTTTAAAAAC ATCTTTTACA
2251 AATCTGTCTT GGAATAAAGT CTATTTTCTG CTTTGTGTT TTTAAAAAAA
2301 AAAAAAAAAA AAAAAAAAAA A
```

BLAST Results

Entry HS203358 from database EMBL:
human STS SHGC-31781.
Score = 1748, P = 1.1e-72, identities = 376/394

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 52 bp to 1443 bp; peptide length: 464
Category: similarity to known protein

```

1 MALVALVAGA RLGRRLSGPG LGRGHWTAAR RSRSRREAAE AEAEPVVQY
51 VGERAARADR VFVWGFSSFG ALGVPSFVVP SSGPGPRAGA RPRRRIQPVP
101 YRLELDQKIS SAACGYGFTL LSSKTADVTK VWGMGLNKDS QLGFRHSRKD
151 KTRGYEYVLE PSPVSLPLDR PQETRVLQVS CGRAHSLVLT DREGVFSMGN
201 NSYGQCGRKV VENIYSESH RVHRMQDFDG QVVQVACQD HSLFLTDKGE
251 VYSCGWGADG QTGLGHYNIT SSPTKLGGDL AGVNVIVQVAT YGDCCLAVSA
301 DGGFLFGWNS EYLQLASVTD STQNVNPRCL HFSGVGKVRQ AACGGTGCAV
351 LNGEHVFW GYGILGKGN LVESAVPEMI PPTLFGLTEF NPEIQVSRIR
401 CGLSHFAALT NKGELEFWGK NIRGCLGIGR LEDQYFPWRV TMPGEPVDVA
451 CGVDHMTLA KSEI

```

BLASTP hits

Entry CEW09G3_5 from database TREMBLNEW:
gene: "W09G3.3"; Caenorhabditis elegans cosmid W09G3
Score = 395, P = 9.3e-37, identities = 111/330, positives = 165/330

Entry Y032_HUMAN from database SWISSPROT:
HYPOTHETICAL PROTEIN KIAA0032.
Score = 309, P = 1.0e-24, identities = 96/308, positives = 143/308

Entry B38919 from database PIR:
hypothetical protein 2 - human (fragment)
Score = 309, P = 1.0e-24, identities = 96/308, positives = 143/308

Entry AF060219_1 from database TREMBLNEW:
product: "RCC1-like G exchanging factor RLG"; Homo sapiens RCC1-like G
exchanging factor RLG mRNA, complete cds.
Score = 273, P = 4.0e-21, identities = 84/262, positives = 124/262

Entry S71752 from database PIR:
giant protein p619 - human
Score = 282, P = 1.1e-19, identities = 86/287, positives = 144/287

Alert BLASTP hits for DKFZphtes3_21d4, frame 1

No Alert BLASTP hits found

Pendant information for DKFZphtes3_21d4, frame 1

Report for DKFZphtes3_21d4.1

```

[LENGTH]      464
[MW]           49997.08
[pI]           8.74
[HOMOL]        TREMBL:CEW09G3_5 gene: "W09G3.3"; Caenorhabditis elegans cosmid W09G3 5e-34

[FUNCAT]       04.07 rna transport [S. cerevisiae, YGL097w] 2e-09
[FUNCAT]       03.07 pheromone response, mating-type determination, sex-specific proteins
               [S. cerevisiae, YGL097w] 2e-09
[FUNCAT]       08.01 nuclear transport [S. cerevisiae, YGL097w] 2e-09
[FUNCAT]       04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S.
cerevisiae, YGL097w] 2e-09
[FUNCAT]       04.01.04 rrna processing [S. cerevisiae, YGL097w] 2e-09
[FUNCAT]       04.03.03 trna processing [S. cerevisiae, YGL097w] 2e-09
[FUNCAT]       30.03 organization of cytoplasm [S. cerevisiae, YGL097w] 2e-09

```

```

[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YAL020c] 4e-06
[BLOCKS] BL008701
[BLOCKS] BL00625B Regulator of chromosome condensation (RCC1) proteins
[BLOCKS] BL00625A Regulator of chromosome condensation (RCC1) proteins
[PIRKW] blocked amino end 3e-16
[PIRKW] nucleus 3e-16
[PIRKW] duplication 4e-08
[PIRKW] tandem repeat 3e-16
[PIRKW] DNA binding 3e-16
[PIRKW] mitosis 3e-16
[PIRKW] leucine zipper 3e-21
[SUPFAM] pheromone response pathway component SRM1 4e-08
[SUPFAM] WD repeat homology 3e-21
[PROSITE] MYRISTYL 7
[PROSITE] RCC1_2_2
[PROSITE] AMIDATION 2
[PROSITE] CAMP_PHOSPHO_SITE 1
[PROSITE] CK2_PHOSPHO_SITE 5
[PROSITE] TYR_PHOSPHO_SITE 2
[PROSITE] GLYCOSAMINOGLYCAN 3
[PROSITE] PKC_PHOSPHO_SITE 7
[PROSITE] ASN_GLYCOSYLATION 2
[PFAM] Regulator of chromosome condensation (RCC1)
[KW] All Beta
[KW] LOW_COMPLEXITY 13.58 %

```

```

SEQ MALVALVAGARLGRRLSGPGLGRGHWTAARRSRSRREAAEAEVPPVQYVGERAARADR
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD ccchhhhhhhhhheeeccccccccchhhhhhhhhhhhhhhhhhhhhceeeeeehhhhhhhhh

```

```

SEQ VFWWGFSGALGVPSFVVPSSGPGPRAGARPRRIQVPYRLELDQKISSAACGYGFTL
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD eeeccccccccccceeeccccccccccccccccccccccccchhhhhhhheeeccccceee

```

```

SEQ LSSKTADVTKVWGMGLNKDSQLGFHRSRKDKTRGYEYVLEPSPVSLPLDRPQETRVLQVS
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD eccccccccceeeccccccccccccccccccccccccccccceeeccccccccccccccccceee

```

```

SEQ CGRAHSLVLTDRGVFSMGNNISYQCGRKVVENEIYSESHRVHRMQDFDQVQVACGQD
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD cccccceeeccccceeeccccccccccccccccccccccccccccccccccccceeecccccc

```

```

SEQ HSLFLTDKGEVYSCGWGADGQTGLGHYNITSSPTKLGDLAGVNVIQVATYGDCLAVSA
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD eeeeeccccceeeccccccccccccccccccccccccccccccccccccceeeccccceeeec

```

```

SEQ DGGLFGWGNSEYLQLASVTDSTQVNVPRCLHFSGVGKVRQAACGGTGCAVLNGEGHVFW
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD cccccccccccccccccccccccccccccccccccccccccccccceeeccccceeeccccceee

```

```

SEQ GYGILGKGNLVSAPPEMIPPTLFLGLTEFNPEIQVSRIICGLSHFAALTNGELFVWGK
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD cccccccccccccccccccccccccccccccccccccccccccccceeeccccceeeccccceec

```

```

SEQ NIRGCLGIGRLEDQYFPWRVTMPGEPVDVACGVDMVTLAKSFI
SEG .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD cccccccccccccccccccccceeeccccceeecccccccccccccccccc

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Prosite for DKFZphtes3_21d4.1

PS00001	200->204	ASN_GLYCOSYLATION	PDOC00001
PS00001	268->272	ASN_GLYCOSYLATION	PDOC00001
PS00002	17->21	GLYCOSAMINOGLYCAN	PDOC00002
PS00002	82->86	GLYCOSAMINOGLYCAN	PDOC00002
PS00002	333->337	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	14->18	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	34->37	PKC_PHOSPHO_SITE	PDOC00005
PS00005	122->125	PKC_PHOSPHO_SITE	PDOC00005
PS00005	147->150	PKC_PHOSPHO_SITE	PDOC00005
PS00005	190->193	PKC_PHOSPHO_SITE	PDOC00005
PS00005	219->222	PKC_PHOSPHO_SITE	PDOC00005
PS00005	246->249	PKC_PHOSPHO_SITE	PDOC00005
PS00005	410->413	PKC_PHOSPHO_SITE	PDOC00005
PS00006	34->38	CK2_PHOSPHO_SITE	PDOC00006
PS00006	147->151	CK2_PHOSPHO_SITE	PDOC00006
PS00006	190->194	CK2_PHOSPHO_SITE	PDOC00006
PS00006	290->294	CK2_PHOSPHO_SITE	PDOC00006
PS00006	317->321	CK2_PHOSPHO_SITE	PDOC00006

PS00007	209->217	TYR_PHOSPHO_SITE	PDOC00007
PS00007	208->217	TYR_PHOSPHO_SITE	PDOC00007
PS00008	9->15	MYRISTYL	PDOC00008
PS00008	20->26	MYRISTYL	PDOC00008
PS00008	133->139	MYRISTYL	PDOC00008
PS00008	238->244	MYRISTYL	PDOC00008
PS00008	277->283	MYRISTYL	PDOC00008
PS00008	302->308	MYRISTYL	PDOC00008
PS00008	344->350	MYRISTYL	PDOC00008
PS00009	12->16	AMIDATION	PDOC00009
PS00009	206->210	AMIDATION	PDOC00009
PS00626	179->190	RCC1_2	PDOC00544
PS00626	235->246	RCC1_2	PDOC00544

Pfam for DKFZphtes3_21d4.1

HMM_NAME	Regulator of chromosome condensation (RCC1)		
HMM	*IAaGqHHTVCLTqDGRVYtWG*		
	+A GQ+H++ LT++G VY++G		
Query	235	VACGQDHSFLTKGEVYSCG	255

DKFzphtes3_21j15

group: transcription factors

DKFzphtes3_21j15 encodes a novel 898 amino acid protein with similarity human NY-CO-33 protein.

NY-CO-33 is a protein recognised by autologous antibodies of human colon cancer patients. The novel protein contains 4 C2H2 Zinc fingers and is a new putativ transcription factor.

The new protein can find application in modulating/blocking the expression of genes controlled by this transcription factor.

strong similarity to "NY-CO-33"

complete cDNA, complete cds, potential start at bp 27, EST hits

Sequenced by LMU

Locus: unknown

Insert length: 4407 bp

Poly A stretch at pos. 4321, polyadenylation signal at pos. 4301

```
1 CGCTGCAGCA GGTGTACAG AGCCGCATGC TCCCGGAGCC CAGCCTCTTC
51 AGCACCGTGC AGCTGTACCG GCAGAGCAGC AAGCTCTATG GCTCCATCTT
101 CACGGGGGGCC AGCAAGTTCC GCTGTAAGGA CTGCAGCGCT GCCTACGACA
151 CCCTGGTGGA GTTGACAGTG CACATGAACG AGACGGGGCA TTACCGCGAC
201 GACAACCATG AGACCGATAA CAACAACCCC AAGCGTGGT CCAAGCCTCG
251 CAAACGCTCC TTGCTGGAAG TGGAAGGGAA GGAAGACGCC CAGAAGGTGC
301 TGAAGTGCAT GTACTGTGGC CACTCCTTTG AGTCCCTGCA GGATTGAGT
351 GTCCATATGA TCAAAACAAA ACACTACCAA AAAGTGCCTC TGAAGGAACC
401 CGTCACTCCT GTCGCCGCCA AAATCATCCC TGCCACTCGG AAGAAAGCTT
451 CCCTGGAGCT GGAGCTCCCC AGCTCCCCAG ATTCCACAGG TGAACCCCC
501 AAAGCCACCA TCTCAGACAC CAACGATGCA CTTCAGAAGA ACTCCAACCC
551 TTACATCAGC CCAATAATC GGTACGGCCA CCAGAATGGG GCCAGCTATG
601 CATGGCACTT TGAGGGCCCG AAGTCGCAGA TCCTGAAGTG CATGGAGTGT
651 GGGAGCTCGC ATGACACCCCT GCAGGAGCTC ACTGCCACA TGATGGTCAC
701 TGGCCACTTC ATCAAGGTCA CCAACTCTGC TATGAAAAG GGAAGCCCA
751 TTGTGGAGAC GCCTGTCACA CCTACCATCA CAACCCTGCT GGATGAGAAG
801 GTCCAGTCCG TGCCCTGGC AGCCACCACC TTCACGTCCC CCTCCAATAC
851 ACGTGCCAGC ATCTCCCAA AACTGAATGT GGAGGTCAAG AAGGAAGTCG
901 ACAAGGAGAA AGCGGTCACT GACGAGAAAC CTAAGCAAAA AGACAAGCCT
951 GGCGAAGAAG AGGAGAAGTG TGACATCTCT TCCAAATACC ATTACTTGAC
1001 TGAAAATGAC TTAGAAGAGA GTCCCAAGGG GGGGCTTGAT ATCCTCAAAT
1051 CCTTGGAAAA CACAGTGACA TCCGCAATCA ACAAGGCCA GAACGGCACT
1101 CCTAGCTGGG GGGGCTATCC CAGCATCCAT GCCGCTTACC AACTTCCCAA
1151 CATGATGAAG TTGTCCCTGG GCTCGTCGGG GAAGAGCACG CCCCTGAAAC
1201 CCATGTTTGG CAACAGTGAG ATTGTCTCCC CGACGAAAA CCAGACCCTG
1251 GTCTCTCCAC CCAGCAGCCA GACGTCCCC ATGCCAAGA CAAACTTTCA
1301 TGCCATGGAG GAGCTGGTGA AAAAGGTCAC TGAGAAAGTT GCCAAAGTGG
1351 AGGAGAAGAT GAAGGAGCCG GATGGGAAGC TTTCCCCGCC CAAGCGGGCC
1401 ACTCCCTCCC CATGTAGCAG CGAAGTCGGG GAACCCATCA AGATGGAGGC
1451 ATCCAGCGAT GGGGGCTTCC GCAGCCAGGA GAACAGCCCC AGCCCCCGC
1501 GGGATGGGTG CAAGGATGGG AGCCCCCTCG CTGAGCCGGT GGAGAATGGC
1551 AAGGAGCTGG TGAAGCCCC AGCCAGCAGT TTGAGTGGCA GCACGGCCAT
1601 CATCACCGAC CACCCGCTTG AACAGCCTTT TGTTAACCTT TTGAGCGCCC
1651 TGCACTCAGT CATGAACATT CACCTGGGCA AGGCCGCCA GCCCTCCCTG
1701 CCTGCCCTGG ACCCCATGAG CATGCTTTTC AAGATGAGCA ACAGCCTGGC
1751 GGAGAAGGCT GCTGTGGCCA CCCC GCCGCC CTTGCAGTCC AAGAAGGCAG
1801 ACCACCTCGA CCGCTATTTC TACCACGTCA ACAACGACCA GCCCATAGAC
1851 TTGACAAAAA GGAAGAGTGA CAAAGGCTGC TCCTTGGGTT CAGTGCTTCT
1901 GTCAACCCAG TCCACAGCCC CGGCACCTC CTCATCCACG GTGACAACCG
1951 CAAAGACATC TGCCGTCGTA TCATTATGAT CAAACTCGCC GCTACGCGAG
2001 AATGCCTTGT CAGATATATC CGATATGCTG AAGAAGTTGA CAGAGAGCCA
2051 CACGTCAAAG TCCTCCACTC CTTCCAGCAT CTCCGAGAAG TCTGACATTG
2101 ACGGGGGCAC TCTGGAGGAG GCTGAGGAGT CGACGCCCGC CCAGAAGAGG
2151 AAGGGCCGCC AGTCAAACCT GAACCCCGAG CACCTCCTGA TCCTCCAGGC
2201 CCAGTTTGGC GCGAGCTTCC GGCAGACCTC AGAAGGGAAG TACATCATGT
2251 CAGACCTGAG CCCCAGGAG CGGATGCATA TCTCCAGGTT CACCGGGCTG
2301 TCCATGACCA CCATCAGCCA CTGGCTGGCC AACGTGAAAT ACCAGCTTCG
2351 AAGGACAGGT GGAACAAAGT TCCTCAAAAA CTTGGACACT GGCCACCCCG
2401 TCTTCTTTTG TAACGATTGT GCGTCCCAAA TCAGGACTCC TTCCACGTAC
2451 ATCAGTCACC TAGAGTCACA CTTAGGCTTC CGGCTACGGG ACTTATCCAA
2501 ACTGTCCACC GAACAGATTA ACAGTCAGAT AGCACAACCC AAGTCACCGT
2551 CAGAAAAAAT GGTGACGTCC TCCCCGAGG AAGACCTGGG GACTTCCTAT
2601 CAGTGCAAAC TTTGCAATCG GACCTTTGCC AGCAAGCACG CTGTTAAACT
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2651 TCACCTTAGC AAAACACACG GGAATCTCC GGAAGACCAC CTTCTGTATG
2701 TCTCTGAGTT AGAGAAGCAG TAGCATTTGC TTTTGATAGA AAGGACTGCA
2751 GTTTGCTTTG AGGGAACTG TGGAAGGCAC CTTCAGGCC CCTCTGACTT
2801 GTTGTCTTTG GCACATGTTT TTAATTTAAC TGCAGAGAAT CACTCTGGGC
2851 TGGACTGTTT TGTATAACTG TACAGTGTTC AATAGAGGTG CATAATCAGC
2901 TGTTGTACTT GGTAAATATAT GAAGGTAAAT ATGCAGTGGT AAGTGTTTGG
2951 AACTTTGTGT AAACGGGATT TAGTTGTGAG CATCCTCCCG ATGCTTCAAG
3001 CTGCATGCAT TAACAGACAG TTTAATTAAG CATTTATAAC GGAATCAGGC
3051 ACACCTTTTC CACGAGACTC GAGTGTGCTG GCATTTCTCA CCTTTTCATC
3101 TTTAGCCCTC TGAGTACTTT GAAGCACTTT TGCATTAATT TGGTTAAAAA
3151 ATAAAAATAA ATAATAATAA TGTATGAAGC TCTGTTTTTT AAACCTCCTA
3201 CCAGCTTAGT TATAATGAAT AATATGAACC TCCATTATG CAGGTCTGCA
3251 GGGGTATAAC ACGCCTTGAA ATTTAAAAAG ATATTATTTT CACATTGAAA
3301 CATAGATGTA TATATTGTAT AGATTTTCAGA CTCTCTTATG AAAAAAATG
3351 TGATTGTGGT TAAATGACCT TTTCTTGCA TTTATAGCAA CAGTGTTTTA
3401 TGCACCTGCT ATGCTCTGGG CATAAGCTGT GCCTATGTAT AGTGTATATT
3451 TCTTTTTTTC TTTTTTTTAA GGTCTATGGG TTTGTTTTTT TACATGCAAA
3501 CATTTGTAAT TATACAGAAG ATACCACAGA TAGCATTAT AAAGTATACA
3551 GAAACATTAT CTGAAAGCAA AGTATGATAG TTTGTTTGC TATACAGTAC
3601 ATCTATATTG ATAGAGGTTC ATGTTTAAAT TATACATATT TATTAGCATC
3651 ATATTGTCAT TTGTTTGTAG CAGTCTGAAT AAACGAGACC GGGAAAGACA
3701 TCCCTGGCAG GCATCAGAAC TATTTTGCAC ATGATTTTAA AAGGTATTTA
3751 TTAGAAATCA AAGAACAAC AAAATAAACT CAGTGCTCAA AGGGTTAAGT
3801 CTATTGTAAT AGGTTAAAAA AAAGAACAAA AAAAAAAGAA GAACCTGTAC
3851 TGTATTTCCT AAACATTGAT AAAGCCTTTA AAATGTTTGT ACTGTAATAC
3901 TTTGCTTAAA AGTCATGAGG CATTCTGTGA TCCAACCTCT TTCACTTATT
3951 TATAAGCCCT CTGTTTGTCT ATTCCATATT GTAGGATGCC TTTCTATTTC
4001 AATTGGTAAC TTTCTGTTTT GTTCTTCTTA ATTATTCTCC CAAGATCCCA
4051 CACTGCAGCT TTATCTTTAG GCTTATGAAA GGTAACCCGT GGTACCAGGC
4101 TCTCCAAGTG ATTCTGTTCT TCTCCATTTT TGGCAGTTAA TTTGCAAGAG
4151 TAACTGACAG CTGACACCAT ATGAGAACCT TTGTATAAAA TATTGGCATG
4201 TAAACAGCAC AGACACCGTA ACACACTCTG TGCCCTGTTT GGTGTTGAC
4251 AATGAAGCAC CATTATGTGA CTCTTCATAT AACCTTTTTC TCTACGGCAG
4301 CATTAAATTT GTCTTTTTCG TATAAAAAAA AAAAAAAGAA AAAAAAAGAA
4351 AAAAAAAGAA AAAAAAAGAA AAAAAAAGAA AAAAAAAGAA AAAAAAAGAA
4401 AAAAAAAGAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 27 bp to 2720 bp; peptide length: 898
Category: strong similarity to known protein

```
1 MLPEPSLFST VQLYRQSSKL YGSIFTGASK FRCKDCSAA YDTLVELTVHM
51 NETGHYRDDN HETDNNPNKR WSKPRKRSLL EMEGKEDAQK VLKCMYCGHS
101 FESLQDLSVH MIKTKHYQKV PLKEPVTPVA AKIIPATRKK ASLELELPSS
151 PDSTGGTPKA TISDTNDALQ KNSNPYITPN NRYGHONGAS YAWHFEARKS
201 QILKMECCGS SHDTLQELTA HMMVTGHFIK VINSAMKKGK PIVETPVPTPT
251 ITTLLEKVVQ SVPLAATTFT SPSNTPASIS PKLNVEVKKE VDKEKAVTDE
301 KPKQKDKPGE EEEKCDISSK YHYLTENDLE ESPKGGDLIL KSLNVTVISA
351 INKAQNGTPS WGGYPSIHAA YQLPNMMKLS LGSSGKSTPL KPMFGNSEIV
401 SPTKNQTLVS PPSSQTSMPM KTNFHAMEEL VKKVTEKVA VEEKMKEPDG
451 KLSPPKRATP SPCSSEVGEP IKMEASSDGG FRSQENSPSP PRDGCKDGGSP
501 LAEPVENGKE LVKPLASSLS GSTAIITDHP PEQPFVNPLS ALQSVMNHIL
551 GKAAKPSLPA LDPMSMLFKM SNSLAEKAAV ATPPPLOSKK ADHLDRYFYH
601 VNNDQPIDLT KGKSDKGCSL GSVLLSPTST APATSSSTVT TAKTSAVVSF
651 MSNSPLRENA LSDISMLKN LTESHTSKSS TPSSISEKSD IDGATLEEAE
701 ESTPAQKRKG RQSNWNPOHL LILQAOFAAS LRQTSSEKYY MSDLSPOERM
751 HISRFTGLSM TTISHWLANV KYQLRRTGGT KFLKNLDTGH PVFFCNDCAS
801 QIRTPSTYIS HLESHLGFR LRLSKLSTEQ INSQIAQTKS PSEKMTVSSP
851 EEDLGTSYQC KLCNRTFASK HAVKLHLSKT HGKSPEDHLL YVSELEKQ
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_21j15, frame 3

TREMBL:AF039698_1 gene: "NY-CO-33"; product: "antigen NY-CO-33"; Homo sapiens antigen NY-CO-33 (NY-CO-33) mRNA, complete cds., N = 1, Score = 1039, P = 5.5e-105

PIR:A38437 probable homeotic protein tsh - fruit fly (Drosophila melanogaster), N = 3, Score = 158, P = 7.2e-09

TREMBL:CE33058_1 gene: "unc-89"; product: "UNC-89"; Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds., N = 2, Score = 175, P = 3.3e-07

>TREMBL:AF039698_1 gene: "NY-CO-33"; product: "antigen NY-CO-33"; Homo sapiens antigen NY-CO-33 (NY-CO-33) mRNA, complete cds.
Length = 687

HSPs:

Score = 1039 (155.9 bits), Expect = 5.5e-105, P = 5.5e-105
Identities = 244/504 (48%), Positives = 319/504 (63%)

Query: 170 QKNSNPYITPNNRYGHQNGASYAWHFEARKSQILKMECGSSHDTLQELTAHMMVTGHFI 229
KQ +NPY+TPNNRYG+QNGASY W FEARK+QILKMECGSSHDTLQ+LTAHMMVTGHF+
Sbjct: 14 QKAANPYVTPNNRYGYQNGASYTWQFEARKAQILKMECGSSHDTLQQLTAHMMVTGHFL 73

Query: 230 KVTNSAMKKGKPIVETPVTPTITTLDEKQSVPLAATTFTS-PSNT----PASISPKLN 284
KVT SA KKGK +V PV ++EK+QS+PL TT T P+++ P S +
Sbjct: 74 KVTTSASKKGKQLVLDPV-----VEEKIQSIPLPPTHTRLPASSIKKQPDSPAGSTT 126

Query: 285 VEVKKEVDKEKA-VTDEKPKQKDKPGESEKCDISSKYHYLTENDLEESPKGGDLILKSL 343
E KKE +KEK V + K K++ + EK + S+ Y YL E DL++SPKGGDLILKSL
Sbjct: 127 SEEKKEPEKEKPPVAGDAEKIKEESEDSELEKFEPTLYPYLREEDLDDSPKGGDLILKSL 186

Query: 344 ENTVTSAINKAQNGTPSWGYPYPSIAAAYQLPNMMKLSLGSSGKSTPLKPMF-GNSEIVSP 402
ENTV++AI+KAQNG PSWGGYPYPSIAAAYQLP +K L ++ +S ++P + G + +S
Sbjct: 187 ENTVSTAISKAQNGAPSWGYPYPSIAAAYQLPGTVK-PLPAVQSVQVQPSYAGGVKSLSS 245

Query: 403 TKNQTLVSPSSQTSMPKTNFAMEELVKKVTEKV-AKVEEKMKEPDGKLSPPKRATPS 461
++ L+ P S T P K+N AMEELV+KVT KV K EE+ E + K S K A S
Sbjct: 246 AEHNALLHSPGSLTPPHKSNVSAEELVEKVTGKVNIIKKEERPPEKE-KSSLAKAA--S 302

Query: 462 PCSSEVGEPIKMEASSDGGFRSQENSPSPPRDGCKDGSPLAEPVENGKELVKPLASSLSG 521
P + E + K E S + Q+ P K PL + NG E +K ++
Sbjct: 303 PIAKENKDFPKTEEVSG---KPQKKGPEAETWEAKKEGPLDVHTPNGTEPLKAKVTNGCN 359

Query: 522 STAIITDHPPEQPFVNPLSALQSVNMNIHLGKAAKPSLPALDPMMLFKMSNSLAEKAABA 581
+ II DH PE F+NPLSALQS+MN HLKG +KP P+LDP++ML+K+SNS+ +K
Sbjct: 360 NLGIIMHSPSPSFNPLSALQSIMNTHLGKVSQKPVSPSLDPLAMLYKISNSMLDKPVYP 419

Query: 582 TPPPLQSKKADHLDYFYHVNNDQPIDLTGKGSCK-GCSLGSVLLSPTSTAPATSSSTVT 640
P K+AD +DRY+Y N+DQPIDLTGK K+ S+ + SP + S +
Sbjct: 420 ATPV---KQADAIDRYYYE-NSDQPIDLTGKSKNKLVSVAADSVASPLRESALMDISDMV 475

Query: 641 TAKTSAVVSFMSN-SPLRENALSDISDMLKNLTE 673
T + S S + E + +D S + L E
Sbjct: 476 KNLTGRLTPKSSSTPSTVSEKSDADGSSFEALDE 509

Score = 865 (129.8 bits), Expect = 7.4e-95, P = 7.4e-95
Identities = 211/434 (48%), Positives = 268/434 (61%)

Query: 447 EPDGLKSPPKRATPSPCSSEVG--EPIKMEASSDGGFRSQENSPSPPRDG-CKDGSPLAE 503
E + L P TP P S V E + + + +E P + K SP+A+
Sbjct: 247 EHNALLHSPGSLTPPHKSNVSAEELVEKVTGKVNIIKKEERPPEKEKSSLAKAASPIAK 306

Query: 504 -----P-VE--NGKELVK-PLASSLSGSTAIITD-HPPE--QPFVNPLSALQSVNMNIHLG 551
P E +GK K P A + D H P +P ++ + + I +
Sbjct: 307 ENKDFPKTEEVSGKPKKGPEAETWEAKKEGPLDVHTPNGTEPLKAKVTNGCNLGIIMD 366

Query: 552 KAAKPSLPALDPMMLFKMSNSLAEKAABATPPPLQSKKADHLDYFYHVNNDQPID 608
+ +PS ++P+S L + N+ K + P L D L Y ++N D+P+
Sbjct: 367 HSPEPSF--INPLSALQSIMNTHLGKVSQKPVSPSL-----DPL-AMLYKISNSMLDKPV- 417

Query: 609 LTKGKSDKGCGLSVLLSPTSTAPATSSSTVTTAKTSAVVSFMSNSPLRENALSDISDML 668
K S P + + S+V ++ SPLRE+AL DISDM+
Sbjct: 418 -YPATPVKQADAIDRYYYENSQPIDLTGKSKNKLVSVAADSVASPLRESALMDISDMV 475

Query: 669 KNLTESHTSKSSTPSSISEKSDIDGATLEEA-EESTPAQKRKRQSNWNPNQHLLILQAQF 727
KNLT T KSSTPS++SEKSD DG++ EEA +E +P KRKRQSNWNPNQHLLILQAQF

Score = 98 (14.7 bits), Expect = 7.4e-95, P = 7.4e-95
Identities = 32/95 (33%), Positives = 47/95 (49%)

Score = 81 (12.2 bits), Expect = 4.6e-93, P = 4.6e-93
Identities = 13/29 (44%), Positives = 20/29 (68%)

Pedant information for DKFZphtes3 21j15, frame 3

Report for DKFZphtes3 21j15.3

```

SEQ      MLPEPSLFSTVQLYRQSSKLYGSIFTGASKFRCKDCSAAAYDTLVELTVHMNETGHYRDDN
SEG      .....
PRD      cccccceeeeeeeccccceeeeeeeccccceeecccchhhhhhhhhhhcccccccccccc

SEQ      HETDNNNPKRWSKPRKRSLLEMEGKEDAQVKVLKCMYCGHSFESLQDLSVHMIKTKHYQKV
SEG      .....
PRD      cccccccccccccccchhhhhhhccchhhhhhhhhhhccccchhhhhheeeeeeeceeee

SEQ      PLKEPVTTPVAAKIIIPATRKKASLELELPSSPDSTGGTPKATISDTNDALQKNSNPYITPN
SEG      .....
PRD      eccccccccceeeeeehhhhhhhhhhhccccccccccccccccceeeecchhhhhcccccccc

SEQ      NRYGHQNGASYAWHFARKSQILKCMCEGSSSDHTLQELTAHMMVTGHFIKVTNSAMKKGK
SEG      .....
PRD      cccccccchhhhhhhhhhhhhhhhhccccccccccchhhhhhhhhhhceeeeecccccccc

SEQ      PIVETPVTPTITTLDEKVSQVPLAATTFTPSPSNTPASISPKNLNVKKEVDKEKAVTDE
SEG      xxxxxxxxxxxxxxxx.....xxxxxxxxxxxxxxxxxxxx
PRD      cccccccccchhhhhhhhhccccccccccccccccccccccccccccccccchhhhhhec

SEQ      KPKOKDKPGEETEEKCDISSKYHYLTENDLEESPKGGLDILKSLNTVTSAINKAQNGTPS

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Prosite for DKFZphtes3 21j15.3

713

PS00006	810->814	CK2_PHOSPHO_SITE	PDOC00006
PS00006	840->844	CK2_PHOSPHO_SITE	PDOC00006
PS00006	848->852	CK2_PHOSPHO_SITE	PDOC00006
PS00006	884->888	CK2_PHOSPHO_SITE	PDOC00006
PS00006	893->897	CK2_PHOSPHO_SITE	PDOC00006
PS00007	732->740	TYR_PHOSPHO_SITE	PDOC00007
PS00007	883->892	TYR_PHOSPHO_SITE	PDOC00007
PS00008	22->28	MYRISTYL	PDOC00008
PS00008	156->162	MYRISTYL	PDOC00008
PS00008	188->194	MYRISTYL	PDOC00008
PS00008	362->368	MYRISTYL	PDOC00008
PS00008	479->485	MYRISTYL	PDOC00008
PS00008	494->500	MYRISTYL	PDOC00008
PS00008	498->504	MYRISTYL	PDOC00008
PS00008	617->623	MYRISTYL	PDOC00008
PS00008	757->763	MYRISTYL	PDOC00008
PS00028	795->816	ZINC_FINGER_C2H2	PDOC00028
PS00028	860->882	ZINC_FINGER_C2H2	PDOC00028
PS00028	33->56	ZINC_FINGER_C2H2	PDOC00028
PS00028	94->117	ZINC_FINGER_C2H2	PDOC00028

Pfam for DKFZphtes3_21j15.3

HMM_NAME Zinc finger, C2H2 type

HMM *CpwpDCgKtFrrwsNLrRHMR..T.H*
 C++ C ++ + +L+ HM+ H
 Query 33 CKD--CSAAYDTLVELTVHMNET-GH 55

26.69 (bits) f: 94 t: 116 Target: dkfzphes3_21j15.3 strong similarity to "NY-CO-33"
 Alignment to HMM consensus:

Query *CpwpDCgKtFrrwsNLrRHMR..T.H*
 C + CG +F + +L HM+ H
 dkfzphes3 94 CMY--CGHSFESLQDLSVHMIKT-KH 116

Query f: 795 t: 815 Target: dkfzphes3_21j15.3 strong similarity to "NY-CO-33"
 Alignment to HMM consensus:

HMM *CpwpDCgKtFrrwsNLrRHMRTH*
 C++ C R++S+++ H+ +H
 Query 795 CND--CASQIRTPSTYISHLESH 815

27.12 (bits) f: 860 t: 881 Target: dkfzphes3_21j15.3 strong similarity to "NY-CO-33"
 Alignment to HMM consensus:

Query *CpwpDCgKtFrrwsNLrRHMR.T.H*
 C+ C++TF +++ + H+ H
 dkfzphes3 860 CKL--CNRTFASKHAVKLHLSK-TH 881

DKFZphtes3_21116

group: intracellular transport and trafficking

DKFZphtes3_21116 encodes a novel 66 amino acid protein nearly identical to rat ribosome attached membrane protein 4 (ramp4).

The novel protein seems to be the human orthologue of rat ramp 4. Ramp4 is involved in the regulation of translocation of proteins into endoplasmic reticulum, e.g. of the MHC class II associated invariant (gamma) chain.

The new protein can find application in modulation of protein translocation into the endoplasmic reticulum.

identical to rat ribosome attached membrane protein 4

ORF Bp 316-513 (66 aa) see BLASTX

Sequenced by LMU

Locus: unknown

Insert length: 2488 bp

Poly A stretch at pos. 2464, polyadenylation signal at pos. 2442

```
1 CTTCTCTTT CACTCCGCGC TCACGGCGGC GGCCAAAGCG GCGGCGACGG
51 CGGCGCGAGC ACGACCCGGC GGCCAGTTCT CTTCCTCCTG CGCACCTGCC
101 CCGCTCGGTC AGTCAGTCGG CGGCCGGCGC CCGCCTTGTC CTCAGACCTC
151 GCGCTTGCGG CGCCCAGGCC CAGCGGCCGT AGCTAGCGTC TGGCCTGAGA
201 ACCTCGGCGC TCCGGCGGCG CGGGCACCAC GAGCCGAGCC TCGCAGCGGC
251 TCCAGAGGAG GCAGGCGAGT GAGCGAGTCC GAGGGGTGGC CGGGGCAGGT
301 GGTGGCGCGC CGAAGATGGT CGCCAAGCAA AGGATCCGTA TGGCCAACGA
351 GAAGCACAGC AAGAACATCA CCCAGCGCGG CAACGTCGCC AAGACCTCGA
401 GAAATGCCCC CGAAGAGAAG GCGTCTGTAG GACCCTGGTT ATTGGCTCTC
451 TTCATTTTGG TTGTCTGTGG TTCTGCAATT TTCCAGATTA TTCAAAGTAT
501 CAGGATGGGC ATGTGAAGTG ACTGACCTTA AGATGTTTCC ATTCTCCTGT
551 GAATTTTAAC TTGAATCAT TCCTGATGTT TGATACCCTG GTTGAAAACA
601 ATTCAGTAAA GCATCCTGCC TCAGAATGAC TTTCCTATCA TGCTTCATGT
651 GTCATTCCAA GGTTCCTTCA TGAGTCATTC CAAGTTTCT AGTCCATACC
701 ACAGTGCCCT GCAGAAAACA CCACATGAAT AAAGCAATAA AATTTGATTG
751 TTAAGATACA GTAGTGACC CTAATTATTC AGTCAATTAA GAGTAAGTTT
801 TTTTATGTGG TTATTAAGAC AGTATGAACA ATTAGTCTAA CTCTGCATAG
851 ACAGGGTCTA GATTTTGTGA ACCCAAATGT ATAACGTCAG TTAGCTTAAA
901 TTACAATTTG AAGTCTGTGG GTTTTTATAT AGCTAGGCAC TTTATTACTC
951 TTTTGAACCT AAAGCACACT CCCTTATAGG TTCATGTAAC TGTCCTGTAA
1001 TAAGGTGCTT ATAAATGGAA CAACTACACA GCCTAGTTTT GCCACAACCT
1051 TTAGCATCTA AAAAGTTTAA AAAGCTTCTA AATGTCTAAT ATAAAGGGAG
1101 ATGCTTATAG CCACAACATC TATTTTACCA ATATTGTTTC CATTACACTA
1151 CCTTGGATTT TGCATGAGTG AGTATAGTAA CCCAAGATGC CATAAAAAAA
1201 AACTTGATCG TTTTCTGACT TAATTAGTTA CTGTGGTTTC ACTAAAAGCT
1251 ACCGTGGTGG GTGAAGTCA GTCAGGGAAG GTTTGTTTAT GTTACATTTA
1301 TTTCACCAGA ACTATTTTAA TATATCAAAG GGGTTTACTA TGCCAAACAA
1351 AATTCTAGGG AAAAATACTG CTAAAAATGG ATGCCTCATC AGAACATGCT
1401 GTTGAGTCCA ATGTGCCATA AGACATTTTA GCATGTAAAA TAGCACTTTT
1451 AATAGCAAAA AAAGGCACAT CAACTGCGAA GTTATCCTTA GTTTGCAAAAT
1501 GCTTTTCTA GATTAATGAT TTTTCAATCA TTAGGGTACT AGACACATCA
1551 GCCTAAAGTG GCATCTGGAA TTGAATGGAT TTAATGATAA TGATCAGTCT
1601 TTAGTCTTCC CTTTGTATTA TGACTTTATA GGTTATGATT GATCAAATTT
1651 ACGTTTACT AATGGTAAGG GTGAGGGTCA TAGGGCAGGT TTTGGGTTTT
1701 CTAGTACTGT TGAAAACTGC AAGTATTGGC TATTTGTATA CTTAGCCATA
1751 ACTTGGTGAA AAAAACCTG AGCAGTGTCT ATGTATTAAT GCGTTGGAAA
1801 GAAAGCTGCT TGTGTTTGCT TTGTAAATTG CCTCAGGATA TTTCTTTTAA
1851 AATAAGCTGT TTGAAGAGGA ACAGAAGGGA AATCTGCTAC CTAGTCTATA
1901 CACAGCGTGA ACCTCACAGG GGGCTTCTGA TACCCTCAAA CATGGAGAAC
1951 AGTAAGGGAG CAGAGTGGTT AAGGACTTTC AGGAACCTAA CTATTCTGGA
2001 ATAAGGAATG AATCAACTGA CCTTGGGCCA GCAGGTTTTT AACTAAATTTG
2051 TTAATGCGCT TTCTCACCCA GTTAATCAGT CTCTGTACTT GTTTCCCTTT
2101 TTGAACAAGT TGTCTTGGTT AACTAATCTT GTTTTATGGT TGTGCTAAAT
2151 TCATAGCAGG TGCCTTATTC TTTGCTTTTA GTCAAACCAT TCCATATCAG
2201 AATTTTCTCT GGTTTACTAT AGATATTGGT CTTTAAGTTG TTGTTTGTGT
2251 TTTTAAATGT ACAATCTTCT CATAAATTTT ACTGTTAAAT TGCTATAGCT
2301 AGCAATCATG TTACATATGT AAAAAATTGC ATTCCCTTTG TATTTTATGT
2351 GTAATTCACC AATTAAGTGC AGTTTATATT CAGGTTGGAT TATGCATGTT
2401 TAGGTAACAG AAAGCTGTGT CTTACTTGAT TTATCTTTA AAAATAAAGT
2451 TCCCTGAATA TTTGAAAAAA AAAAAAAA AAAAAAA
```

BLAST Results

Entry HSCDN13 from database EMBL:
H.sapiens (TL5) mRNA from LNCaP cell line
Score = 1075, P = 5.8e-41, identities = 219/221

Entry AF100470.1 from database TREMBLNEW:
gene: "RAMP4"; product: "ribosome attached membrane protein 4"; Rattus norvegicus ribosome attached membrane protein 4 (RAMP4) mRNA, complete cds.
Score = 331, P = 3.9e-28, identities = 66/66, positives = 66/66, frame +1

Entry HSG19910 from database EMBL:
human STS A002B48.
Score = 530, P = 2.1e-17, identities = 108/109

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 316 bp to 513 bp; peptide length: 66
Category: strong similarity to known protein
Classification: Intracellular transport and traffic

1 MVAQQRIRMA NEKHSKNITQ RGNVAKTSRN APEEKASVGP WLLALFIFVV
51 CGSAIFQIIQ SIRMGM

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_21116, frame 1

TREMBLNEW:RNO238236.1 gene: "ramp4"; product: "ribosome associated membrane protein RAMP4"; Rattus norvegicus mRNA for ribosome associated membrane protein RAMP4, N = 1, Score = 331, P = 6.2e-30

TREMBL:AF100470.1 gene: "RAMP4"; product: "ribosome attached membrane protein 4"; Rattus norvegicus ribosome attached membrane protein 4 (RAMP4) mRNA, complete cds., N = 1, Score = 331, P = 6.2e-30

>TREMBLNEW:RNO238236.1 gene: "ramp4"; product: "ribosome associated membrane protein RAMP4"; Rattus norvegicus mRNA for ribosome associated membrane protein RAMP4
Length = 75

HSPs:

Score = 331 (49.7 bits), Expect = 6.2e-30, P = 6.2e-30
Identities = 66/66 (100%), Positives = 66/66 (100%)

Query: 1 MVAQQRIRMANEKHSKNITQ RGNVAKTSRNAPEEKASVGPWLLALFIFVCGSAIFQIIQ 60
MVAQQRIRMANEKHSKNITQ RGNVAKTSRNAPEEKASVGPWLLALFIFVCGSAIFQIIQ
Sbjct: 10-MVAQQRIRMANEKHSKNITQ RGNVAKTSRNAPEEKASVGPWLLALFIFVCGSAIFQIIQ 69

Query: 61 SIRMGM 66
SIRMGM
Sbjct: 70 SIRMGM 75

No Pedant data available

DKFZphtes3_21n23

group: testes derived

DKFZphtes3_15j18 encodes a novel 148 amino acid protein with strong similarity to rat 7acomp protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

strong similarity to rat 7acomp protein

on genomic level encoded by AF107885

Sequenced by LMU

Locus: /map="14q24.3"

Insert length: 3122 bp

Poly A stretch at pos. 3070, polyadenylation signal at pos. 3045

```
1  GGAAAACTCTC GTGGGCTCAG CCCGGGAGAA AGGGCCAGGG AAGTTGGGTG
51  GTTCTGTGCT TGGTCTGTCA ATGGAGGAGA TCAAAGTTT ACGAAGGGTG
101 AAGGAGGAGA ATGATCGGCG AGGTGGATTT ATTCGCATAT TTCTTACATC
151 TGAGACATGG GAAATATATG GGTCTACCT CGAGCATAAG ACCTCAATGA
201 ACTATATGCT GGCAACACGC CTCTTCCAGG ACAGGGGAAA CCAAGAAGA
251 AGCTTATTGA CAGGAAGAAC ACGAATGACT GCTGATGGAG CGCCAGAATT
301 GAAGATAGAG AGTCTGAATT CAAAGGCCAA GCTGCATGCT GCACCTTACG
351 AGAGGAAGCT CCTGTCTCTG GAGGTGCGAA AACGTAGACG ACGGAGTAGC
401 AGATTGAGGG CAATGAGGCC AAAATACCCA GTGATTACCC AACCAGCTGA
451 AATGAATGTT AAAACTGAGA CAGAGAGTGA AGAGGAGGAA GAAGTCGCAT
501 TAGATAATGA AGATGAAGAA CAGGAGGCTT CCCAGGAGGA GTCTGCAGGA
551 TTTCTTAGAG AAAATCAAGC CAAATATACA CCCTCATTGA CAGCTTTGGT
601 AGAAAAATACA CCAAAAGAAA ATTCCATGAA AGTTCGTGAA TGGAAATAA
651 AAGGTGAGCA CTGCTGCAAA CTGAGACTC AGGAGCTAGA GCCTAAATTT
701 AACCTGATGC AGATTCTTCA AGATAATGGC AATCTTAGCA AAATGCAGGC
751 CCGAATAGCA TTCTCTGCCT ATCTCCAGCA TGTTCAAATT CGCTTGATGA
801 AAGACAGTGG CGGTGAGACG TTCAGTGCCA GTTGGGCTGC CAAAGAGGAT
851 GAACAGATGG AGCTGGTTGT TCGTTTCCTC AAGCGAGCAT CAAATAACCT
901 CCAGCATTCA CTGAGGATGG TATTACCCAG TCGACGATTG GCACCTTCTG
951 AACGCAGAAG AATCCTGGCC CACCAGCTGG GTGACTTTAT CATTGTATAC
1001 AACAAAGGAAA CACAACAAAT GGCTGAAAAG AAATCAAAGA AGAAACTTGA
1051 GGAAGAAGAG GAAGATGGGG TGAATATGGA AAACCTTTCAG GAGTTCATCA
1101 GACAAGCAAG CTGAGGCTGAA CTGGAGGAGG TGTTGACTTT TTATACCCAA
1151 AAGAACAAGT TCGCTAGTGT CTTCTGTTGG ACTCACTCTA AAATTTCTAA
1201 GAACAACAAC AATTATTCTG ATAGTGGGGC AAAAGGTGAT CACCCTGAGA
1251 CTATAATGGA AGAAGTGAAA ATAAAGCCAC CTAAACAGCA ACAGACGACA
1301 GAAATTCATT CTGATAAATT ATCTCGATTT ACCACTTCAG CAGAAAAAGA
1351 GGCAAAATTA GTTTATAGCA ATTCCTCCTC TGGTCTACT GCTACTCTGC
1401 AGAAAAATTC CAACACCCAT TTGTCACTCTG TTACAACCTC TGACCTCTCT
1451 CCAGGGGCTT GCCACCATTC TTCTTTATCT CAAATTCCTT CAGCTATCCC
1501 CAGCATGCCT CACCAGCCAA CAATTTTACT GAACACAGTC TCTGCCAGTG
1551 CTCTCTCCCTG CCTACATCCC GGGGCACAGA ACATCCCAAG CCCTACTGGC
1601 CTGCCACGCT GTCGATCAGG AAGTCACACC ATTGGTCCCT TTCTTTCTTT
1651 CCAAAGTGCT GCACACATCT ATAGCCAGAA ACTGTCTCGT CCCTCTTCAG
1701 CAAAGGCAGG ATCGTGCTAT CTAAACAAGC ATCATTTCAG AATAGCCAAA
1751 ACACAAAAAG AGGGAGAAAG TGCTTCTTTA TATAGCAAAC GGTACAACCA
1801 AAGTATGGTT ACAGCTGAAC TTCAGCGGCT AGCTGAGAAG CAGGCAGCGA
1851 GACAGTATTC TCCATCCAGC CACATCAACC TCCTCACCCA ACAGGTAACA
1901 AACCTGAATT TGGCAACTGG CATCATAAAC AGAAGCAGTG CTTGAGCTCC
1951 CCCAACCTCT CGACCCATCA TCAGTCCTAG TGGCCCCGAC TGGTCTACAC
2001 AGTCAGACCC CCAAGCTCCC GAGAATCACT CCAGCTCTCC TGGAAAGCAG
2051 AGCCTGCAGA CAGGGGGATT TGCCTGGGAA GGAGAAGTAG AAAACAACGT
2101 GTACAGCCAG GCTACAGGGG TGGTCCCCCA GCACAAGTAT CACCCACAG
2151 CAGGCAGCTA TCAGCTTCAA TTGCCCCTGC AGCAACTTGA ACAACAAAAA
2201 CTTCAGTCCC GGCAGCTCCT GGACCAGAGT CGAGCCCGGC ACCAGGCAAT
2251 CTTTGGGAGC CAGACACTAC CTAACCTCAA TTTATGGACA ATGAATAATG
2301 GTGCAGGTTG TAGAATTTC AGTGCCACAG CTAGTGCCCA GAAGCCAACC
2351 ACTCTGCCAC AAAAAGTGGT ACCACCTCCA AGTTCTTGCG CCTCCCTGGT
2401 TCCCAAACCC CCACCAACCC ACGAACAAGT GCTCAGAAGG GCAACATCCC
2451 AGAAAGCTTC CAAATACCCG TFCAGATCCT CTTTCAAAA CTATTTGTGG
2501 TATTTCTTCC AAGCAGTCAG CTGAACCTAG GACGACAGCC TACAAACAAC
2551 TACATGCATC TGAACCTGCT CTTGTAAATG AGCTTTTTTC AGAGCCAGAA
2601 TCATACTCTC CAGGAAATAT GGAGAAAGAA ACCTGAGGAG ATTGAAGTTT
2651 GCCAGGCACA AGGGCAAAAC TCAGACTGAA TGAATTTGAA AGGGTGGGGC
2701 CAAAGATGTT GTAACCTGGG AGACTTCTCT GAAGAAAGAA AACTGTTTAA
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2751 GAAACACAGA CTGAACTGCA GTACTTTTCC TTAAATAGCT GAGATGACCT
2801 TCTTTACCTT GGGCTTAGGT GATTCTCATC AGGGTGACCT GAGTGGGAAGT
2851 TGGTGGTAAC GACTGTTCTG TGTCAGCACC CAGGACAGTG GTGTCTGTTA
2901 AGGCTGCCAG GGATTAGCAG GGAGGAAAGC CATCAGGACT GGGTAGCCTG
2951 GTAGCACCAA ATCCCAATTA ATGTTACCTG AACATGTGGT GAGGTCAGCC
3001 GTATGATCAA AGATGTTTAA GAGATTAATG TCAGAAGAAT ATGAAAATAA
3051 ACACCGGCTT AAAAAATGTT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3101 AAAAAAAAAA AAAAAAAAAA AA

```

BLAST Results

Entry AF107885 from database EMBL:
Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
Score = 3042, P = 3.0e-219, identities = 610/612
5 exons matching 1893-3070

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 71 bp to 2521 bp; peptide length: 817
Category: strong similarity to known protein

```

1 MEEIKVLRV KEENDRRGGF IRIFPTSETW EIYGSYLEHK TSMNYMLATR
51 LFQDRGNPRR SLLTGTRMT ADGAPELKIE SLNSKAKLHA ALYERKLLSL
101 EVRKRRRRSS RLRMRPKYP VITQPAEMNV KTETSEEEEE EVALDNEDEE
151 QEASQEEESAG FLRENQAKYT PSLTALVENT PKENSMKVRE WNNKGGHCCK
201 LETQLEPKF NLMQILQDNG NLSKMQARIA FSAYLQHVQI RLMKDSGGQT
251 FSASWAAKED EQMELVVRFL KRASNNLQHS LRMVLPSSRL ALLERRRILA
301 HQLGDFIIVY NKETEQMAEK KSKKKVEEEE EDGVNMENFQ EFIRQASEAE
351 LEEVLTFTYQ KNKSASVFLG THSKISKNNN NYSDSGAKGD HPETIMEEVK
401 IKPPKQQOTT EIHSCLKSRF TTSAEKEAKL VYSNSSSGPT ATLQKIPNTH
451 LSSVTSDLS PGPCHHSSL S QIPSAIPSM HQTILLNTV SASASPCLHP
501 GAQNIPSPPTG LPRCRSGSHT IGPFSSFSQA AHIIYQKLSR PSSAKAGSCY
551 LNKHHSGIAK TQKEGEDASL YSKRYNQSMV TAELORLAEK QAARQYSPSS
601 HINLLTQQVT NLNLATGIIN RSSASAPPTL RPIISPSGPT WTSQSDPQAP
651 ENHSSSPGSR SLQTGGFAWE GEVENNVYSQ ATGVVPOHKY HPTAGSYQLQ
701 FAIQLEQOK LSRQLLDQS RARHQAIFGS QTLPSNLWT MNNGAGCRIS
751 SATASGQKPT TLQKVVPPP SSCASLVKPK PPNHEQVLR ATSQKASNTR
801 FRSSFQNYLW YFFQAVS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_2ln23, frame 2

TREMBL:AF064856_1 product: "7acomp protein"; Rattus sp. 7acomp protein mRNA, complete cds., N = 1, Score = 1845, P = 2.2e-190

TREMBL:AF107885_3 product: "unknown"; Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes., N = 1, Score = 443, P = 5.3e-41

TREMBL:AF107885_4 product: "unknown"; Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes., N = 1, Score = 265, P = 8.2e-22

>TREMBL:AF064856_1 product: "7acomp protein"; Rattus sp. 7acomp protein mRNA, complete cds.
Length = 436

HSPs:

Score = 1845 (276.8 bits), Expect = 2.2e-190, P = 2.2e-190
Identities = 369/435 (84%), Positives = 395/435 (90%)


```

SEQ    TTSAEKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPGCHHSSLSQIPSAIPSM
SEG    .....
PRD    hhhhhhhheeeccccccccceeecccccccccccccccccccccccccccccccccccccc

SEQ    HQPTILLNTVSASASPCLHPGAQNIPSTGLPRCRSGSHTIGPFSSFQSAAHYISQKLSR
SEG    .....
PRD    cccceeeccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhccc

SEQ    PSSAKAGSCYLNKHHSGIAKTQKEGEDASLYSKRYNQSMVTAEQLRLAEKQAARQYSPSS
SEG    .....
PRD    cccccccccceeeccccccccccccccccccccceeeccchhhhhhhhhhhhhhhhhhhhhccc

SEQ    HINLLTQVQTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQSDPQAPENHSSSPGSR
SEG    ..xxxxxxxxxxxxx.....
PRD    cccccccccccccccccccccccccccccccccceeecccccccccccccccccccccccccc

SEQ    SLQTGGFAWEGEVENNVYSQATGVVPQHKYHPTAGSYQLQFALQQLEQQKLQSRQLLDQS
SEG    .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....
PRD    cccccccccceeeccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhh

SEQ    RARHQAIFGSQTLPNSNLWTMNGAGCRISSATASGQKPTTLPOKVVPPPPSSCASLVPKP
SEG    .....
PRD    hhhhhhhhhccccccccceeeccccccccceeecccccccccccccecccccccccecccccc

SEQ    PPNHEQVLRRATSQKASNTRFRSSFQNYLWYFFQAVS
SEG    .....
PRD    cccchhhhhhhhhhhccccccccccccceeeeeecccc

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Prosites for DKFZphtes3_2ln23.2

PS00001	221->225	ASN_GLYCOSYLATION	PDOC00001
PS00001	362->366	ASN_GLYCOSYLATION	PDOC00001
PS00001	381->385	ASN_GLYCOSYLATION	PDOC00001
PS00001	434->438	ASN_GLYCOSYLATION	PDOC00001
PS00001	576->580	ASN_GLYCOSYLATION	PDOC00001
PS00001	620->624	ASN_GLYCOSYLATION	PDOC00001
PS00001	652->656	ASN_GLYCOSYLATION	PDOC00001
PS00004	106->110	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	107->111	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	271->275	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	789->793	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	64->67	PKC_PHOSPHO_SITE	PDOC00005
PS00005	109->112	PKC_PHOSPHO_SITE	PDOC00005
PS00005	180->183	PKC_PHOSPHO_SITE	PDOC00005
PS00005	185->188	PKC_PHOSPHO_SITE	PDOC00005
PS00005	280->283	PKC_PHOSPHO_SITE	PDOC00005
PS00005	287->290	PKC_PHOSPHO_SITE	PDOC00005
PS00005	322->325	PKC_PHOSPHO_SITE	PDOC00005
PS00005	359->362	PKC_PHOSPHO_SITE	PDOC00005
PS00005	414->417	PKC_PHOSPHO_SITE	PDOC00005
PS00005	535->538	PKC_PHOSPHO_SITE	PDOC00005
PS00005	543->546	PKC_PHOSPHO_SITE	PDOC00005
PS00005	561->564	PKC_PHOSPHO_SITE	PDOC00005
PS00005	572->575	PKC_PHOSPHO_SITE	PDOC00005
PS00005	629->632	PKC_PHOSPHO_SITE	PDOC00005
PS00005	793->796	PKC_PHOSPHO_SITE	PDOC00005
PS00006	35->39	CK2_PHOSPHO_SITE	PDOC00006
PS00006	132->136	CK2_PHOSPHO_SITE	PDOC00006
PS00006	134->138	CK2_PHOSPHO_SITE	PDOC00006
PS00006	136->140	CK2_PHOSPHO_SITE	PDOC00006
PS00006	154->158	CK2_PHOSPHO_SITE	PDOC00006
PS00006	180->184	CK2_PHOSPHO_SITE	PDOC00006
PS00006	347->351	CK2_PHOSPHO_SITE	PDOC00006
PS00006	394->398	CK2_PHOSPHO_SITE	PDOC00006
PS00006	422->426	CK2_PHOSPHO_SITE	PDOC00006
PS00006	455->459	CK2_PHOSPHO_SITE	PDOC00006
PS00006	561->565	CK2_PHOSPHO_SITE	PDOC00006
PS00006	643->647	CK2_PHOSPHO_SITE	PDOC00006
PS00007	563->572	TYR_PHOSPHO_SITE	PDOC00007
PS00008	195->201	MYRISTYL	PDOC00008
PS00008	248->254	MYRISTYL	PDOC00008
PS00008	510->516	MYRISTYL	PDOC00008
PS00008	557->563	MYRISTYL	PDOC00008
PS00008	746->752	MYRISTYL	PDOC00008
PS00008	756->762	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_2ln23.2)

DKFZphtes3_22c23

group: testes derived

DKFZphtes3_22c23 encodes a novel 223 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, 3 EST hits (two from a testis library)

Sequenced by LMU

Locus: /map="9q34"

Insert length: 1113 bp

Poly A stretch at pos. 1073, polyadenylation signal at pos. 1055

```
1 GGTGGGCAAA GGCATCTTCC TCTGGGAAGG ACTGGCACAA GCACTTGGTC
51 CCTGGGTTGT GTGCCGTGGA GGCCGGGATC AGGGCTGGCC CTCTTTCTCC
101 CTGGCAAAGC AAAACCTCCC TTTTACTACT ATCAAGGGGA AGTAACTTGA
151 AGGTGCCTGT GGCAGGCAGC ACCTTGAGCC AACAGGAACC ATTGACATGC
201 GAGGCCCAAG GCAGGCAGAC TGTGCAGTGG CCATTGGGCG GCCCTCGGG
251 GAGGTGGTGA CCCTCCGCCT CTTTCAGAGT TCTCTCAACT GCACTGCGGG
301 GGACATGTTG CTGCTTTGGG GCCGGCTCAC CTGGAGGAAG ATGTGCAGGA
351 AGCTGTTGGA CATGACTTTC AGCTCCAAGA CCAACACGCT GGTGGTGAGG
401 CAGCGCTGCG GCGGCCAGG AGGTGGGGTG CTGCTGCGGT ATGGGAGCCA
451 GCTTGCTCCT GAAACCTTCT ACAGAGAATG TGACATGCAG CTCTTTGGGC
501 CCTGGGGTGA AATCGTGAGC CCCTCGCTGA GTCCAGCCAC GAGTAATGCA
551 GGGGGCTGCC GGCTCTTCAT TAATGTGGCT CCGCACGCAC GGATTGCCAT
601 CCATGCCCTG GCCACCAACA TGGGCGCTGG GACCGAGGGA GCCAATGCCA
651 GCTACATCTT GATCCGGGAC ACCCAGAGCT TGAGGACCAC AGCGTTCCAT
701 GGGCAGCAGG TGCTCTACTG GGAGTCAGAG AGCAGCCAGG CTGAGATGGA
751 GTTCAGCGAG GGCTTCCTGA AGGCTCAGGC CAGCTGCGG GGCCAGTACT
801 GGACCCTCCA ATCATGGGTA CCGGAGATGC AGGACCCTCA GTCTTGAAG
851 GGAAAGGAAG GAACCTGAGG GTCATTGAAC ATTTGTTCG TGTCTGGCCA
901 GCCCTGGAGG GTTGACCCCT GGTCTCAGTG CTTTCCAATT CGAACTTTTT
951 CCAATCTTAG GTATCTACTT TAGAGTCTTC TCCAATGTCC AAAAGGCTAG
1001 GGGGTTGGAG GTGGGGAAGC TGGAAAAGCA GCCCCATTTC CCTCGGGTAC
1051 CAATAAATAA AACATGCAGG CTGAAAAAAA AAAAAAAAAA AAAAAAAAAA
1101 AAAAAAAAAA AAA
```

BLAST Results

Entry HSAC1644 from database EMBL:
Genomic sequence from Human 9q34, complete sequence.
Score = 2072, P = 8.8e-225, identities = 422/430
5 exons Bp 41969-38232

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 197 bp to 865 bp; peptide length: 223
Category: putative protein

```
1 MRGPGQADCA VAIGRPLGEV VTLRVLESSL NCSAGDMLLL WGRLTWRKMC
51 RKLLDMTESS KTNLTVVRQR CGRPGGGVLL RYGSQALPET FYRECDMLF
101 GPWGEIVSPS LSPATSNAGG CRLFINVAPH ARIAIHALAT NMGAGTEGAN
151 ASYILIRDTH SLRTTAFHQ QVLYWESESS QAEMEFSEGF LKAQASLRGQ
201 YWTLQSWVPE MQDPQSWKKG EGT
```


BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_22c23, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3_22c23, frame 2

Report for DKFZphtes3_22c23.2

[LENGTH] 223
[MW] 24546.19
[pI] 8.57
[PROSITE] MYRISTYL 4
[PROSITE] CK2_PHOSPHO_SITE 2
[PROSITE] PKC_PHOSPHO_SITE 6
[PROSITE] ASN_GLYCOSYLATION 2
[KW] Alpha_Beta

SEQ MRGPGQADCAVAIGRPLGEVVTLRVLESSLNCAGDMLLLWGRLTWRKMCRLDLMTFSS
PRD ccc

SEQ KTNTLVVRQRCGRPGGVLLRYGSQLAPETFYRECDMQLFGPWGEIVSPSLSPATSNAGG
PRD ccc

SEQ CRLFINVAPHARIAHALATNMGAGTEGANASYILIRDTHSLRTTAFHGQQVLYWESESS
PRD ccc

SEQ QAEMEFSEGFLKAQASLRGQYWTLSQSWPEMQDPQSWKGKEGT
PRD hhhhhhhcchhh

Prosite for DKFZphtes3_22c23.2

PS00001	31->35	ASN_GLYCOSYLATION	PDOC00001
PS00001	150->154	ASN_GLYCOSYLATION	PDOC00001
PS00005	22->25	PKC_PHOSPHO_SITE	PDOC00005
PS00005	45->48	PKC_PHOSPHO_SITE	PDOC00005
PS00005	59->62	PKC_PHOSPHO_SITE	PDOC00005
PS00005	161->164	PKC_PHOSPHO_SITE	PDOC00005
PS00005	196->199	PKC_PHOSPHO_SITE	PDOC00005
PS00005	216->219	PKC_PHOSPHO_SITE	PDOC00005
PS00006	33->37	CK2_PHOSPHO_SITE	PDOC00006
PS00006	180->184	CK2_PHOSPHO_SITE	PDOC00006
PS00008	5->11	MYRISTYL	PDOC00008
PS00008	145->151	MYRISTYL	PDOC00008
PS00008	148->154	MYRISTYL	PDOC00008
PS00008	199->205	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_22c23.2)

DKFZphtes3_22g2

group: nucleic acid management

DKFZphtes3_22g2 encodes a novel 1230 amino acid protein with nearly identical to rat TIP120.

TATA-binding protein TBP is a central component for transcriptional regulation and is a target for various transcription regulators. TBP-interacting protein 120 (TIP120) is a protein interacting with the TATA-binding protein (TBP). The novel protein is the human ortholog of rat TIP120. The novel TBP-binding protein is considered to participate in transcription regulation through the interaction with TBP.

The new protein can find application in modulation of gene transcription.

KIAA0829, complete cds, nearly identical to rat TIP120

complete cDNA, complete cds, EST hits,

Sequenced by LMU

Locus: /map="387.3 cR from top of Chr12 linkage group"

Insert length: 5387 bp

Poly A stretch at pos. 5352, polyadenylation signal at pos. 5335

```
1 GGGAGCGAGT GCGGAGCGAG TGGGAGCGAG ACGGCCCTGA GTGGAAGTGT
51 CTGGCTCCCC GTAGAGGCCG TTCTGTACGC CCCGCCGCCG ATGAGCTCGT
101 TCTCAGCGCA ACAGCGCCGT CGTTAGGCTG GCTCTGTAGC CTCGGCTTAC
151 CCCGGGACAG GCCCAGCCCT CGCCAGGGAG GGGGCAGCCC GTCGAGGCGC
201 CTCCTAGTGC AGCGTCGGCG TCGCGCTGCG ACCCTGGAAG CGGGAGCCGC
251 CGCGAGCGAG AGGAGGAGCT CCAGTGGCGG CGCGGGCGGC GGCAGCGGCA
301 GCGGGCAGCA GCTCCAGCAG CGCCAGCAGG CGGGATCGAG GCCGTCAACA
351 TGGCGAGCGC CTCGTACCAC ATTTCCAATT TGCTGGAAAA AATGACATCC
401 AGCGACAAGG ACTTTAGGTT TATGGCTACA AATGATTTGA TGACGGAACT
451 GCAGAAAGAT TCCATCAAGT TGGATGATGA TAGTGAAAGG AAAGTAGTGA
501 AAATGATTTT GAAGTTATTG GAAGATAAAA ATGGAGAGGT ACAGAATTTA
551 GCTGTCAAAT GTCTTGGTCC TTTAGTGAGT AAAGTGAAAG AATACCAAGT
601 AGAGACAATT GTAGATACCC TCTGCACTAA CATGCTTTCT GATAAAGAAC
651 AACTTCGAGA CATTTCAAGT ATTGGTCTTA AAACAGTAAT TGGAGAAGTT
701 CCTCCAGCTT CCACTGGCTC TGCATTAGCT GCTAATGTAT GTAAAAAGAT
751 TACTGGACGT CTTACAAGTG CAATAGCAAA ACAGGAAGAT GTCTCTGTTC
801 AGCTAGAAGC CTTGGATATT ATGGCTGATA TGTGAGCAG GCAAGGAGGA
851 CTTCTTGTTA ATTTCCATCC TTCAATTCTG ACCTGTCTAC TTCCCCAGTT
901 GACCAGCCCT AGACTTGCAG TGAGGAAAAG AACCATTATC GCTCTTGGCC
951 ATCTGGTTAT GAGCTGTGCA AATATAGTTT TTGTAGATCT TATTGAACAT
1001 CTGTTGTCTAG AGTTGTCCAA AAATGATTCT ATGTCAACAA CAAGAACCTA
1051 CATACAATGT ATTGCTGCTA TTAGTAGGCA AGCTGGTCAAT AGAATAGGTG
1101 AATACCTTGA GAAGATAAAT CCTTGGTGG TAAAATTTTG CAATGTAGAT
1151 GATGATGAAT TAAGAGAGTA CTGTATTCAA GCCTTTGAAT CATTTGTAAG
1201 AAGATGTCTT AAGGAAGTAT ATCCTCATGT TTCTACCATT ATAAATATTT
1251 GTCTTAAATA TCTTACCTAT GATCCAAATT ATAATTACGA TGATGAAGAT
1301 GAAGATGAAA ATGCAATGGA TGCTGATGGT GGTGATGATG ATGATCAAGG
1351 GAGTGATGAT GAATACAGTG ATGATGATGA CATGAGTTGG AAAGTGAGAC
1401 GTGCAGCTGC GAAGTGCTTG GATGCTGTAG TTAGCACAAAG GCATGAAATG
1451 CTTCCAGAAT TCTACAAGAC CCTCTCTCCT GCACTAATAT CCAGATTTAA
1501 AGAGCGTGAA GAGAATGTAA AGGCAGATGT TTTTCACGCA TACCTTTCTC
1551 TTTTGAAGCA AACTCGTCCT GTACAAAGTT GGCTATGTGA CCCTGATGCA
1601 ATGGAGCAGG GAGAAACACC TTTAACAATG CTTCAGAGTC AGGTTCCCAA
1651 CATTGTTAAA GCTCTTCACA AACAGATGAA AGAAAAAAGT GTGAAGACCC
1701 GACAGTGTG TTTTAAACATG TTAACGTAGC TGGTAAATGT ATTACCTGGG
1751 GCCTTAATC AACACATTCC TGTACTTGTA CCAGGAATCA TTTTCTCACT
1801 GAATGATAAA TCAAGCTCAT CGAATTTGAA GATCGATGCT TTGTCTATGC
1851 TATACGTAAT CCTCTGTAAC CATCTCTCCT AAGTCTTCCA TCCTCACGTT
1901 CAGGCTTTGG TTCTCCAGT GGTGGCTTGT GTTGGAGACC CATTTTACAA
1951 AATTACATCT GAAGCACTTC TTGTTACTCA ACAGCTTGTG AAAGTAATTC
2001 GTCCCTTAGA TCAGCCTTCC TCGTTTGATG CAACTCCTTA TATCAAAGAT
2051 CTATTTACCT GTACCAATTA GAGATTAAAA GCAGCTGACA TTGATCAGGA
2101 AGTCAAGGAA AGGCTATTT CCTGTATGGG ACAAATTATT TGCAACCTTG
2151 GAGACAATTT GGGTCTGAC TTGCCTAATA CACTTCAGAT TTTCTTGGAG
2201 AGACTAAAGA ATGAAATTAC CAGGTTAACT ACAGTAAAGG CATTGACACT
2251 GATTGCTGGG TCACCTTTGA AGATAGATT GAGGCCTGTT CTGGGAGAAG
2301 GGGTTCCTAT CCTTGCTTCA TTTCTTAGAA AAAACCAGAG AGCTTTGAAA
2351 CTGGGTACTC TTTCTGCCCT TGATATTCTA ATAAAAAAT ATAGTGACAG
2401 CTTGACAGCT GGCATGATTG ATGCAGTTCT AGATGAGCTC CCACCTCTTA
2451 TCAGCGAAAG TGATATGCAT GTTTCACAAA TGGCCATCAG TTTTCTTACC
2501 ACTTTGGCAA AAGTATATCC CTCTCCCTT TCAAAGATAA GTGGATCCAT
2551 TCTCAATGAA CTTATTGGAC TTGTGAGATC ACCCTTATTG CAGGGGGGAG
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2601 CTCTTAGTGC CATGCTAGAC TTTTCCAAG CTCTGGTGT CACTGGAACA
2651 AATAATTTAG GATACATGGA TTTGTTGCGC ATGCTGACTG GTCCAGTTTA
2701 CTCTCAGAGC ACAGCTCTTA CTCATAAGCA GTCTTATTAT TCCATTGCCA
2751 AATGTGTAGC TGCCCTTACT CGAGCATGCC CTAAAGAGGG ACCAGCTGTA
2801 GTAGGTCAGT TTATTCAAGA TGTCAGAAGC TCAAGGTCTA CAGATTCCAT
2851 TCGTCTCTTA GCTCTACTTT CTCTTGGAAG AGTTGGGCAT CATATTGACT
2901 TAAGTGGACA GTTGGAACTA AAATCTGTAA TACTAGAAGC TTTCTCATCT
2951 CCTAGTGAAG AAGTCAAATC AGCTGCATCC TATGCATTAG GCAGCATTAG
3001 TGTGGGCAAC CTTCTGAAT ATCTGCCGTT TGTCCTGCAA GAAATAACTA
3051 GTCACCCCAA AAGGCAGTAT CTTTTACTTC ATTCTTGAA GGAAATTATT
3101 AGCTCTGCAT CAGTGGTGGG CCTTAAACCA TATGTTGAAA ACATCTGGGC
3151 CTTATTACTA AAGCACTGTG AGTGTGCAGA GGAAGGAACC AGAAATGTTG
3201 TTGCTGTAAG TCTAGGAAAA CTCACTCTAA TTGATCCAGA AACTCTCCTT
3251 CCACGGCTTA AGGGTACTT GATATCAGGC TCATCATATG CCCGAAGCTC
3301 AGTGGTTACG GCTGTGAAAT TTACAATTTT TGACCATCCA CAACCTATTG
3351 ATCCACTGTT AAAGAACTGC ATAGGTGATT TCCTAAAAAC TTTGGAAAGC
3401 CCAGATTTGA ATGTGAGAAG AGTAGCCTTG GTCACATTTA ATTCAGCAGC
3451 ACATAACAAG CCATCATTAA TAAGGGATCT ATTGGATACT GTTCTTCCAC
3501 ATCTTTACAA TGAAACAAAA GTTAGAAAGG AGCTTATAAG AGAGGTAGAA
3551 ATGGGTCCAT TTAACATAC GGTGTATGAT GGTCTGGATA TTAGAAAGGC
3601 AGCATTTGAG TGTATGTACA CACTTCTAGA CAGTTGTCTT GATAGACTTG
3651 ATGCTGTAAG ATTTCTAAAT CATGTTGAAG ATGGTTTGAA GGACCATTAT
3701 GATATTAAGA TGCTGACATT TTTAATGTTG GTGAGACTGT CTACCCTTTG
3751 TCCAAGTGCA GTACTGCAGA GGTGGACCG ACTTGTGAG CCATTACGTG
3801 CAACATGTTA AACTAAGGTA AAGGCAAACT CAGTAAAGCA GGAGTTTGAA
3851 AAACAAGATG AATTAAAGCG ATCTGCCATG AGAGCAGTAG CAGCACTGCT
3901 AACCATTCCA GAAGCAGAGA AGAGTCCACT GATGAGTGAA TTCCAGTCAC
3951 AGATCAGTTC TAACCCCTGAG CTGGCGGCTA TCTTTGAAAG TATCCAGAAA
4001 GATTTCATCAT CTACTAATTT GGAATCAATG GACACTAGTT AGATGTTTGT
4051 TCACCATGGG GACCATTACA TATGACCATA CAATGCATG AATTGACAGG
4101 TTAATCATAA GACATGGAAA GAGAAGTGTC TAAAAGCTTC AAAATGTTCC
4151 ACTTTTTTTT CCTTCATGGA GACTGTTTGT TTGGCTTTCT TCCATTGTTG
4201 TTTTGTAGC ATTTATTTCA GAAATGTGTA TTTCCATAAT CCAGAGTTG
4251 TAAAACCACT AGTGTTTTAG TGGTTACAGC AACATTTGAA ATGGAAACTA
4301 AAAGTTAGGA TTTTATGGAG TATGGAGATA GGGTCCAGTA TCTATTTACC
4351 CTGTAATGTT TAGGATTAAA ATGTTAAAAA TTTGTGACCA TGAATTTCTT
4401 TCTTTTATAA ATTTTCTCAT TTAATAATCA AAAATCTTGC AAAACAAAAA
4451 CCATGTTTCT TTTTCTTGTA TAACTTTTTG TTTTCAGCAA CATAAATTGA
4501 TTTTGTAGCTG GCAGACAAGA ATATCCATAT AAGATTGTTT AACCATTTCA
4551 GAGAGTTTGG CAATTTTTAA AAGATAATAA GGTATCATTT TTAAGTATGA
4601 AAATTAACAA TATCCCTGTT GCGCACACTA ATTTTGATG AGTAAGTTTA
4651 CAAATATGTA TCGTCTGTAA AGCAGCATGT GCAGATTATT CATAATATAG
4701 AAGTTAAAAA AAGTATTAGT GCAATTTTCA GATATTTATT TTTGCACAGA
4751 AAACACATTA TCTGGAGAGA AAGAAAGGAG AATTTTGTAG ACTTGGGTTT
4801 TCTTAATGCC AGTGTGAATT TGCAGATGTT TTCAGAAAAT CAAGTCACAG
4851 TAACAATTGG CCACTTTTTT CTATTATAAA TCTCTTACT TAAATTTTGA
4901 ATATTTAGTT TTTCTCAGTT ACCCATTTGT GTGTGTGTGA TTCCACTTAG
4951 AAATTCCTAA AACAGATT TTCTTTCATT CCGTTTGAT GTCTACATTC
5001 CTTATCAAAG GATATAAATA CTGTGTATGC TTTTGAATTT TATTTTTAGG
5051 AAAATTCCTA AGCCAGCTAT CACAGGTTTG TTAGCTAATA ATAGTATTTT
5101 CTTTGTAGTT AGTTAGGTTT TTCCCATCT CCTGTAGAGC GAATTTACAT
5151 ATTGTATTGG GTAAGTGTTC ACTACTTTTC CTGATTAAGG GATCTGTGCT
5201 GGGGAACAAA GCTTTTGCAG TACCTTATAT TGAGTTAAA ATTTTATTTA
5251 ACATATCCTT CAGTGAGCTC ATTTACACT GTAGCCTCTT CCTTAAAAAT
5301 TGTGGTGTCT CTGTAACAGT AAGAACTAAT TCTGAAATAA AAGACATCTC
5351 CTAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

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BLAST Results

Entry HS793345 from database EMBL:
human STS WI-12457.
Score = 1985, P = 1.3e-83, identities = 433/460

Medline entries

97127450:
Molecular cloning of a novel 120-kDa TBP-interacting
protein.

Peptide information for frame 2

ORF from 350 bp to 4039 bp; peptide length: 1230

Category: known protein
 Classification: Nucleic acid management

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1 MASASYHISN LLEKMTSSDK DFRFMATNDL MTELQKDSIK LDDDSERKVV
51 KMILKILLEDK NGEVQNLAVK CLGPLVSKVK EYQVETIVDT LCTNMLSDKE
101 OLRDISSIGL KTVIGELPPA SSGSALAANV CKKITGR LTS AIKQEDVSV
151 QLEALDIMAD MLSRQGGLLV NFHPSILTCL LPQLTSPRLA VRKRTIIALG
201 HLVMSCGNIV FVDLIEHLLS ELSKNDMSMT TRTYIQCIAA ISRQAGHRIG
251 EYLEKIIPLV VKFCNVDDDE LREYCIQAFE SFVRRCPKEV YPHVSTIINI
301 CLKYLTYDPN YNYDDEDEDE NAMDADGGDD DDQGSDDDEYS DDDDMSWKVR
351 RAAAKCLDAV VSTRHEMLPE FYKTVSPALI SRFKEREENV KADV FHAYLS
401 LLKQTRPVQS WLCDDPDAMEQ GETPLTMLQS QVPNIVKALH QMKESKSVKT
451 RQCCFNMLTE LVNVLPGALT QHIPVLVPGI IFSLNDKSSS SNLKIDALSC
501 LYVILCNHSP QVFHPPHVAL VPPVVACVGD PFYKITSEAL LVTQQLVKVI
551 RPLDQSSFD ATPYIKDLET CTIKRLKAAD IDQEVKERAI SCMGQIICNL
601 GDNLGSDLPN TLQIFLERLK NEITRLTTVK ALTLIAGSPL KIDLRPVLGE
651 GVPILASFLR KNQRAKLKGT LSALDILIKN YSDSLTAAMI DAVLDELPLP
701 ISESDMHVSQ MAISFLTTLA KVPSSLSKI SGSLNELIG LVRSPLLQGG
751 ALSAMLDFFQ ALVVTGTNNL GYMDLLRMLT GPVYSQSTAL THKQSYYSIA
801 KCVAAALTRAC PKEGPAVVGQ FIQDVKNRSR TDSIRLLALL SLGEVGHHD
851 LSGQLELKS V ILEAFSSPSE EVKSAASYAL GSISVGNLPE YLPFVLOEIT
901 SQPKROYLLL HSLKEIISSA SVVGLKPYVE NIWALLLKHC ECAEEGTRNV
951 VAECLGKLT L IDPETLLPRL KGYLISGSSY ARSSVVAVK FTISDHPQPI
1001 DPLLKNCIGD FLKTLEDPLD NVRRVALVTF NSAAHNKPSL IRDLLDTVLP
1051 HLYNETKVVR ELIREVEMGP FKHTVDDGLD IRKAAFECMY TLLDSCDLRL
1101 DIFEFNLHVE DGLKDHYDIK MLTFLMLVRL STLCPSAVLQ RLDRLVEPLR
1151 ATCTTKVKAN SVKQEFKQD ELKRSAMRAV AALLTIPEAE KSPLMSEFQS
1201 QISSNPELAA IFESI QKDSS STNLESMDTS

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_22g2, frame 2

TREMBL:AB020636_1 gene: "KIAA0829"; product: "KIAA0829 protein"; Homo sapiens mRNA for KIAA0829 protein, partial cds., N = 1, Score = 5986, P = 0

TREMBL:RND6711_1 gene: "tip120"; product: "TIP120"; Rattus norvegicus mRNA for TIP120, complete cds., N = 1, Score = 6203, P = 0

>TREMBL:RND6711_1 gene: "tip120"; product: "TIP120"; Rattus norvegicus mRNA for TIP120, complete cds.
 Length = 1,230

HSPs:

Score = 6203 (930.7 bits), Expect = 0.0e+00, P = 0.0e+00
 Identities = 1227/1230 (99%), Positives = 1228/1230 (99%)

```

Query:      1 MASASYHISN LLEKMTSSDK DFRFMATNDL MTELQKDSIK LDDDSERKVV KMILKILLEDK 60
            MASASYHISN LLEKMTSSDK DFRFMATNDL MTELQKDSIK LDDDSERKVV KMILKILLEDK
Sbjct:      1 MASASYHISN LLEKMTSSDK DFRFMATNDL MTELQKDSIK LDDDSERKVV KMILKILLEDK 60

Query:      61 NGEVQNLAVK CLGPLVSKVKEYQVETIVDT LCTNMLSDKEQLRDISSIGL KTVIGELPPA 120
            NGEVQNLAVK CLGPLVSKVKEYQVETIVDT LCTNMLSDKEQLRDISSIGL KTVIGELPPA
Sbjct:      61 NGEVQNLAVK CLGPLVSKVKEYQVETIVDT LCTNMLSDKEQLRDISSIGL KTVIGELPPA 120

Query:     121 SSGSALAANVCKKITGR LTS AIKQEDVSVQLEALDIMAD MLSRQGGLLVNFHPSILTCL 180
            SSGSALAANVCKKITGR LTS AIKQEDVSVQLEALDIMAD MLSRQGGLLVNFHPSILTCL
Sbjct:     121 SSGSALAANVCKKITGR LTS AIKQEDVSVQLEALDIMAD MLSRQGGLLVNFHPSILTCL 180

Query:     181 LPQLTSPRLAVRKR TIIALGHLVMSCGNIVFVDLIEHLLSELSKNDMSMTTRTYIQCIAA 240
            LPQLTSPRLAVRKR TIIALGHLVMSCGNIVFVDLIEHLLSELSKNDMSMTTRTYIQCIAA
Sbjct:     181 LPQLTSPRLAVRKR TIIALGHLVMSCGNIVFVDLIEHLLSELSKNDMSMTTRTYIQCIAA 240

Query:     241 ISRQAGHRIG EYLEKIIPLVVKFCNVDDDELREYCIQAFESFVRRCPKEVYPHVSTIINI 300
            ISRQAGHRIG EYLEKIIPLVVKFCNVDDDELREYCIQAFESFVRRCPKEVYPHVSTIINI
Sbjct:     241 ISRQAGHRIG EYLEKIIPLVVKFCNVDDDELREYCIQAFESFVRRCPKEVYPHVSTIINI 300

Query:     301 CLKYLTYDPN YNYDDEDEDE NAMDADGGDDDDQGSDDDEYS DDDDMSWKVRRAAAKCLDAV 360
            CLKYLTYDPN YNYDDEDEDE NAMDADGGDDDDQGSDDDEYS DDDDMSWKVRRAAAKCLDAV
Sbjct:     301 CLKYLTYDPN YNYDDEDEDE NAMDADGGDDDDQGSDDDEYS DDDDMSWKVRRAAAKCLDAV 360

Query:     361 VSTRHEMLPEFYKTVSPALISRFKEREENVKADV FHAYLSLLKQTRPVQSWLCDPDAMEQ 420
            VSTRHEMLPEFYKTVSPALISRFKEREENVKADV FHAYLSLLKQTRPVQSWLCDPDAMEQ
Sbjct:     361 VSTRHEMLPEFYKTVSPALISRFKEREENVKADV FHAYLSLLKQTRPVQSWLCDPDAMEQ 420

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Query: 421 GETPLTMLQSQVFNIVKALHKQMKEKSVKTRQCCFNMLTELNVNLPALTQHIPVLVPGI 480
 GETPLTMLQSQVFNIVKALHKQMKEKSVKTRQCCFNMLTELNVNLPALTQHIPVLVPGI
 Sbjct: 421 GETPLTMLQSQVFNIVKALHKQMKEKSVKTRQCCFNMLTELNVNLPALTQHIPVLVPGI 480

Query: 481 IFSLNDKSSSSNLKIDALSCLYVILCNHSPQVFHHPVQALVPPVVACVGDPPFYKITSEAL 540
 IFSLNDKSSSSNLKIDALSCLYVILCNHSPQVFHHPVQALVPPVVACVGDPPFYKITSEAL
 Sbjct: 481 IFSLNDKSSSSNLKIDALSCLYVILCNHSPQVFHHPVQALVPPVVACVGDPPFYKITSEAL 540

Query: 541 LVTQQLVKVIRPLDQPSFDPATPYIKDLFTCTIKRLKAADIDQEVKERAISCMGQIICNL 600
 LVTQQLVKVIRPLDQPSFDPATPYIKDLFTCTIKRLKAADIDQEVKERAISCMGQIICNL
 Sbjct: 541 LVTQQLVKVIRPLDQPSFDPATPYIKDLFTCTIKRLKAADIDQEVKERAISCMGQIICNL 600

Query: 601 GDNLGSDLPNTLQIFLERLKNEITRLTTVKALTLIAGSPLKIDLRPVLGEGVPILASFLR 660
 GDNLG DL NTLQIFLERLKNEITRLTTVKALTLIAGSPLKIDLRPVLGEGVPILASFLR
 Sbjct: 601 GDNLGSDLPNTLQIFLERLKNEITRLTTVKALTLIAGSPLKIDLRPVLGEGVPILASFLR 660

Query: 661 KNQRALKGLTSLALDILIKNYSDSLTAAMIDAVLDELPLPSESMDMHVSQMAISFLTTLA 720
 KNQRALKGLTSLALDILIKNYSDSLTAAMIDAVLDELPLPSESMDMHVSQMAISFLTTLA
 Sbjct: 661 KNQRALKGLTSLALDILIKNYSDSLTAAMIDAVLDELPLPSESMDMHVSQMAISFLTTLA 720

Query: 721 KVPSSLSKISGSILNELIGLVRSPLQGGALSAMLDFFQALVVTGTNNLGMDLLRMLT 780
 KVPSSLSKISGSILNELIGLVRSPLQGGALSAMLDFFQALVVTGTNNLGMDLLRMLT
 Sbjct: 721 KVPSSLSKISGSILNELIGLVRSPLQGGALSAMLDFFQALVVTGTNNLGMDLLRMLT 780

Query: 781 GPVYSQSTALTHKQSYYSIAKCVAAALTRACPKEGPAVVGQFIQDVKNRSRSTDSIRLLALL 840
 GPVYSQSTALTHKQSYYSIAKCVAAALTRACPKEGPAVVGQFIQDVKNRSRSTDSIRLLALL
 Sbjct: 781 GPVYSQSTALTHKQSYYSIAKCVAAALTRACPKEGPAVVGQFIQDVKNRSRSTDSIRLLALL 840

Query: 841 SLGEVGHIDLSGQLELKSIVILEAFSSPSEEVKSAASYALGSISVGNLPEYLPFVLQEI 900
 SLGEVGHIDLSGQLELKSIVILEAFSSPSEEVKSAASYALGSISVGNLPEYLPFVLQEI
 Sbjct: 841 SLGEVGHIDLSGQLELKSIVILEAFSSPSEEVKSAASYALGSISVGNLPEYLPFVLQEI 900

Query: 901 SQPKRQYLLHSLKEIISASVVGKPYVENIALLKHCECAEEGTRNVVAECLGKLT 960
 SQPKRQYLLHSLKEIISASVVGKPYVENIALLKHCECAEEGTRNVVAECLGKLT
 Sbjct: 901 SQPKRQYLLHSLKETIISASVVGKPYVENIALLKHCECAEEGTRNVVAECLGKLT 960

Query: 961 IDPETLLPRLKGYLISGSSYARSSVVTAVKFTISDHPQPIDPLKNCIGDFLKTLED 1020
 IDPETLLPRLKGYLISGSSYARSSVVTAVKFTISDHPQPIDPLKNCIGDFLKTLED
 Sbjct: 961 IDPETLLPRLKGYLISGSSYARSSVVTAVKFTISDHPQPIDPLKNCIGDFLKTLED 1020

Query: 1021 NVRRVALVTFNSSAAHNKPSLIRDLLDVLPHLYNETKVRKELIREVEMGPFKHTVDDGLD 1080
 NVRRVALVTFNSSAAHNKPSLIRDLLD+VLPHLYNETKVRKELIREVEMGPFKHTVDDGLD
 Sbjct: 1021 NVRRVALVTFNSSAAHNKPSLIRDLLDVLPHLYNETKVRKELIREVEMGPFKHTVDDGLD 1080

Query: 1081 IRKAAFECMYTLLDSCDLRLDIFEFNLHVEDGLKDHYDIKMLTFLMLVRLSTLCPSAVLQ 1140
 IRKAAFECMYTLLDSCDLRLDIFEFNLHVEDGLKDHYDIKMLTFLMLVRLSTLCPSAVLQ
 Sbjct: 1081 IRKAAFECMYTLLDSCDLRLDIFEFNLHVEDGLKDHYDIKMLTFLMLVRLSTLCPSAVLQ 1140

Query: 1141 RDLRLVEPLRATCTTKVKANSVKQEFKQDELKRSAMRAVAALLTIPEAEKSPLMSEFQS 1200
 RDLRLVEPLRATCTTKVKANSVKQEFKQDELKRSAMRAVAALLTIPEAEKSPLMSEFQS
 Sbjct: 1141 RDLRLVEPLRATCTTKVKANSVKQEFKQDELKRSAMRAVAALLTIPEAEKSPLMSEFQS 1200

Query: 1201 QISSNPELAAIFESI QKDSSTNLESMDTS 1230
 QISSNPELAAIFESI QKDSSTNLESMDTS
 Sbjct: 1201 QISSNPELAAIFESI QKDSSTNLESMDTS 1230

Pedant information for DKFZphtes3_22g2, frame 2

Report for DKFZphtes3_22g2.2

[LENGTH] 1230
 [MW] 136376.58
 [pI] 5.52
 [HOMOL] TREMBL:RND6711_1 gene: "tip120"; product: "TIP120"; Rattus norvegicus mRNA for
 TIP120, complete cds. 0.0
 [KW] TRANSMEMBRANE 1
 [KW] LOW_COMPLEXITY 5.28 %

SEQ MASASYHISNLEKMTSSDKDFRFRMATNDLMTLQKDSIKLDDDSERKVVKMILKLEDK
 SEG
 PRD cccccchhhhhhhhhccccceeeehhhhhhhhhccccccccchhhhhhhhhhhhhcc
 MEM

SEQ NGEVQNLAVKCLGPLVSKVKEYQVETIVDTLCTNMLSQKEQIRDISSIGLKTVIGELPPA
 SEG
 PRD cccccceeeeeeeceeeehhhhhhhhhhhccccchhhhhccccccccchhhhhhhhhhhcc

MEM
SEQ SSGSALAANVCKKITGRLTSAIAKQEDVSVQLEALDIMADMLSRQGGLLVNFHPSILTCL
SEG xxxxxxxx.....
PRD cccccchhhhhhhccchhhhhhhcccccchhhhhhhhhhhhhhhhhccceeeecchhhhhh
MEM
SEQ LPOLTSPLAVRKRTIIALGHLVMSCGNIVFVDLIEHLLSELSKNDSMSTRTYIOCIAA
SEG
PRD hccccchhhhhhhhhhhheeeecceeeehhhhhhhhhhhhhcccccchhhhhhhhhhh
MEMMMMMMMMMMMMMMM.....
SEQ ISRQAGHRIGEYLEKIIPLVVKFCNVDDDELREYCIQAFESFVRRCPKEVYPHVSTIINI
SEG
PRD hhhccccccccchhhhhhhheeeecchhhhhhhhhhhhhhhhhcccccceecchhhhhh
MEM
SEQ CLKYLTYDPNINYDDEDEDENAMDADGGDDDDQGSDDDEYSDDDDMSWKVRRRAAKCLDAV
SEGxx.....
PRD hhhhhccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhh
MEM
SEQ VSTRHEMLPEFYKTVSPALISRFKEREENVKADVHAYLSLLKQTRPVQSWLCDPDAMEQ
SEG
PRD hhhhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccceeeeccecccccc
MEM
SEQ GETPLTMLQSQVPNIVKALHKQMKESVKTRQCCFNMLTELNVNLPGALTQHIPVLVPGI
SEG
PRD cccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhhhcccccceeeecce
MEM
SEQ IFSLNDKSSSSNLKIDALSCLYVILCNHSPQVFHPHVQALVPPVACVGDPPFYKITSEAL
SEGxxxxxxxxxxxxxxxx.....
PRD eeeecccccccccchhhhhhhheeeecceccccccccceeeecceeeecceccccchhhhhhhh
MEM
SEQ LVTQQLVKVIRPLDQPSFDPATPYIKDLFTCTIKRLKAADIDQEVKERAISCMGQICNL
SEG
PRD hhhhhhhhhhhccccccccccccccchhhhhhhhhhhhhhhhhccchhhhhhhhhhhheeeecce
MEM
SEQ GDNLGSDLPNTLQIFLERLKNEITRLTTVKALTLAGSPLKIDLRPVLGEGVPILASFLR
SEG
PRD cccccccccchhhhhhhhhccchhhhhhhhhhhheeeecceccccccccceehhhhhhhhhhh
MEM
SEQ KNQRALKGLTSLDILIKNYSDSLTAAMIDAVLDELPLISESDMHVSQMAISFLTTLA
SEG
PRD hhhhhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhh
MEM
SEQ KVYPSSLSKISGSILNELIGLVRSPLLQGGALSAMLDFFQALVVTGTNNLGYMDLLRMLT
SEG
PRD cccccceecchhhhhhhhhhhcccccchhhhhhhhhhhheeeecceccccchhhhhhhhhc
MEM
SEQ GPVYSQSTALTHKQSYYSIAKVAALTRACPKEGPAVVGQFIQDVKNRSTDSIRLLALL
SEG
PRD cccccccccchhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhcccccchhhhhhhh
MEM
SEQ SLGEVGHHDLSGQLELKSIVILEAFSSPSEEVKSAASYALGSISVGNLPEYLPFVLQEIT
SEG
PRD hccccccccccccccccceeeecceccccchhhhhhhhhhhcccccceccccchhhhhhhh
MEM
SEQ SQPKRQYLLHSLKEIISASVVGKPYVENIWALLLKHCECAEEGTRNVVAECLGKLT
SEG
PRD cccchhhhhhhhhhhhhhhccceehhhhhhhhhhhhhhhhhcccccceeeeccecccccc
MEM
SEQ IDPETLLPRLKGYLISGSSYARSSVVTAVKFTISDHPQPIDPFLKNCIGDFLKTLEDPLD
SEG
PRD cccccccccccccccccccchhhhhhhhhhhhhhhhhcccccceccccchhhhhhhhhhhccccc
MEM
SEQ NVRRVALVTFNSAAHNKPSLIRDLLDTVLPHLYNETKVRKELIREVEMGPFKHTVDDGLD
SEG
PRD ccceeeeeeccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccceccccch
MEM

```

SEQ      IRKAAFECEMYTLLDSCDLRLDIFEFNLHVEDGLKDHYDIKMLTFLMLVRLSTLCPSAVLQ
SEG      .....
PRD      hhhhhhhhhhhhhhhccccccceeeccccccccccchhhhhhhhhhhhhhhccccchhh
MEM      .....

SEQ      RDLRLVEPLRATCTTKVKANSVKQEFQDELKRSAMRAVAALLTIPEAEKSPLMSEFQS
SEG      .....
PRD      hhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccchhhh
MEM      .....

SEQ      QISSNPELAAIFESIQKDSSTNLESMDTS
SEG      .....
PRD      hhhccccchhhhhhhhhhhcccccccccccccc
MEM      .....

```

(No Prosite data available for DKFZphtes3_22g2.2)

(No Pfam data available for DKFZphres3_22g2.2)

DKFZphtes3_22n13

group: testes derived

DKFZphtes3_22n13 encodes a novel 677 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes.

dJ1042K10.3, complete

Sequenced by LMU

Locus: /map="22q13.1-13.2"

Insert length: 3353 bp

Poly A stretch at pos. 3315, polyadenylation signal at pos. 3298

```
1 ATGGAACAC TATCCCCACT GCCAAGTCCA CCCCCACACT CATTAAAGCAA
51 AGCCAACCCA AGTCTGCCAG TGAGAAGTCA CAGCGCAGCA AGAAGGCCAA
101 GGAGCTGAAG CCAAAGGTGA AGAAGCTCAA GTACCACCAG TACATCCCCC
151 CGGACCAGAA GCAGGACAGG GGGGCACCCC CCATGGACTC ATCCTACGCC
201 AAGATCCTGC AGCAGCAGCA GCTCTTCCTC CAGCTGCAGA TCCTCAACCA
251 GCAGCAGCAG CAGCACCACA ACTACCAGGC CATCCTGCCT GCCCCGCCAA
301 AGTCAGCAGG CGAGGCCCTG GGAAGCAGCG GGACCCCCC AGTACGCAGC
351 CTCTCCACTA CCAATAGCAG CTCCAGCTCG GGGCCCCCTG GGCCCTGTGG
401 GCTGGCACGT CAGAACAGCA CCTCACTGAC TGGCAAGCCG GGAGCCCTGC
451 CGGCCAACCT GGACGACATG AAGGTGGCAG ACCTGAAGCA GGAGCTGAAG
501 TTGCGATCAC TGCCTGTCTC GGGCACCAAA ACTGAGCTGA TTGAGCGCCT
551 TCGAGCCTAT CAAGACCAAA TCAGCCCTGT GCCAGGAGCC CCAAGGCCCC
601 CTGCCGCCAC CTCTATCCTG CACAAGGCTG GCGAGGTGGT GGTAGCCTTC
651 CCAGCGGCCC GGCTGAGCAC GGGGCCAGCC CTGGTGGCAG CAGGCCCTGGC
701 TCCAGCTGAG GTGGTGGTGG CCACGGTGGC CAGCAGTGGG GTGGTGAAGT
751 TTGGCAGCAC GGGCTCCACG CCCCCCGTGT CTCCCACCCC CTCGGAGCGC
801 TCACTGCTCA GCACGGGCGA TGAAAACCTC ACCCCCCGGG ACACCTTTGG
851 TGAGATGGTG ACATCACCTC TGACGCAGCT GACCCTGCAG GCCTCGCCAC
901 TGCAGATCCT CGTGAAGGAG GAGGGCCCCC GGGCCGGGTC CTGTTGCCTG
951 AGCCCTGGGG GGGGGGGCGA GCTAGAGGGG CGCGACAAGG ACCAGATGCT
1001 GCAGGAGAAA GACAAGCAGA TCGAGGCGCT GACGCGCATG CTCGGGCAGA
1051 AGCAGCAGCT GGTGGAGCGG CTCAAGCTGC AGCTGGAGCA GGAGAAGCGA
1101 GCCCAGCAGC CCGCCCCCGC CCCCCCCCCC CTCGGCACCC CCGTGAAGCA
1151 GGAGAACAGC TTCTCCAGCT GCCAGCTGAG CCAGCAGCCC CTGGGCCCCG
1201 CTCACCCATT CAACCCAGC CTGGCGGCCC CAGCCACCAA CCACATAGAC
1251 CCTTGTGCTG TGGCCCCAGG GCCCCCGTCC GTGGTGGTGA AGCAGGAAGC
1301 CTTGACAGCT GAGCCCCGAG CGGTCCCCGC CCCCCAGTTG CTTCTGGGGC
1351 CTCAGGGCCC CGGCCTCATC AAGGGGGTTG CACCTCCAC CCTCATCACC
1401 GACTCCACAG GGACCCACCT TGTCTCACC GTGACCAATA AGAATGCAGA
1451 CAGCCCTGGC CTGTCCAGTG GGAGCCCCCA GCAGCCCTCG TCCCAGCCTG
1501 GCTCTCCAGC GCCTGCCCCC TCTGCCAGA TGGACCTGGA GCACCCACTG
1551 CAGCCCTCTT TTGGGACCCC CACTTCTCTG CTGAAGAAGG AACCACCTGG
1601 CTATGAGGAA GCCATGAGCC AGCAGCCCAA ACAGCAGGAA AATGGTTCTT
1651 CAAGCCAGCA GATGGACGAC CTGTTTGACA TTCTCATTCA GAGCGGAGAA
1701 ATTTCAAGCA ATTTCAAGGA GCCGCCATCC CTGCCAGGGA AGGAGAAGCC
1751 ATCCCCGAAG ACAGTCTGTG GGTCCCCCCT GGCAGCACAG CCATCACCTT
1801 CTGCTGAGCT CCCCAGGCT GCCCCACCTC CTCCAGGCTC ACCCTCCCTC
1851 CCTGGACGCC TGGAGGACTT CCTGGAGAGC AGCAGGGGGC TGCCCTGCT
1901 GACCAGTGGG CATGACGGGC CAGAGCCCCT TTCCCTCATT GACGACCTCC
1951 ATAGCCAGAT GCTGAGCAGC ACTGCCATCC TGGACCACCC CCGTCAACCC
2001 ATGACACCT CGGAATTGCA CTTTGTTCCT GAGCCAGCA GCACCATGGG
2051 CCTGGACCTG GCTGATGGCC ACCTGGACAG CATGGACTGG CTGGAGCTGT
2101 CGTCAGGTGG TCCCGTGCTG AGCCTAGCCC CCCTCAGCAC CACAGCCCCC
2151 AGCCTCTTCT CACAGACTT CCTCGATGGC CATGATTTCG AGCTGCACTG
2201 GGATTCCTGC TTGTAGCTCT CTGGCTCAAG ACCGGGTGGG GAAGGGGCTG
2251 GGAGCCAGGG TACTCCAATG CGTGGCTCTC CTGCGTGATT CGGCCTCTCC
2301 ACATGGTTGT GAGTCTTGAC AATCACAGCC CCGCTTTTTT CCTTCCCTG
2351 GGAGGCTAGA ACAGAGAAGC CCTTACTCCT GGTTCAGTGC CACCGAGGGC
2401 AGAGGAGAGC AGCTGTCAAG AAGCAGCCCCT GGCTCTCAAG CTGGGGTTTT
2451 GGACACACCG TGAGGGTCAG GGCCATTTCG GCTTGACCTC CTTTTTTGAG
2501 GTCAGGGGGC ACTGTCTGTC TGGCTACAAT TTGGCTAAGG TAGGTGAAGC
2551 CTGGCCAGGC GGGAGGCTTC TCTTCTGACC CAGGGCTGAG ACAGGTTAAG
2601 GGTGGAATCT CTTTCTTTC TCTCCCTGCT TTGCTGTGAA GGGAGAAATT
2651 AGCCTGGGCC TCTACCCCTT ATTCCCTGTG TCTGCCAACC CCAGGATCCC
2701 AGGGCTCCCT GCCATTTTAG TGTCTGGTG TAGTGAACC ATTTAGTGGT
2751 TGGTGGCAAC AATTTTATGT ACAGGTGTAT ATACCTCTAT ATTATATATC
2801 GACATACATA TATATTTTGG GGGGGGGGCG GACAGGAGAT GGTGCAACT
```



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2851 CCCTCCCATC CTACTCTCAC AGAAGGGCCT GGATGCAAGG TTACCCTTGA
2901 GCTGTGTGCC ACAGTCTGGT GCCCAGTCTG GCATGCAGCT ACCCAGGCCC
2951 ACCCATCACG TGTGATTGAC ATGTAGGTAC CCTGCCACGG CCTATGCCCC
3001 ACCTGCCCTG CTTCTGGCT CTTATCAGT GCCATGAGGG CAGAGGTGCT
3051 ACCTGGCCTT CCTGCCAGGA GCTCTCCACC CACTCACATT CCGTCCCCGC
3101 CGCCTCACTG CAGCCAGCGT GGCCTAGGA CAGGAGGAGC TTCGGGCCCCA
3151 GCTTACCCTT GCGGTGGGGC TGAGGGGTGG CCATCTCTG CCCTGGGGCC
3201 ACTGGCTTCA CATTCTGGGC TGA CT CATAG GGGAGTAGGG GTGGAGTCAC
3251 CAAAACCAGT GCTGGGACAA AGATGGGGAA GGTGTGTGAA CTTTTTAAAA
3301 TAAACACAAA AACACAGGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3351 AAG

```

BLAST Results

Entry HS1042K10 from database EMBL:
 Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2.
 Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2,
 Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP
 domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a
 putative CpG island.
 Score = 7997, P = 0.0e+00, identities = 1617/1645
 7 exons

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 183 bp to 2213 bp; peptide length: 677
 Category: similarity to unknown protein
 Classification: unclassified

```

1  MDSYAKILQ  QQQLFLQLQI  LNQQQQQHNN  YQAILPAPPK  SAGEALGSSG
51  TPVRSLSLT  NSSSSSGAPG  PCGLARQNST  SLTGKPGALP  ANLDDMKVAE
101 LKQELKLRSL  PVSQTKTELI  ERLRAYQDQI  SPVPGAPKAP  AATSILHKAG
151 EVVVAFFPAAR  LSTGPALVAA  GLAPAEVVVA  TVASSGVVKF  GSTGSTPPVS
201 PTPSERSLLS  TGDNSTPGD  TFGEMVTSPL  TQLTLQASPL  QILVKEEGPR
251 AGSCCLSPGC  RAELEGRDKD  QMLQEKDKQI  EALTRMLROK  QQLVERLKLO
301 LEQEKRAQQP  APAPAPLGTP  VKQENSFSSC  QLSQQPLGPA  HPFNPSLAAP
351 ATNHIDPCAV  APGPPSVVVK  QEALQPEPEP  VPAPQLLLGP  QGPGLIKGVA
401 PPTLITDSTG  THLVLTVTNK  NADSPGLSSG  SPQPPSSQPG  SPAPAPSAQM
451 DLEHPLQLPF  GTPSLLKKE  PPGYEEAMSQ  QPKQENGSS  SQQMDLFDI
501 LIQSGEISAD  FKEPPSLPGK  EKPSPKTVCG  SPLAAQSPSP  AELPQAAPPP
551 PGSPSLPGRL  EDPLESSTGL  PLLTSGHDGP  EPLSLIDDLH  SQMLSSTAIL
601 DHPFSPMDTS  ELHFVPEPSS  TMGLDLADGH  LOSMDWLELS  SGGPVLSLAP
651 LSTTAPSLFS  TDFLDGHDLQ  LHWDSCL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_22n13, frame 3

TREMBL:HS1042K10_6 gene: "dJ1042K10.3"; product: "dJ1042K10.3 (novel protein)"; Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island., N = 1, Score = 1285, P = 4.9e-131

TREMBL:CEUK06A9_3 gene: "K06A9.1a"; Caenorhabditis elegans cosmid K06A9., N = 2, Score = 149, P = 1.3e-09

TREMBLNEW:SSI132828_1 product: "p210 protein"; Spermatozopsis similis mRNA for p210 protein, partial, N = 1, Score = 171, P = 2.8e-09

>TREMBL:HS1042K10_6 gene: "dJ1042K10.3"; product: "dJ1042K10.3 (novel protein)"; Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC

Length = 243

HSPs :

Score = 1285 (192.8 bits), Expect = 4.9e-131, P = 4.9e-131
Identities = 243/243 (100%), Positives = 243/243 (100%)

Query:	435	PSSQPGSPAPAPSAQMDLEHPLQLFGLTPTSLKKKEPPGYEEAMSQQPKQQENGSSSQM	494
		PSSQPGSPAPAPSAQMDLEHPLQLFGLTPTSLKKKEPPGYEEAMSQQPKQQENGSSSQM	
Sbjct:	1	PSSQPGSPAPAPSAQMDLEHPLQLFGLTPTSLKKKEPPGYEEAMSQQPKQQENGSSSQM	60
Query:	495	DDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCGSPLAQAQPSAELPQAAPPPPGSP	554
		DDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCGSPLAQAQPSAELPQAAPPPPGSP	
Sbjct:	61	DDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCGSPLAQAQPSAELPQAAPPPPGSP	120
Query:	555	SLPGRLEDFLSSTGLPLLTSGHDGPEPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHF	614
		SLPGRLEDFLSSTGLPLLTSGHDGPEPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHF	
Sbjct:	121	SLPGRLEDFLSSTGLPLLTSGHDGPEPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHF	180
Query:	615	VPEPSSTMGLDLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHDLQLHWD	674
		VPEPSSTMGLDLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHDLQLHWD	
Sbjct:	181	VPEPSSTMGLDLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHDLQLHWD	240
Query:	675	SCL 677	
		SCL	
Sbjct:	241	SCL 243	

Pedant information for DKF2phtes3 22n13, frame 3

Report for DKFZphtes3 22n13.3

```
[LENGTH]          677
[MW]               70743.01
[pI]               4.93
[HOMOL]            TREMBL:HS1042K10_6 gene: "dJ1042K10.3"; product: "dJ1042K10.3 (novel protein)";
Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for
Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with
probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative
CpG island. 1e-111
[KW]               TRANSMEMBRANE 1
[KW]               LOW_COMPLEXITY 21.57 %
[KW]               COILED COIL 4.58 %
```

```

SEQ      MDSSYAKILQQOQLFLQLQLLNQQQQQHHNYQAILPAPPKSAGEALGSSSGTPPVRSLSTT
SEG      . . . . . xxxxxxxxxxxxxxxxxxxxxxxx . . . . . xxxxxx
PRD      ccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhccceeeeeeccccceeeccccccccceeecccc
COILS    . . . . .
MEM      . . . . .

SEQ      NSSSSSGAPGPCGLARQNSTSLTGKPGALPANLDDMKVaelKQELKLRSLPVSgTKTELI
SEG      xxxxxxxx . . . . . xxxxxxxxxxxxxxxxxxxxxxxx
PRD      cccccccccccccceccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhcccccchhhhh
COILS    . . . . .
MEM      . . . . .

SEQ      ERLRAYQDQISVPVGAPKAPAATSIHLKAGEVVVAFPAARLSTGPALVAAGLAPAEVVVA
SEG      . . . . . xxxxxxxxxxxxxxxxxxxxxxxx
PRD      hhhhhhhhhhhccccccccccccccccceeeeeeccccceccccccccccccccccceeeeee
COILS    . . . . .
MEM      . . . . . MMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ      TVASSGVVKGSTGSTPPVSPTPSERSLLSTGDENSTPGDTFGEMVTSPLTQLTLQASPL
SEG      xxxxxxxx . . . . . xxxxxxxxxxxxxxxxxxxxxxxx
PRD      eeccccccccccccccccccccccccceeeccccccccccccccccceeeccccceeeccccce
COILS    . . . . .
MEM      M . . . . .

SEQ      QTLVKEEGPRAGSCCLSPCGRAELEGRDKDQMLQEKDKQIEALTRMLRQKQQLVERLKLQ
SEG      . . . . .
PRD      eeeeeccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    . . . . . CCCCCCCCCCCCCCCCCCCCCCCC
MEM      . . . . .

SEQ      LEQEKRAQQPAPAPAPLGTGPVKQENSFSSCQLSQOPLGPAHPFNPSLAAPATNHIDPCA

```

```
SEG      .....xxxxxxxxx.....
PRD      hhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    CCCCCC.....
MEM      .....

SEQ      APGPPSVVVKQEQALQPEPEPVAPQQLLLGPQGPGLIKGVAPPTLITDSTGTHLVLTVTNK
SEG      .....xxxxxxxxx.....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....
MEM      .....

SEQ      NADSPGLSSGSPQQPSSQPGSPAPAPSAQMDLEHPLQPLFGTPTSLLKKEPPGYEAMSQ
SEG      .....xxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....
MEM      .....

SEQ      QPKQQENGSSSQMDDLFDILIQSGEISADFEPPSLPGKEKPSPKTVCGSPLAAQSPSPS
SEG      .....xxxxxxxxx.....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....
MEM      .....

SEQ      AELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGPEPLSLIDDLHSQMLSSTAIL
SEG      .....xxxxxxxxxxxxxxxx.....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....
MEM      .....

SEQ      DHPPSPMDTSELHFVPEPSSTMGLDLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFS
SEG      .....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS    .....
MEM      .....

SEQ      TDFLDGHDQLHWDSCl
SEG      .....
PRD      ccccccccccccccccccc
COILS    .....
MEM      .....
```

(No Prosite data available for DKFZphtes3_22n13.3)

(No Pfam data available for DKFZphtes3_22n13.3)

DKFZphtes3_23111

group: intracellular transport and trafficking

DKFZphtes3_23111 encodes a novel 186 amino acid protein nearly identical to mouse ADP-ribosylation-like factor homolog 6 (Arl6).

Protein secretion through the endoplasmic reticulum and the Golgi vesicular trafficking system is initiated by the binding of ADP-ribosylation factors (ARFs) to donor membranes, leading to recruitment of cocatomer, bud formation, and eventual vesicle release. ARFs are approximately 20-kDa GTPases that are active with bound GTP and inactive with GDP bound. The novel protein contains an ATP/GTP-binding site motif A (P-loop) and seems to be a novel ARF. It seems to have an important role in vesicular transport and vesicular trafficking.

The new protein can find application in modulating vesicle transport and trafficking in cells.

nearly identical to mouse Arl6, ADP-ribosylation-like factor homolog

start at Bp 15 matches kozak consensus ANNatgG

Sequenced by LMU

Locus: unknown

Insert length: 717 bp

Poly A stretch at pos. 689, no polyadenylation signal found

```

1  ATTTGAATCA CATTATGGGA TTGCTAGACA GACTTTCAGT CTTGCTTGGC
51 CTGAAGAAGA AGGAGGTTCA TGTTTTGTGC CTTGGGCTAG ATAATAGTGG
101 CAAAACGACG ATCATTAAACA AACTTAAACC TTCAAATGCT CAATCTCAAA
151 ATATCCTTCC AACAAATAGGA TTCAGCATAG AGAAATTCAA ATCATCCAGT
201 TTGTCATTTA CAGTGTTTGA CATGTCAGGT CAAGGAAGAT ACAGAAATCT
251 CTGGGAACAC TATTATAAAG AAGGCCAAGC TATTATTTT GTCATTGATA
301 GTAGTGATAG ATTAAGAATG GTTGTGGCCA AAGAAGAACT CGATACTCTT
351 CTGAATCATC CAGATATTAA ACACCGTCGA ATTCCAATCT TATTCTTTGC
401 AAATAAAAATG GATCTTAGAG ATGCAGTGAC ATCTGTAAAA GTGTCTCAGT
451 TGCTGTGTTT AGAGAACATC AAAGATAAAC CCTGGCATAT TTGTGCTAGT
501 GATGCCATAA AAGGAGAAGG CTTGCAAGAA GGTGTAGACT GGCTTCAAGA
551 TCAGATCCAG ATGTGAAGA CATGAAAAGA TAATAGTTGG AAACCTCAGC
601 AATTTTCAAT TCAAGGAATC TATCTAAGAC AAATAGAATA CATTTTGTA
651 AAGATGTTTA TGCATCAAAA AATATAATTT TCTGCTTGCA AAAAAAAAAA
701 AAAAAAAAAA AAAAAAG

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 15 bp to 572 bp; peptide length: 186
 Category: strong similarity to known protein
 Classification: Intracellular transport and traffic
 Prosite motifs: ATP_GTP_A (24-32)

```

1  MGLDLRLSVL LGLKKKEVHV LCLGLDMSGK TTIINKLKPS NAQSQNILPT
51  IGFSIEKFKS SLSFTVFDM SGQGRYRNW EHYYKEGQAI IFVIDSSDRL
101 RMVVAKEELD TLLNHPDIKH RRIPIFFAN KMDLRDAVTS VKVSQLLCLE
151 NIKDKPWHIC ASDAIKGEGL QEGVDWLQDQ IQTVKT

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_23111, frame 3

TREMBL:AF031903_1 gene: "Arl6"; product: "ADP-ribosylation-like factor homolog ARL6"; Mus musculus ADP-ribosylation-like factor homolog ARL6 (Arl6) mRNA, complete cds., N = 1, Score = 923, P = 1.1e-92

TREMBL:CEC38D4_5 gene: "C38D4.8"; Caenorhabditis elegans cosmid C38D4, N = 1, Score = 418, P = 3.6e-39

PIR:S66337 ADP-ribosylation factor 1 - Chlamydomonas reinhardtii, N = 1, Score = 373, P = 2.1e-34

SWISSPROT:ARF1_CHLRE ADP-RIBOSYLATION FACTOR 1., N = 1, Score = 372, P = 2.7e-34

>TREMBL:AF031903_1 gene: "Arl6"; product: "ADP-ribosylation-like factor homolog ARL6"; Mus musculus ADP-ribosylation-like factor homolog ARL6 (Arl6) mRNA, complete cds.
Length = 186

HSPs:

Score = 923 (138.5 bits), Expect = 1.1e-92, P = 1.1e-92
Identities = 178/186 (95%), Positives = 184/186 (98%)

Query: 1 MGLLDRLSVLLGLKKKEVHVLCGLDMSGKTTIINKLKPSNAQSQNIPTIGFSIEKFKS 60
MGLLDRLS LLGLKKKEVHVLCGLDMSGKTTIINKLKPSNAQSQ+I+PTIGFSIEKFKS
Sbjct: 1 MGLLDRLSGLLGLKKKEVHVLCGLDMSGKTTIINKLKPSNAQSQDIVPTIGFSIEKFKS 60

Query: 61 SLSFTVFDMMSGQGRYRNLEWHYYKEGQAIIFVIDSSDRLRMVVAKEELDTLLNHPDIKH 120
SLSFTVFDMMSGQGRYRNLEWHYYK+GQAIIFVIDSSD+LRMVVAKEELDTLLNHPDIKH
Sbjct: 61 SLSFTVFDMMSGQGRYRNLEWHYYKDGQAIIFVIDSSDKLRMVVAKEELDTLLNHPDIKH 120

Query: 121 RRIPILFFANKMDLRDVAVTSVKVSQLLCLENIKDKPWHICASDAIKGEGLOEGVDWLQDQ 180
RRIPILFFANKMDLRD+VTSVKVSQLLCLE+IKDKPWHICASDAIKGEGLOEGVDWLQDQ
Sbjct: 121 RRIPILFFANKMDLRDSVTSVKVSQLLCLESIKDKPWHICASDAIKGEGLOEGVDWLQDQ 180

Query: 181 IQTVKT 186
IQ VKT
Sbjct: 181 IQAVKT 186

Pedant information for DKFZphtes3_23111, frame 3

Report for DKFZphtes3_23111.3

[LENGTH] 186
[MW] 21097.69
[pI] 8.72
[HOMOL] TREMBL:AF031903_1 gene: "Arl6"; product: "ADP-ribosylation-like factor homolog ARL6"; Mus musculus ADP-ribosylation-like factor homolog ARL6 (Arl6) mRNA, complete cds. 4e-94

[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YDL192w] 1e-36
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YDL192w] 1e-36
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL192w] 1e-36
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YDL137w] 2e-36
[FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YBR164c] 2e-32
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YBR164c] 2e-32
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YMR138w] 4e-19
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YMR138w] 4e-19
[FUNCAT] r general function prediction [M. jannaschii, MJ1339] 2e-05
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YHR005c] 4e-05
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YHR005c] 4e-05
[FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YHR005c] 4e-05
[FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YKR014c] 2e-04
[FUNCAT] 08.19 cellular import [S. cerevisiae, YKR014c] 2e-04
[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YKR014c] 2e-04
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL005w] 4e-04
[BLOCKS] BL01288C
[BLOCKS] BL01020C SAR1 family proteins
[BLOCKS] BL01019C ADP-ribosylation factors family proteins

```

[BLOCKS]      BL01019B ADP-ribosylation factors family proteins
[BLOCKS]      BL01019A ADP-ribosylation factors family proteins
[SCOP]        dlas3_2 3.29.1.4.12 Transducin (alpha subunit), insertion domai 2e-45
[SCOP]        dimh1_ 3.29.1.4.2 Rac1 [Human (Homo sapiens) 2e-46
[SCOP]        d5p21_ 3.29.1.4.1 cH-p21 Ras protein [human (Homo sapiens) 5e-37
[SCOP]        dlhura_ 3.29.1.4.8 ADP-ribosylation factor 1 (ARF1) [human (Hom 4e-61
[SCOP]        dla2kc_ 3.29.1.4.5 Ran Nuclear transport factor-2 (NTF2) [Do 4e-33
[PIRKW]       glycoprotein 2e-33
[PIRKW]       monomer 3e-31
[PIRKW]       P-loop 2e-35
[PIRKW]       lipoprotein 2e-33
[PIRKW]       GTP binding 2e-35
[SUPFAM]      ADP-ribosylation factor 2e-35
[PROSITE]     ATP_GTP_A 1
[PFAM]        ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
[KW]          Alpha_Beta
[KW]          3D
[KW]          LOW_COMPLEXITY 5.91 %

```

```

SEQ      MGLLDRLSVLLGLKKKEVHVLCGLDMSGKTTIINKLKPSNAQSONILPTIGFSIEKFKS
SEG      ..xxxxxxxxxxxxx.....
lhurA    .....CCCCEEEEETTTTCHHHHHHHHCCCCEEE--EETTEEEEEEE
SEQ      SLSFTVFDMSGQGRYRNLWEHYYKEGQAIIFVIDSSDRLRMVVAKEELDTLLNHPDIKH
SEG      .....
lhurA    TTEEEEEETTTTTTTCCHHHHHHCEEEEEEEETTTTHHHHHHHHHHHHHHTTT--
SEQ      RRIPILFFANKMDLRDAVTSVKVSQLLCLENIKDKPWHICASDAIKGEGLQEGVDWLQDQ
SEG      .....
lhurA    TTTEEEEEETTTTTTTCCHHHHHHHHCGGGTTTCEEEECBTTTBTTHHHHHHHHHHH
SEQ      IQTVKT
SEG      .....
lhurA    HHHHC.

```

Prosite for DKFZphtes3_23111.3

PS00017 24->32 ATP_GTP_A PDOC00017

Pfam for DKFZphtes3_23111.3

```

HMM_NAME      ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
HMM            *GMgWfsIFrkmWGLWNKEMRILMLGLDNAGKTTILYMLKlgE..IVTTI
               MG++ ++ ++GL +KE+++L LGLDN+GKTTI+++LK+ ++
Query          1 -MGLLDRLSVLLGLKKKEVHVLCGLDMSGKTTIINKLKPSNAQSQNIL 48
HMM            PTIGFNVETVeYKNIKFNVDVGGQdsIRPYWRHYypNTDGIWVVDsAD
               PTIGF +E+ + ++F+V+D GQ + R +W HYY + ++II+V+DS+D
Query          49 PTIGFSIEKFKSSLSFTVFDMSGQGRYRNLWEHYYKEGQAIIFVIDSSD 98
HMM            RDRMeEaKqELHaMLNEEEL..rDAP1LIFANKQDLPGaMSesEIREaLG
               R RM AK+EL+ +LN+ ++ R+ P+L FANK DL+++A+++ +++ +L
Query          99 RLRMVVAKEELDTLLNHPDIKHRRIPILFFANKMDLRDAVTSVKVSQLLC 148
HMM            LHeIRCnRPWYIQMCCAvtGEGLYEGMDWLSNYInkrkK*
               L++I+ + PW+I +++A++GEGl+EG DWL ++I+ K
Query          149 LENIK-DKPWHICASDAIKGEGLQEGVDWLQDQIQTVKT 186

```

DKFZphtes3_23n19

group: testes derived

DKFZphtes3_23n19 encodes a novel 387 amino acid protein with similarity to rat protein kinase C-interacting RBCC protein 1.

The novel protein contains not the RING-B box-coiled coil (RBCC) motif of RBCC protein 1, and thus is not a member of this subgroup of RING finger proteins.
No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to rat protein kinase C-interacting RBCC protein 1

start at Bp 209 matches kozak consensus PyNNatgG
similarity to of C-terminal part to N-terminus of RBCK1

Sequenced by LMU

Locus: unknown

Insert length: 1579 bp
Poly A stretch at pos. 1535, polyadenylation signal at pos. 1515

```
1 CGGAGACCCT CGGGCCGTGT CCATTGTGTG GCAAAGCCAG CGGGGCAGGC
51 TTGGCCAGAG TGCACCACTC GCGGCCGTCC CAGGCCCGAC GCTCTGGGCG
101 CGCCCCGAAC CCCAGGTTTCG CGGCCCGTGT TTCCGACCGG CGGAGGGGGC
151 TCAGCGGCCC GATCCCACGG AAGCGCGCTC GGAGGGGTGG GACCCGGCCG
201 GACCGGAGAT GCGGCCGCCA GCGGGCGGGG CGGCGGCGGC GGCCTCGGAC
251 TTGGGCTCCG CCGCAGTGTCT CTTGGCTGTG CACGCCGCGG TGAGGCCGCT
301 GGGCGCGCGG CCAGACGCGG AGGCACAGCT GCGGAGGCTG CAGCTGAGCG
351 CGGACCCTGA GAGGCCTGGG CGCTTCCGGC TGGAGCTGCT GGGCGCGGGA
401 CCTGGGGCGG TTAATTGGA GTGGCCCTG GAGTCAGTTT CCTACACCAT
451 CCGAGGCCCC ACCCAGCACG AGCTACAGCC TCCACCAGGA GGGCCTGGAA
501 CCCTCAGCCT GCACTTCCTC AACCTCAGG AAGCTCAGCG GTGGGCAGTC
551 CTAGTCCGAG GTGCCACCGT GGAAGGACAG AATGGCAGCA AGAGCAACTC
601 ACCACCAGCC TTGGGCCCAG AAGCATGCCC TGTCTCCCTG CCCAGTCCCC
651 CGGAAGCCTC CACACTCAAG GGCCCTCCAC CTGAGGCAGA TETTCCTAGG
701 AGCCCTGGAA ACTTGACGGA GAGAGAAGAG CTGCCAGGGA GCCTGGCCCG
751 GGCTATTGCA GGTGGAGACG AGAAGGGGGC AGCCCAAGTG GCAGCCGTCC
801 TGGCCAGCA TCGTGTGGCC CTGAGTGTTC AGCTTCAGGA GGCCTGCTTC
851 CCACCTGGCC CCATCAGGCT GCAGGTCACA CTTGAAGACG CTGCCTCTGC
901 CGCATCCGCC GCGTCTCTG CACACGTTGC CCTGCAGGTC CACCCCACT
951 GCACTGTTGC AGCTCTCCAG GAGCAGGTGT TCTCAGAGCT CGGTTCCTCCG
1001 CCAGCCGTGC AACGCTGGGT CATCGGACGG TGCCGTGTGTG TGCCTGAGCG
1051 CAGCCTTGCC TCTTACGGGG TTCGGCAGGA TGGGGACCCT GCTTTCCTCT
1101 ACTTGCTGTC AGCTCCTCGA GAAGCCCCAG CCACAGGACC TAGCCCTCAG
1151 CACCCCCAGA AGATGGACGG GGAACCTGGA CGTTGTTTC CCCCATCATT
1201 GGGGTACCC CCAGGCCCCC AGCCAGCTGC CTCCAGCCTG CCCAGTCCAC
1251 TCCAGCCCCG CTGGTCTGT CTTCTCTGCA CCTTCATCAA TGCCCCAGAC
1301 CGCCCTGGCT GTGAGATGTG TAGCACCCAG AGGCCCTGCA CTTGGGACCC
1351 CCTTGTGCA GCTTCCACCT AGCAGCCACC AGAGGTTACA AGGGGAGAGT
1401 GGCCCTTCCC TCACAAGTCC GACATCTCCA GGCCCCCACT GAACTCCGGG
1451 GACCTCTACT GACTGCTTGC TGGGACAGTC ACCAGGGTTG GGGGGAAGGG
1501 CCACAAAATG AAACCATTAA AGACCCTTAA GAGCCAAAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAAAAAA AAAAAAAG
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 209 bp to 1369 bp; peptide length: 387

1	MAPPAGGAAA	AASDLGSAAV	LLAVHAAVRP	LGAGPDAAEQ	LRRLQLSADP
51	ERPGRFRLEL	LGAGVPAVNL	EWPLESVSYT	IRGTQHEQL	PPPGPGPTLS
101	LHFLNPQEAQ	RWAVLVRGAT	VEQGQSKSN	SPPALGPEAC	PVSLSPPEEA
151	STLKGPPPEA	DLPSPFNGIT	EREELAGSLA	RAIAGGDEKG	AAQVAAVLAQ
201	HRVALSVQLQ	ACEFFPGPIR	LQVTLEDAAS	AAAASSAAHV	ALQVPHCTV
251	AALEQGVFSE	LGFFPAVQRW	VIGRCLCVPE	RSLSYGVQR	DGDPVFLYLL
301	SAPREAPATF	PSQPHQKQMD	GLGRLFLPPS	LGLPFGQPPA	ASSLPSFLQP
351	SWSCPSTCI	NAPDRPGECM	GSTORPCTWD	PLAAAST	

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3 23n19, frame 2

PIR:JC5983 protein kinase C-interacting RBCC protein 1 - rat, N = 1,
Score = 353, P = 2.8e-32

TREMBL:AB011369.1 product: "RBCK2"; Rattus norvegicus mRNA for RBCK2, complete cds., $\bar{N} = 1$, Score = 353, $P = 2.8e-32$

TREMBL:U67322_1 gene: "XAP4"; product: "HBV associated factor"; Human
HBV associated factor (XAP4) mRNA, complete cds., N = 1, Score = 286, P
= 8.5e-25

TREMBLNEW:AF124663_1 product: "UbcM4 interacting protein 28"; Mus musculus UbcM4 interacting protein 28 mRNA, complete cds., N = 1, Score = 367, P = 9.3e-34

>TREMBLNEW:AF124663_1 product: "UbcM4 interacting protein 28"; Mus musculus
UbcM4 interacting protein 28 mRNA, complete cds.
Length = 498

HSPs :

Score = 367 (55.1 bits), Expect = 9.3e-34, P = 9.3e-34
Identities = 95/212 (44%), Positives = 129/212 (60%)

Query: 175 LAGSLARAIAGGDEKGAAQVAVLAQHRVALSVQLQEACFPFGPIRLQVLTLEDAASAASA 234
+A SLARA+AGGDE+ A + A LA+ RV LV VQ++ P IRL V++EDA
Sbjct: 1 MALSLARAVAGGDEQAIAIKYATWLARQVRVQVKPEVSTQDILRLCVSEDAYM---- 56

Query: 235 ASSAHVALQVHPCHTVAALQEQVFSELGFPPAVQRWVIGRCLCVPERSLASYGVRQDGD 294
+ + + L V P TVA+L+ + VF + GFPP+Q+WV+G+ L + +L S+G+R+G+D
Sbjct: 57 -HTVTIWLTVPRDMTVASLKDVFVFLDYGFPSPSLOOWVVGARLARDQETLHSHGIRRRNGD 115

```
Query:      295 AFYLLLSAPREAPATGSPSPQHPQK-----MDGELG--RLFPPSSLG-LPPG-PQPAASSSLP 345
            A+LYLLSA      T +PQ Q+      M +LG L S GL P P+P + P
Sbjct:     116 AYLYLLSARN----TSLNPQLQQQRQRLMEDLGKFDKLDTLOSRGLEPVLPPKPRTNOEP 171
```

Query: 346 -----SPLQP--SWSCPSCTFINAPDRPGCEMCSTQRPCTW 379
+P P W CP CTFIN P RPGCEMC RP T+
Sbjct: 172 QPDAAAPESPPVGWQCPGCTFINKPTRPGCEMCRRARPETY 212

Pedant information for DKFZphtes3 23n19, frame 2

Report for DKFZphtes3 23n19.2

```
[LENGTH]      387
[MW]           39949.29
[pI]           5.53
[HOMOL]        TREMBLNEW:AF124663_1 product: "UbcM4 interacting protein 28"; Mus musculus
UbcM4 interacting protein 28 mRNA, complete cds. 1e-22
[BLOCKS]       BL00578B
[KW]           Alpha_Beta
[KW]           LOW COMPLEXITY      17.57 %
```

```
SEQ      MAPPAGGAAAAASDLGSAAVLLAVHAAVRPLGAGPDAEAQLRRLQLSADPERPGRFRLEL  
          .XXXXXXXXXXXXXXXXXXXXXXXXXXXXX  
PRD      ccccccchhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhccccccccceeee
```



```
SEQ    LGAGPGAVNLEWPLESVSYTIRGPTQHELQPPPGGPGTSLHFLNPQEAQRWAVLVRGAT
SEG    .....
PRD    cccccceeeccccceeeccccccccccccccccccccccccccccccccccccchhhhhheeeecce

SEQ    VEGQNGSKSNSPPALGPEACPVSLPSPEASTLKGPPEADLPRSPGNLTEREELAGSLA
SEG    .....
PRD    eccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhh

SEQ    RAIAGGDEKGAAQVAAVLAQHRVALSVQLQEACFPFGPIRLQVTLDAASAASAASSAHV
SEG    .....xxxxxxxxxxxxx...
PRD    hhhhhcccchhhhhhhhhhhhhhhhhhhccccccccccccccccccccchhhhhhhhhhhheee

SEQ    ALQVHPHCTVAALQEQVFSELGFPFPAVQRWVIGRCLCVPERSLASYGVRQDGPFLYLL
SEG    .....
PRD    eeeccccchhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhccccccccccccccccceeeec

SEQ    SAPREAPATGSPSPQHPQKMDGELGRLFPFSLGLPPGPQPAASSLPSPLQPSWSCPSCTFI
SEG    .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx...
PRD    cccccccccchhhhhhhhhhhhhhhhhhhccccccccccccccccccccccccccccccccccccceee

SEQ    NAPDRPGCEMCSTQRPCTWDPLAAAST
SEG    .....
PRD    cccccccccccccccccccccccccccccceeeccc
```

(No Prosite data available for DKFZphtes3_23n19.2)

(No Pfam data available for DKFZphtes3_23n19.2)

similarity to rat protein kinase C-interacting RBCC protein 1

start at Bp 209 matches kozak consensus PyNNatgG

similarity to of C-terminal part to N-terminus of RBCK1

Sequenced by LMU

Locus: unknown

Insert length: 1579 bp

Poly A stretch at pos. 1535, polyadenylation signal at pos. 1515

```
1 CGGAGACCCT CGGGCCGTGT CCATTGTGG GCAAAGCCAG CGGGGCAGGC
51 TTGGCCAGAG TGCACCACTC GGCGCCGTCC CAGGCCCGAC GCTCTGGGCG
101 CGCCCCGAAC CCCAGGTTCG CGGCCCGTGT TTCCGACCAG CGGAGGGGGC
151 TCAGCGGCCC GATCCCACGG AAGCGCGCTC GGAGGGGTGG GACCCGGCCG
201 GACCGGAGAT GCGCGCCGCA GCGGGCGGGG CGGCGCGGCG GCCTTCGGAC
251 TTGGGCTCCG CCGCAGTGCT CTGGGCTGTG CACGCCGCGG TGAGGCCGCT
301 GGGCGCCGGG CCAGACGCGG AGGCACAGCT GCGGAGGCTG CAGCTGAGCG
351 CGGACCCCTGA GAGGCTGGG CGCTTCCGCG TGGAGCTGCT GGGCGCGGGA
401 CCTGGGGCGG TTAATTGGA GTGGCCCTCG GAGTCAGTTT CCTACACCAT
451 CCGAGGCCCC ACCAGCAGCG AGCTACAGCC TCCACCAGGA GGGCCTGGAA
501 CCCTCAGCCT GCACTTCCTC AACCCTCAGG AAGCTCAGCG GTGGGCAGTC
551 CTAGTCCGAG GTGCCACCGT GGAAGGACAG AATGGCAGCA AGAGCAACTC
601 ACCACCAGCC TTGGGCCCAG AAGCATGCCC TGCTCCCTG CCCAGTCCCC
651 CGGAAGCCTC CACACTCAAG GGCCCTCCAC CTGAGGCAGA TCTTCTAGG
701 AGCCCTGGAA ACTTGACGGA GAGAGAAGAG CTGGCAGGGA GCCTGGCCCG
751 GGCTATTGCA GGTGGAGACG AGAAGGGGGC AGCCCAAGTG GCAGCCGTCC
801 TGGCCAGCA TCGTGTGGCC CTGAGTGTTT AGCTTCAGGA GGCCTGTCTC
851 CCACCTGGCC CCATCAGGCT GCAGGTCACA CTGAAGACG CTGCCTCTGC
901 CGCATCCGCG GCGTCTCTG CACACGTTGC CCTGCAGGTC CACCCCACT
951 GCACTGTGTC AGCTCTCCAG GAGCAGGTGT TCTCAGAGCT CGGTTTCCCG
1001 CCAGCCGTGC AACGCTGGGT CATCGGACGG TGCTGTGTG TGCTGTAGCG
1051 CAGCCTTGCC TCTTACGGGG TTCGGCAGGA TGGGACCCT GCTTCTCTCT
1101 ACTTGCTGTC AGCTCTCGA GAAGCCCAG CCACAGGACC TAGCCCTCAG
1151 CACCCCAAGA AGATGGACGG GGAACCTGGA CGCTTGTTC CCCCATCATT
1201 GGGGCTACCC CCAGGCCCCC AGCCAGCTGC CTCCAGCCTG CCCAGTCCAC
1251 TCCAGCCAGC CTGGTCTGT CTTCTCTGCA CTTTCATCAA TGCCCCAGAC
1301 CGCCTTGGCT GTGAGATGTG TAGCACCAG AGGCCCTGCA CTGGGACCC
1351 CTTGTCTGCA GCTTCCACCT AGCAGCCACC AGAGGTTACA AGGGGAGAGT
1401 GGCCCTTCCC TCACAAGTCC GACATCTCCA GGCCCCACT GAACTCCGGG
1451 GACCTTACT GACTGCTTGC TGGGACAGTC ACCAGGGTTG GGGGGAAGGG
1501 CCACAAAATG AAACCATTA AGACCCTTA GAGCCAAAAA AAAAAAAAAG
1551 AAAAAAAAAG AAAAAAAAAG AAAAAAAG
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 209 bp to 1369 bp; peptide length: 387
 Category: similarity to known protein
 Classification: Cell signaling/communication

```

1 MAPPAGGAAA AASDLGSAV LLAVHAAVRP LGAGPDAEAQ LRLQLSADP
51 ERPGFRFRLEL LGAGPGAVNL EWPLESVSYT IRGPTQHELQ PPPGGPGTSL
101 LHFLNPQEAQ RWAVLVRGAT VEGQNGSKSN SPPALGPEAC PVSLLSPPEA
151 STLKGPPEA DLPRSPGNLT EREELAGSLA RAIAGGDEKG AAQVAAVLAQ
201 HRVALSVQLQ EACFPFGPIR LQVTLEDAAS AASAASSAHV ALQVHPHCTV
251 AALQEQQVFE LGFPPAVQRW VIGRCLCVPE RSLASYGVRQ DGDPAFLYLL
301 SAPREAPATG PSPQHPQKMD GELGRLFPFS LGLPPGPQPA ASSLPSPLPQ
351 SWSCPSCFTI NAPDRPGCEM CSTQRPCTWD PLAAAST

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_23n19, frame 2

PIR:JC5983 protein kinase C-interacting RBCC protein 1 - rat, N = 1,
 Score = 353, P = 2.8e-32

TREMBL:AB011369_1 product: "RBCK2"; Rattus norvegicus mRNA for RBCK2,
 complete cds., N = 1, Score = 353, P = 2.8e-32

TREMBL:U67322_1 gene: "XAP4"; product: "HBV associated factor"; Human
 HBV associated factor (XAP4) mRNA, complete cds., N = 1, Score = 286, P
 = 8.5e-25

TREMBLNEW:AF124663_1 product: "UbcM4 interacting protein 28"; Mus
 musculus UbcM4 interacting protein 28 mRNA, complete cds., N = 1, Score
 = 367, P = 9.3e-34

>TREMBLNEW:AF124663_1 product: "UbcM4 interacting protein 28"; Mus musculus
 UbcM4 interacting protein 28 mRNA, complete cds.
 Length = 498

HSPs:

Score = 367 (55.1 bits), Expect = 9.3e-34, P = 9.3e-34
 Identities = 95/212 (44%), Positives = 129/212 (60%)

```

Query:   175 LAGSLARAIAGGDEKGAAQVAAVLAQHRVALSVQLQEACFPFGPIRLQVTLEDAASAASA 234
          +A SLARA+AGGDE+ A + A LA+ RV L VQ++ P IRL V++EDA
Sbjct:   1 MALSLARAVAGGDEQAATKYATWLAEQRVPLRVQVKPEVSPTQDIRLCVSVEDAYM---- 56

Query:   235 ASSAHVALQVHPHCTVAALQEQQVSELGFPPAVQRWVIGRCLCVPERSLASYGVRQDGDG 294
          + + L V P TVA+L++ VF + GFPP++Q+VV+G+ L + +L S+G+R++GD
Sbjct:   57 -HTVTIWLTVRPDMTVASLKMVFLDYGFPPSLQQWVVGQRLARDQETLHSHGIRNRNGD 115

Query:   295 AFLYLLSAPREAPATGSPSPQHPQK-----MDGELG--RLFPFSLG-LPPG-PQPAASSLP 345
          A+LYLLSA T +PQ Q+ M +LG L S G L P P+P + P
Sbjct:   116 AYLYLLSARN----TSLNPQELQRQRQLRMLEDLGFKDLTLSRGPLEPVLPKPRTNQEP 171

Query:   346 -----SPLQP--SWSCPSCFTFINAPDRPGCEMCSTQRPCTW 379
          +P P W CP CTFIN P RPGCEMC RP T+
Sbjct:   172 GQPDAAPESPVPVWQCPCGCTFINKPTRPGCEMCCRARPETY 212

```

Pedant information for DKFZphtes3_23n19, frame 2

```
[LENGTH]          387
[MW]               39949.29
[pI]               5.53
[HOMOL]            TREMBLNEW:AF124663_1 product: "UbcM4 interacting protein 28"; Mus musculus
UbcM4 interacting protein 28 mRNA, complete cds. 1e-22
[BLOCKS]           BLO0578B
[KW]               Alpha_Beta
[KW]               LOW COMPLEXITY      17.57 %
```

(No Pfam data available for DKF2phtes3 23n19.2)

DKFZphtes3_26g22

group: intracellular transport/trafficking

DKFZphtes3_26g22 encodes a novel 898 amino acid protein with similarity to kinesins.

The novel protein contains a ATP/GTP-binding site motif A (P-loop) and a kinesin motor domain signature. Kinesin is a microtubule-associated force-producing protein that play a role in organelle transport. It is an oligomeric complex composed of two heavy chains and two light chains. The kinesin motor activity is directed toward the microtubule's plus end. The heavy chain contains a large globular N-terminal domain which is responsible for the motor activity of kinesin, which is known to hydrolyze ATP and to bind and move on microtubules. Several proteins involved in chromosome segregation and cell division contain this motor domain, such as drosophila claret segregational protein (ncd), Drosophila kinesin-like protein (nod), human CENP-E and human mitotic kinesin-like protein-1 (MKLP-1). The novel protein is a new kinesin like propein.

The new protein can find application in modulating chromosome transport in mitosis and meiosis and modulation of cell division.

strong similarity to kinesins

Sequenced by EMBL

Locus: unknown

Insert length: 3032 bp

No poly A stretch found, no polyadenylation signal found

```
1 CTGAAGCGCT GGGAGGCGGA CATTAAAGTG AAGTGGTTGC GGTAACCTGG
51 CCTGGGCCCTG AAGTGAGTGA GAGGCACATG AAGAGAAGTA TTCAAGTATT
101 TATACAGATA GGAATCAAGA TAATCAACAA TGCTGTCTAC TGAGGAAGAC
151 CTGTGCCACC ATATGAAAGT AGTAGTTCGT GTACGTCCGG AAAACACTAA
201 AGAAAAAGCA GCTGGATTTC ATAAAGTGGT TCATGTTGTG GATAAACATA
251 TCCFAGTTTT TGATCCCAA CAAGAAGAAG TCAGTTTTTI CCATGGAAAG
301 AAAACTACAA ATCAAAATGT TATAAAGAAA CAAAATAAGG ATCTTAAATT
351 TGTATTTGAT GCTGTTTTTG ATGAAACGTC AACTCAGTCA GAAGTTTTTG
401 AACACACTAC TAAGCCAATT CTTCGTAGTT TTTTGAATGG ATATAATTGC
451 ACAGTACTTG CCTATGGTGC CACTGGTGCT GGGGAAGACCC ACACTATGCT
501 AGGATCAGCT GATGAACCTG GAGTGATGTA TCTAACAATG TTACACCTTT
551 ACAATGTCAT GGATGAGATT AAAGAAGAGA AAATATGTAG TACTGCAGTT
601 TCATATCTGG AGGTATATAA TGAACAGATT CGTGATCTCT TAGTAAATTC
651 AGGGCCCACTT GCTGTCCGGG AAGATACCCA AAAAGGGGTG GTCGTTTCATG
701 GACTTACTTT ACACCAGCCC AAATCCTCAG AAGAAATTTT ACATTTATTG
751 GATAATGGAA ACAAAACAG GACACAACAT CCCACTGATA TGAATGCCAC
801 ATCTTCTCGT TCTCATGCTG TTTTCCAAAT TTACTTGGCA CAACAAGACA
851 AAACAGCAAG TATCAATCAA AATGTCCGTA TTGCCAAGAT GTCACCTATT
901 GACCTGGCAG GATCTGAGCG AGCAAGTACT TCCGGTGCTA AGGGGACCGG
951 ATTTGTAGAA GGCACAAATA TTAATAGATC ACTTTTAGCT CTTGGGAATG
1001 TCATCAATGC CTTAGCAGAT TCAAGAGAAA AGAATCAGCA TATCCCTTAC
1051 AGAAATAGTA AGCTTACTCG CTTGTAAAG GATTCTCTTG GAGGAAACTG
1101 TCAAACATAA ATGATAGCTG CTGTTAGTCC TTCTCTGTA TTCTACGATG
1151 ACACATATAA CACTCTTAAG TATGCTAACC GGGCAAAGGA CATTAATCTT
1201 TCTTTSAAGA GCAATGTTCT TAATGTCAAT AATCATATAA TCATATATGT
1251 AAAGATCTGT AATGAGCAGA AGGCAGAGAT TTTATTGTTA AAAGAAAAAC
1301 TAAAGCCTTA TGAAGAACAG AAAGCCTTCA CTAATGAAAA TGACCAAGCA
1351 AAGTTAATGA TTTCAAACCC TCAGGAAAAA GAAATCGAAA GGTTCGAAGA
1401 AATCCTGAAC TGCTTGTTCC AGAATCGAGA AGAAATTAGA CAAGAATATC
1451 TGAAGTTGGA AATGTTACTT AAAGAAAATG AACTTAAATC ATTCTACCAA
1501 CACAGTGCC ATAAACAAAT AGAAATGATG TGTCTGAAG ACAAGTAGA
1551 AAAGGCCACT GGAAACGAG ATCATAGACT TGCAATGTTG AAAACTCGTC
1601 GCTCCTACCT GGAGAAAAGG AGGGAGGAGG AATTGAAGCA ATTTGATGAG
1651 AATACTAATT GGTCCATCG TGTCGAAAAA GAAATGGGAC TCTTAAGTCA
1701 AAACGGTCAAT ATTCCAAAGG AACTCAAGAA AGATCTTCAT TGTACCATT
1751 TGCACCTCCA GAACAAAGAT TTGAAAGCAC AAATTAGACA TATGATGGAT
1801 CTAGCTTGTG TCTCAGGAACA GCAACACAGG CAGACTGAAG CAGTATTGAA
1851 TGCTTTACTT CCAACCCTAA GAAACAAATA TTGCACATTA AAAGAAGCCG
1901 GCCTGTCAAA TGCTGCTTTT GAATCTGACT TCAAAGAGAT CGAACATTTG
1951 GTAGAGAGTA AAAAAGTGGT AGTTTGGGCT GACCAAACCT CCGAACAAAC
2001 AAAGCAAAAC GATCTACCAG GGATTCTGT TCTTATGACC TTTCCACAAC
2051 TTGGACCAGT TCAGCCTATT CCTTGTTCCT CATCTTCAGG TCGAACTAAT
2101 CTGGTTAAGA TTCTTACAGA AAAAAGAACT CGGAGAAAAA TAATGCCATC
2151 TCCTTGAAA GGACAGCATA CTCTAAAGTC TCCACCATCT CAAAGTGTGC
2201 AGCTCAATGA TTCTCTTAGC AAAGAACTTC AGCCTATTGT ATATACACCA
2251 GAAGACTGTA GAAAAGCTTT TCAAAATCCG TCTACAGTAA CCTTAATGAA
2301 ACCATCATCA TTTACTACAA GTTTTCAGGC TATCAGCTCA AACATAAACA
2351 GTGATAATTG TCTGAAAATG TTGTGTGAAG TAGCTATCCC TCATAATAGA
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2401 AGAAAAGAAT GTGGACAGGA GGAAGTGGAC TCTACATTTA CTATATGTGA
2451 AGACATCAAG AGCTCGAAGT GTAAATTACC CGAACAAGAA TCACTACCAA
2501 ATGATAACAA AGACATTTTA CAACGGCTTG ATCCTTCTTC ATTCTCAACT
2551 AAGCATTCTA TGCCTGTACC AAGCATGGTG CCATCCTACA TGGCAATGAC
2601 TACTGCTGCC AAAAGGAAAC GGAAATTAAC AAGTCTTACA TCAAACAGTT
2651 CGTTAACTGC AGACGTAAAT TCTGGATTG CCAAACGTGT TCGACAAGAT
2701 AATTCAAGTG AGAAGCACTT ACAAGAAAAC AAACCAACAA TGGAACATAA
2751 AAGAAACATC TGTAATAATA ATCCAAGCAT GGTTAGAAAA TTTGGAAGAA
2801 ATATTTCAAA AGGAAATCTA AGATAAATCA CTTCAAAACC AAGCAAAATG
2851 AAGTTGATCA AATCTGCTTT TCAAAGTTTA TCAATACCCT TTCAAAAATA
2901 TATTTAAAT CTTTGAAAGA AGACCCATCT TAAAGCTAAG TTTACCCAAG
2951 TACTTTGAGC AAGCAGAAAA ATGAAACTCT TTGTTTCTT CTTTGTGTT
3001 CTAAAAAAT AAAATTTCAA AAGAAAAAAA AA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 130 bp to 2823 bp; peptide length: 898
 Category: strong similarity to known protein
 Classification: Cell structure/motility
 Prosite motifs: ATP_GTP_A (113-121)
 KINESIN_MOTOR_DOMAIN1 (252-264)

```

1 MSVTEEDLCH HMKVVVRVRP ENTKEKAAGF HKVVHVVDKH ILVFDPKQEE
51 VSFHGKKT NQNVIKKQNK DLKFVFDVAV DETSTQSEVF EHTTKPILRS
101 FLNGYNTVL AYGATGAGKT HTMLGSADEP GVMYLTMLHL YKCMDEIKKE
151 KICSTAVSYL EVYNEQIRDL LVNSGPLAVR EDTQKCVVH GLTLHQPSS
201 EELHLLDNG NKNRTQHPTD MNATSSRSHA VFQIYLRQD KTASINQNV
251 IAKMSLIDLA GSERASTSGA KGTRFVEGTN INRSLALGN VINALADSKR
301 KNQHIPPYRN KLTRLKDSL GGNCQTIMIA AVSPSSVFYD DTYNLKYAN
351 RAKDIKSSLK SNVLNVNNHI TOYVKICNEQ KAEILLKKEK LKAYEEOKAF
401 TNENDQAKLM ISNPQKEIE RFQEIILNCLF QNREEIRQY LKLEMLLKEN
451 ELKSIFYQQQC HKQIEMMCSE DKVEKATGKR DHRLAMLKTR RSYLEKRREE
501 ELKQFDENTN WLHRVEKEMG LLSQNGHIPK ELKKDLHCHH LHLQNKDLKA
551 QIRHMDLAC LQEQHROTE AVLNALLPTL RKQYCTLKEA GLSNAAFESD
601 FKEIEHLVER KVVVWADQT AEQPKQNDLP GISVLMTFPQ LGPVQPIPC
651 SSSGGTNLVK IPTEKTRRK LMPSPKGGH TLKSPPSQSV QLNDLSKEL
701 QPIVYTPEDC RKAQNPSTV TLMKPSSTF SFOAISSNIN SDNCLKMLE
751 VAIPHNRKE CGQEDLDSTF TICEDIKSSK CKLPEQESLP NDNKDILQRL
801 DPSSFSTKHS MPVPSMPSY MAMTTAAKRK RKLTSSTNS SLTADVNSGF
851 AKRVRQDNSS EKHLQENKPT MEHKNICKI NPSMVRKFR NISKGNLR

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_26g22, frame 1

SWISSPROT:YB3D_SCHPO PUTATIVE KINESIN-LIKE PROTEIN C2F12.13., N = 3,
 Score = 874, P = 9e-93

TREMBL:DMU89264_1 product: "kinesin like protein 67a"; Drosophila
 melanogaster kinesin like protein 67a mRNA, complete cds., N = 1, Score
 = 880, P = 4.2e-88

TREMBL:SPBC649_1 gene: "SPBC649.01c"; product: "putative kinesin-like
 protein"; S.pombe chromosome II cosmid c649., N = 3, Score = 814, P =
 9.8e-86

PIR:S64238 kinesin-related protein KIP3 - yeast (Saccharomyces
 cerevisiae), N = 2, Score = 802, P = 2.5e-83

>TREMBL:DMU89264_1 product: "kinesin like protein 67a"; Drosophila

melanogaster kinesin like protein 67a mRNA, complete cds.
Length = 814

HSPs:

Score = 880 (132.0 bits), Expect = 4.2e-88, P = 4.2e-88
Identities = 181/345 (52%), Positives = 238/345 (68%)

Query: 11 HMKVVVRVRPENTKEKAAGFHKKVVHVVDKHLVFDPKQEEVSFF-HGKKTTNQNVIKKQN 69
++KV VRVRP N +E ++ V+D+ L+FDP +E+ FF G K +++ K+ N
Sbjct: 8 NIKVAVRVRPYNVRELEQKORSIIKVMDSALLFDPDEEDDEFFQGAQKQPYRDITKRMN 67

Query: 70 KDLKFVFDVAFDETSTQSEVFEHTTKPILRSFLNGYNCTVLAYGATGAGKTHMLGSADE 129
K L FD VFD ++ ++FE T P++ + LNGYNC+V YGATGAGKT TMLGS
Sbjct: 68 KKLTMEFDRVFDIDNSNQDLFEECTAPLVDVAVLNGYNCVSVFYGATGAGKTFTMLGSEAH 127

Query: 130 PGVMYLTMLHLYKCMDEIKEEKICSTAVSYLEVYNEQIRDLLVNSGPLAVREDTQKGVVV 189
PG+ YLTM L+ + + + VSYLEVYNE + +LL SGPL +RED GVVV
Sbjct: 128 PGLTYLTMQDLFDKIQAQSDVRKFDVGVSYLEVYNEHVMNLLTKSGPLKLRDNN-GVVV 186

Query: 190 HGLTLHQPKSSEEILHLLDNGNKNRTOHPTDMNATSSRSHAVFQIYLRQQDKTASINQNV 249
GL L S+EE+L +L GN +RTQHPTD NA SSRSAH+FQ+++R ++ + V
Sbjct: 187 SGCLCTPIYSAEELLRLMLGNSHRTQHPTDANAESSRSAHFQVHIRITERKTDTRKRTV 246

Query: 250 RIAKMSLIDLAGSERASTSGAKGTRFVEGTNINRSLALGNVINALADSKRKNQHIPPYRN 309
K+S+IDLAGSERA+++ G RF EG +IN+SLLALGN IN LAD + HIPYR+
Sbjct: 247 ---KLSMIDLAGSERAASATKGIGVRFEGASINKSLLALGNCINKLADGLK---HIPYRD 300

Query: 310 SKLTRLLKDSLGGNCQTIMIAAVSPSSVFYDDTYNTLKYANRAKDI 355
S LTR+LKDSLGGNC+T+M+A VS SS+ Y+DTYNTLKYA+RAK I
Sbjct: 301 SNLTRILKDSLGGNCRTLMVANVSMSSLTIEDTYNTLKYASRAKKI 346

Pedant information for DKFZphtes3_26g22, frame 1

Report for DKFZphtes3_26g22.1

[LENGTH] 898
[MW] 102281.63
[pI] 9.09
[HOMOL] SWISSPROT:YB3D_SCHPO PUTATIVE KINESIN-LIKE PROTEIN C2F12.13. 3e-97
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YGL216w] 2e-88
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YGL216w] 2e-88
[FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YGL216w] 2e-88
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YGL216w] 2e-88
[FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YPR141c] 5e-42
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR141c] 5e-42
[FUNCAT] 03.13 meiosis [S. cerevisiae, YPR141c] 5e-42
[FUNCAT] 11.01 stress response [S. cerevisiae, YPR141c] 5e-42
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YPR141c] 5e-42
[FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YPR141c] 5e-42
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YKL079w] 4e-28
[BLOCKS] BL00411H
[BLOCKS] BL00411G
[BLOCKS] BL00411F
[BLOCKS] BL00411E Kinesin motor domain proteins
[BLOCKS] BL00411C Kinesin motor domain proteins
[BLOCKS] BL00411B Kinesin motor domain proteins
[BLOCKS] BL00411A Kinesin motor domain proteins
[SCOP] d2kin.1 3.29.1.5.3 Kinesin [Rat (Rattus norvegicus) 1e-117
[SCOP] d3kar_ 3.29.1.5.4 Kinesin [Baker's yeast (Saccharomyce 1e-112
[PIRKW] nucleus 6e-87
[PIRKW] heterodimer 4e-68
[PIRKW] DNA binding 9e-60
[PIRKW] heterotetramer 2e-54
[PIRKW] mitosis 9e-60
[PIRKW] microtubule binding 4e-68
[PIRKW] ATP 6e-87
[PIRKW] phosphoprotein 5e-59
[PIRKW] heterotrimer 4e-68
[PIRKW] purine nucleotide binding 1e-26
[PIRKW] P-loop 6e-87
[PIRKW] coiled coil 4e-68
[PIRKW] heptad repeat 3e-62
[PIRKW] methylated amino acid 2e-54
[PIRKW] hydrolase 2e-54
[PIRKW] GTP binding 1e-60

[PIRKW] cell division 5e-57
 [SUPFAM] kinesin-related protein KIP1 3e-50
 [SUPFAM] kinesin-related protein CIN8 7e-33
 [SUPFAM] kinesin heavy chain 2e-54
 [SUPFAM] suppressor protein SMY1 1e-26
 [SUPFAM] kinesin-related protein KIF3 4e-68
 [SUPFAM] kinesin-related protein KIF2 1e-46
 [SUPFAM] kinesin-related protein unc-104 7e-60
 [SUPFAM] unassigned kinesin-related proteins 6e-87
 [SUPFAM] centromere protein E 3e-54
 [SUPFAM] kinesin-related protein KLP61F 5e-57
 [SUPFAM] kinesin-related protein MKLP-1 2e-28
 [SUPFAM] pleckstrin repeat homology 7e-60
 [SUPFAM] kinesin-related protein KIF1B 4e-61
 [SUPFAM] kinesin motor domain homology 6e-87
 [SUPFAM] kinesin-related protein KLPA 1e-43
 [SUPFAM] kinesin-related protein nodA 1e-30
 [SUPFAM] kinesin-related protein Eg5 5e-59
 [PROSITE] ATP_GTP_A 1
 [PROSITE] KINESIN_MOTOR_DOMAIN1 1
 [PFAM] Kinesin motor domain
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 8.57 %

SEQ MSVTEEDLCHHMKVVVRPENTKEKAAGFHKVVHVVDKHLVFDPKQEEVSFFHGKKT
 SEG
 3kar-TBEEE

 SEQ NQNVIKKQNKDLKFVDFDAVFDETSTQSEVFEHTTKPILRSFLNGYNCTVLAYGATGAGKT
 SEG
 3kar- EEEETTTTTTEEEEEETETTTTCHHHHHHHHHH-HHHGGGGCCCCEEEEECTTTTCHH

 SEQ HTMLGSADPEGVMYLTMLHLYKCMDEIKEEKICSTAVSYLEVYNEQIRDLLVNSGPLAVR
 SEG
 3kar- HHHHTTTT--THHHHHHHHHHHHHHHGGGCEEEEEEEEEETTEEEETT-TCCCCCEE

 SEQ EDTQKGVVHGLTLHQPKSSEELHLLDNGNKNRTQHPDMDNATSSRSHAVFQIYLRQQD
 SEG
 3kar- EETTTEEEETTCCCEEECCGGHHHHHHHHHHHCCTTTTCHHHHHHCCEEEEEEEEEEE

 SEQ KTASINQNVRIAKMSLIDLAGSERASTSGAKGTRFVEGTNINRSLLAGNVINALADSKR
 SEG
 3kar- TTTTCEE---EEEEEEECCECCCCCCC---HHHHHHHHHHHHHHHHHHHHHHHTTTT

 SEQ KNQHI PYRNSKLTRLKDSLGCNCQTIMIAAVSPSSVFYDDTYNTLKYANRAKDIKSSLK
 SEG
 3kar- TTTCTTTTTHHHHHHGGGCTTTTEEEEEEECCCGGGHHHHHHHHHHHH.....xxxxx

 SEQ SNVLNVNNHITQYVKICNEQAEILLLEKLKAYEEQKFTNENDQAKLMISNPQEKIE
 SEG xxxxxxxx.....xxxxxxxxxxxxxxxxxxxxxxxx.....
 3kar-

 SEQ RFQEILNCLFQNRREEIRQEYLKLEMLKENELKSFYQQQCHKQIEMMCSEDKVEKATGKR
 SEG
 3kar-xxxxxx

 SEQ DHRLAMLKTRRSYLEKRREEELKQFDENTNWLHRVEKEMGLLSQNGHIPKELKKDLHCHH
 SEG
 3kar-xxxxxx

 SEQ LHLQNKDLKAQIRHMDLACLQEQHRQTEAVLNALLPTLRKQYCTLKEAGLSNAAFESD
 SEG xxx.....
 3kar-

 SEQ FKEIEHLVERKKVVWADQTAEQPKQNDLPGISVLMTFPQLGPVQPI PCCSSSGGTNLVK
 SEG
 3kar-

 SEQ IPTEKRTRRKLMPFSLKGQHTLKSPPSQSVQLNDSLKELQPIVYTPEDCRKAFQNPSTV
 SEG
 3kar-

 SEQ TLMKPSSFTTSFQAISNINSNCLKMLCEVAIPHNRKCEQGEDLDSTFTICEDIKSSK
 SEG
 3kar-

 SEQ CKLPEQESLPNDNKDILQRLDPSSFSTKHSMPVPSMVPSYAMTTAAKRKRKLTSSSTSNS
 SEG
 3kar-xxxxxx

SEQ SLTADVNSGFAKRVQRQDNSSEKHLQENKPTMEHKRNICKINPSMVRKFGRNISKGNLR
 SEG xxx.....
 3kar-

Prosite for DKFZphtes3_26g22.1

PS00017 113->121 ATP_GTP_A PDOC00017
 PS00411 252->264 KINESIN_MOTOR_DOMAIN1 PDOC00343

Pfam for DKFZphtes3_26g22.1

HMM_NAME Kinesin motor domain

HMM *RCRPLNeREindgcscvVQWpPwtGyktvhnghegds.....
 R+RP N +E+++G +VV + + + + +E S

Query 17 RVRPENTKEKAAGFHKVHVVD-KHILVFDPKQEEVSFFHGKKTNNQNV 64

HMMphksFtFDHVFwWncTQedVYdtvAHPIVDDcFhGYNCTIFAYGQ
 + F+FD VF+ ++TQ +V++ + PI+ +++GYNCT++AYG

Query 65 IKKQNKDLKFVFDVAFDETSTQSEVFHTTKPILRSLNGYNCTVLAYGA 114

HMM TGSgKTYTMMGpggehPDHmGIIPRCCHDIFdrIdkfgekDhdFWHvkCS
 TG+GKT+TM G + D+ G+ + +++++ D + + + +S

Query 115 TGAGKTHTMLG---SADEPGVMYLTMLHLYKCMDEIK-EEKIC-STAVS 158

HMM YMEIYNeeIYDLLCPnPqhMkpLnIHEHPNMGpYVqGCTEfHVcSYeDac
 Y+E+YNE+I+DLL+ N ++PL+++E+ G+ V G+T+ +S E+++

Query 159 YLEVYNEQIRDLLV-N---SGPLAVREDTQKGVVHGLTLHQPKSSEEIL 204

HMM hWIWqGnknRHVAaTnMndhSSRShtIFTIHVeQrHk..qcdehvcHskM
 H+++ GNKNR+ +T MN++SSRSH++F+I ++Q K + V++ KM

Query 205 HLLDNGNKNRTQHPDMMNATSSRSHAVFQIYLRQDKTASINQNVRIAKM 254

HMM NLVDLAGSERvnrTGAEGQRlKEGcNINqSLttLGnVInaLaDgqTKYmY
 +L+DLASER++ +GA G+R+ EG+NIN+SL++LGNVINALAD +

Query 255 SLIDLAGSERASTSGAKGTRFVEGTNINRSLALGNVINALADSK----- 299

HMM gghgHIPYRDSKLTWlLQDSLGGNcKtcmIACIWPadWNYEETLSTLRYA
 +++HIPYR SKLT+LL+DSLGCNC T MIA+++P+ + Y++T +TL+YA

Query 300 RKNQHlPYRNSKLTRLKDSLGGNCQTIMIAAVSPSSVFYDDTYNTLKYA 349

HMM dRAKnIkNkPQINEDPcamalWRrYheQIqdmKhqL*
 +RAK+IK + N + + + +Y + + K++

Query 350 NRAKDIKSSLKSNVLNVN-NHITQYVKICNEQKAEI 384

DKFZphtes3_27d1

group: metabolism

DKFZphtes3_27d1 encodes a novel 712 amino acid protein similar to ubiquitin-specific proteases (EC 3.1.2.15).

The novel protein contains both, a ubiquitin carboxyl-terminal hydrolases family 2 signature 1 and signature 2. Pfam predicts a new member of the ubiquitin carboxyl-terminal hydrolases family 2. The ubiquitin system is responsible for the turn over of proteins. Ubiquitin carboxyl-terminal hydrolases (EC 3.1.2.15) (UCH) (deubiquitinating enzymes) are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins.

The novel protein is a new member of the ubiquitin carboxyl-terminal hydrolases family 2, represented by proteins such as yeast UBPI-16, human tre-2, human isopeptidase T and others.

The novel protein can find application in modulation of ubiquitin- and protein metabolism in cells.

similarity to ubiquitin-specific proteases

complete cDNA, complete cds, 4 EST hits

Sequenced by GBF

Locus: unknown

Insert length: 2871 bp

Poly A stretch at pos. 2836, no polyadenylation signal found

```
1 CCAAACCTGA AAGAGGTTGA TTGTAAATGA TTTGCAGGGG GGCAGTGGAG
51 GCAGCGGCCA GGACTTTTCA CTAGGAGAT CAGCATTTGC CCTGATGGAA
101 ACTGGGCGAT CCTGCAGGGA CTGACCTCTG AGTTATCCAA AGGCCGACCT
151 GGGGAAAGAC TGATTTTGAG GTTTAATAG TTTTCAGATG CTTCAAGTGT
201 TGTGAACAGA GACTTGTGTT GATTATGCAT TTCTCAGCTA GACTAAATAA
251 ATGCTAGCAA TGGATACGTG CAAACATGTT GGGCAGCTGC AGCTTGCTCA
301 AGACCATGCC AGCCTCAACC CTCAGAAATG GCACTGTGTG GACTGCAACA
351 CGACCGAGTC CATTTGGGCT TGCCTTAGCT GCTCCCATGT TGCTGTGGA
401 AGATATATTG AAGAGCATGC ACTCAAGCAC TTTCAAGAAA GCAGTCATCC
451 TGTGTCATTG GAGGTGAATG AGATGTACGT TTTTGTGTAC CTTGTGATG
501 ATTATGTTCT GAATGATAAC GCAACTGGAG ACCTGAAGTT ACTACGACGT
551 ACATTAAGTG CCATCAAAAG TCAAAATTAT CACTGCACAA CTCGTAGTGG
601 GAGGTTTTTA CCGTCCATGG GTACAGGTGA TGATTCTTAT TTCTTACATG
651 ACGGTGCCCA ATCTCTGCTT CAAAGTGAAG ATCAACTGTA TACTGCTCTT
701 TGGCACAGGA GAAGGATACT AATGGGTAAA ATCTTTGCAA CATGGTTTGA
751 ACAATCACCC ATTGGAAGAA AAAAGCAAGA AGAACCATTT CAGGAGAAAA
801 TAGTAGTAAA AAGAGAAGTA AAGAAAAGAC GGCAGGAATT GGAGTATCAA
851 GTTAAAGCAG AATTGGAAG TATGCCTCCA AGAAAGAGTT TACGTTTACA
901 AGGGCTCGCT CAGTCGACCA TAATAGAAAT AGTTTCTGTT CAGGTGCCAG
951 CACAAACGCC AGCATCACCA GCAAAAGATA AAGTACTCTC TACCTCAGAA
1001 AATGAAATAT CTCAAAAAGT CAGTGACTCC TCAGTTAAAC GAAGGCCAAT
1051 AGTAACCTCT GGTGTAACAG GATTGAGAAA TTTGGGAAAT ACTTGCTATA
1101 TGAATTCGTG TCTTCAGGTG TTGAGTCATT TACTTATTTT TCGACAATGT
1151 TTTTAAAGC TTGATCTGAA CCAATGGCTG GCTATGACTG CTAGCGAGAA
1201 GACAAGATCT TGTAAGCATC CACCACTCAC AGATACAGTA GTATATCAAA
1251 TGAATGAATG TCAGGAAAAA GATACAGGTT TTGTTTGCTC CAGACAATCA
1301 AGTCTGTCAT CAGGACTAAG TGGTGGAGCA TCAAAAGGTA GAAAGATGGA
1351 ACTTATTCAG CCAAAGGAGC CAACTTCACA GTACATTTCT CTTTGTCTATG
1401 AATTGCATAC TTTGTTCCAA GTCATGTGGT CTGGAAAGTG GCGGTTGGTC
1451 TCACCATTTG CTATGCTACA CTCAGTGTGG AGACTCATTC CTGCCTTCG
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1551 AAATACAAGG TGAATTAGAG ACAACTGGTA CCAGTTTACC AGCTCTTATC
1601 CCCACTTCTC AAAGGAAACT CATCAACAA GTTCTGAATG TTGTAATAAA
1651 CATTTTTCAT GGACAACCTC TTAGTCAGGT TACATGTCTT GCATGTGACA
1701 ACAAATCAAA TACCATAGAA CCTTTCTGGG ACTTGTCTAT GGAGTTTCCA
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1901 CCAGTTGTAC TCACAGAAGC CCAGAAACAA CTTATGATAT GCCACCTACC
1951 TCAGCTTCTC ACAGTGCACC TCAAACGATT CAGCTGGTCA CGACGTAAAT
2001 ACCGAGAGAA GATTGGTGTT CATGTTGGCT TTGAGGAAAT CTTAAACATG
2051 GAGCCCTATT TGTTCAGGGA GACCTGAAA TCCCTCAGAC CAGAATGCTT
2101 TATCTATGAC TTGTCCCGCG TGGTGTATGCA CCATGGGAAA GGATTGGCT
2151 CAGGGCACTA CACTGCCTAC TGCTATAAAT CTGAAGGAGG GTTCTGGGTA
2201 CAGTGCAATG ATTCCAAAC AAGCATGTGC ACTATGGATG AAGTATGCAA
2251 GGCTCAAGCT TATATCTTGT TTTATACCCA ACGAGTTACT GAGAATGGAC
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2301 ATTCTAAACT TTTGCCTCCA GAGCTCCTGT TGGGGAGCCA ACATCCCAAT
2351 GAAGACGCTG ATACCTCGTC TAATGAAATC CTTAGCTGAT CCAAAGACAA
2401 TGGGGGTTTC TTCTGTGAT TTATATATAT ACTTTTAAAG AGACTGATGT
2451 ACCATTTTAA ACTTCATTTT TTCTTGTGAA TCAGTGTATA CTACATTAT
2501 ACATTTTATA TCTAACAATT TTTTCTTTT ACAGAGTATA AATGTATATA
2551 TCAACTGAAG GTAACACTCT TTTTCATATT TGGAGTTTAA AACTTTTGGT
2601 GTTACCTCA GACTGATGTT ACCTCTTTTA TATTTTATG TCTTAATTGG
2651 CTCGGATGAT GAACTTGTGC AATCTTCTAC CAACAAAGTT CAAGTGGCAT
2701 CATTTTATAT ACATGTATCT TTTTCAGGTA TTTTCTATAC AAATCTTAA
2751 TAGATGGAAA ATTAGACTCT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2801 AAAAAAAAAA AAAAAAAAAA AAGGGGCGGC CGCTCTAAA AAAAAAAAAA
2851 AAAAAAAAAA AAAAAAAAAA G

```

BLAST Results

No BLAST result

Medline entries

98072201:
Regulation of ubiquitin-dependent processes by deubiquitinating enzymes.

98431658:
The ubiquitin system.

Peptide information for frame 2

ORF from 251 bp to 2386 bp; peptide length: 712
Category: similarity to known protein
Prosite motifs: UCH_2_1 (274-290)
UCH_2_2 (619-638)
UCH_2_2 (619-638)

```

1 MLAMDTCKHV GQLQLAQDHS SLNPQKWHCV DCNTTESIWA CLSCSHVACG
51 RYIEEHALKH FQESSHPVAL EVNEMYVFCY LCDDYVLNDN ATGDLKLLRR
101 TLSAIKSONY HCTTRSGREF RSMGTGDSY FLHDGAQSL QSEDQLYTAL
151 WHRRRILMGK IFRWFQSP IGRKKQEEPF QEKIVVKREV KRRRQEELEYQ
201 VKAELESMP RSLRLQGLA QSTIIIEIVSV QVPAQTPASP AKDKVLSTSE
251 NEISOKVSDS SVKRRPIVTP GVTGLRNLGN TCYMSVLOV LSHLLIFROC
301 FLKLDLNLWL AMTASEKTRS CKHPPVTDV VYQMECQEK DTGFVCSRQS
351 SLSSGLSGGA SKGRKMELIQ PKEPTSQYIS LCHELHTLFQ VMWSGKWALV
401 SPFAMLHVSF RLIPAFRGYA QDQAQELCE LLDKIQRELE TTGTSPLALI
451 PTSQRKLIKQ VLNVVNNIFH QQLLSQVTCL ACDNKSNTIE PFWDLSEFP
501 ERYQCSGKDI ASQPCLVTEM LAKFTETEAL EGKIYVCDQC NSKRRRFSSK
551 PVLVTEAQKQ LMIHLPQVL RLHLKRFWS GRNNREKIGV HVGFEELNM
601 EBYCCRETLK SLRPECFIYD LSAVVMHHGK GFGSGHYTAY CYNSEGGFWV
651 HCNDSKLSMC TMDEVCKAQA YILFYTORVT ENHSHKLLPP ELLLSQHPN
701 EDADTSSNEI LS

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_27d1, frame 2

PIR:S57591 hypothetical protein YMR223w - yeast (Saccharomyces cerevisiae), N = 4, Score = 218, P = 8.4e-38

SWISSPROT:UBPB_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (K1AA0055).. N = 2, Score = 300, P = 9.3e-31

TREMBL:AF079565_1 gene: "Ubp41"; product: "ubiquitin-specific protease UBP41"; Mus musculus ubiquitin-specific protease UBP41 (Ubp41) mRNA, complete cds., N = 3, Score = 187, P = 8.7e-30

PIR:I58376 hypothetical protein unip - mouse, N = 3, Score = 214, P = 1.2e-28

>SWISSPROT:UBPB_HUMAN_UBIQUITIN_CARBOXYL-TERMINAL_HYDROLASE_11 (EC 3.1.2.15)
 (UBIQUITIN_THIOLESTERASE_11) (UBIQUITIN-SPECIFIC_PROCESSING_PROTEASE_13)
 (DEUBIQUITINATING_ENZYME_11) (KIAA0055).
 Length = 1,118

HSPs:

Score = 300 (45.0 bits), Expect = 9.3e-31, Sum P(2) = 9.3e-31
 Identities = 95/301 (31%), Positives = 149/301 (49%)

Query: 381 LCHELHTLFQVMWSGKVALVSPFAMLSVWRLIPAFRGYAQQDAQEFLCELLDKIQREL- 439
 + E + + +W+G++ +SP ++ ++ F GY+QQD+QE L L+D + +L
 Sbjct: 826 VAEFGIIMKALWTGQYRYISPKDFKITIGKINDQFAGYSQQDSQELLLFLMDGLHEDLN 885
 Query: 440 -----ETTGTSLPALIPTSQRKLIKQVLN--VVNNIFHGQLLSQVTCCLACDNKSNT 488
 E L + LN ++ +F GQ S V CL C KS T
 Sbjct: 886 KADNRKRYKEENNNDHDDFKAAEHAHQKHLQNLNESIIVALFQGGQFKSTVQCLTCHKKSRT 945
 Query: 489 IEPFWDLSLEFPERYQCSGKDIASQPCLVTEMLAKFTETEALLEGKIYVCDQCNSKRRRFS 548
 E F LSL +C+ +D CL + +K E + + + C C ++R
 Sbjct: 946 FEAFMYLSLPLASTSKCTLQD-----CL--RLFSK--EEKLTDNNRFYCSHCRRARR---- 992
 Query: 549 SKPVVLTEAQKQLMICHLPOVLRHLKRFWRSGRNNREKIGVHVGFEEILNMEPYCC-- 605
 ++ K++ I LP VL +HLKRF + GR ++K+ V F E L++ Y
 Sbjct: 993 -----DSLKKIEIWKLPVLLVHLKRFESYDGRW-KQKLQTSVDFPLENLDLSQYVIGP 1044
 Query: 606 RETLKSRLPECFIYDLSAVVMHMGKFGSGHYTAYCYNSEGGFWVHCNDSKLSMCTMDEV 665
 + LK Y+L +V H+G G GHYTAYC N+ W +D ++S ++ V
 Sbjct: 1045 KNNLKK-----YNLFSVSNHYG-GLDGGHYTAYCKNAARQRWFKFDDHEVSDISVSSV 1096
 Query: 666 CKAQAYILFYTQ---RVTE 681
 + AYILFYT RVT+
 Sbjct: 1097 KSSAAYILFYTSLGPRVTD 1115

Score = 126 (18.9 bits), Expect = 9.3e-31, Sum P(2) = 9.3e-31
 Identities = 41/116 (35%), Positives = 63/116 (54%)

Query: 200 QVKAELSMPPR--KSLRLQGLAQSTIIIEIVSVQVPAQTPASPAKDKVLSTSENEISQKV 257
 Q+ AE + P + +S + Q+ I+ + P TP ++K + EIS ++
 Sbjct: 701 QIPAERDREPSKLKRSYSSPDITQA--IQEEKKRKPVTPTVNRENKPTCYPKAEIS-RL 757
 Query: 258 SDSSVKR-RPIVT---PGVTGLRNLGNTCYMNSVLQVLS---HLLIF--RQCFLKLDLNQ 308
 S S ++ P+ P +TGLRNLGNTCYMNS+LQ L HL + R C+ D+N+
 Sbjct: 758 SASQIRNLNPFVGGSGPALTGLRNLGNTCYMNSILQCLCNAPHLADYFNRCYQD-DINR 816

Score = 50 (7.5 bits), Expect = 8.3e-23, Sum P(2) = 8.3e-23
 Identities = 29/106 (27%), Positives = 51/106 (48%)

Query: 173 RKKEOEPFOEKIVVKREVKKRRQLELEYOVKAELSMPPRKSLRLQGLAQSTIIIEIVSVQV 232
 + KQE+ +E+ +++ K R++E E + K + E+ + Q A+ + + S Q
 Sbjct: 475 KNKQEKELRERQEQEKEKLKREEEQEKAKKKQEA-EENEITEKQKAKEEMEKKESEQA 533
 Query: 233 PAQ---TPASPAKD---KVLSTSENEIS--QKVSDDSSVKRRPIVTPGV 272
 + T A K+ K S SE+E S +K + KR P TP +
 Sbjct: 534 KKEDKTSARKGKEITGVKRQSKSEHETSDAKKSVEDRGKRCP--TPEI 580

Score = 42 (6.3 bits), Expect = 5.7e-22, Sum P(2) = 5.7e-22
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 167 EQSPIGRKKEEPFOEKIVVKREVKKRRQLELEY-QVKAELSMPPRKSLRLQGLAQST 223
 EQ +KKQE E +++ K+ ++ E Q K E + ++ + G+ + +
 Sbjct: 498 EQEQAKKKQEAENEITEKQKAKEEMEKKESEQAKKEDKTSARKGKEITGVKRQS 555

Pedant information for DKFZphtes3_27d1, frame 2

Report for DKFZphtes3_27d1.2

[LENGTH] 712
 [MW] 81155.71
 [pI] 8.21
 [HOMOL] SWISSPROT:UBPB_HUMAN_UBIQUITIN_CARBOXYL-TERMINAL_HYDROLASE_11 (EC 3.1.2.15)
 (UBIQUITIN_THIOLESTERASE_11) (UBIQUITIN-SPECIFIC_PROCESSING_PROTEASE_13) (DEUBIQUITINATING
 ENZYME_11) (KIAA0055). 4e-32
 [FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YMR223w] 5e-33
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation,
 palmitoylation, farnesylation and processing) [S. cerevisiae, YMR223w] 5e-33

[FUNCAT] 06.13 proteolysis [S. cerevisiae, YBL067c] 3e-19
 [FUNCAT] 10.03.99 other osmosensing activities [S. cerevisiae, YDR069c] 2e-17
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDR069c] 2e-17
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YDR069c] 2e-17
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDR069c] 2e-17
 [FUNCAT] 09.25 vacuolar and lysosomal biogenesis [S. cerevisiae, YDR069c] 2e-17
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YNL186w] 4e-17
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YHL010c] 3e-12
 [BLOCKS] BL00970A Nuclear transition protein 2 proteins
 [BLOCKS] BL00972D
 [BLOCKS] BL00972C
 [BLOCKS] BL00972B
 [BLOCKS] BL00972A
 [EC] 3.1.2.15 Ubiquitin thiolesterase 5e-06
 [PIRKW] alternative splicing 2e-11
 [PIRKW] thiolester hydrolase 5e-06
 [PIRKW] hydrolase 1e-14
 [SUPFAM] RING finger homology 7e-11
 [SUPFAM] deubiquinating enzyme SSV7 5e-16
 [PROSITE] MYRISTYL 5
 [PROSITE] AMIDATION 2
 [PROSITE] CAMP_PHOSPHO_SITE 1
 [PROSITE] CK2_PHOSPHO_SITE 10
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] UCH_2_2_1
 [PROSITE] PKC_PHOSPHO_SITE 17
 [PROSITE] ASN_GLYCOSYLATION 4
 [PROSITE] UCH_2_1_1
 [PFAM] Ubiquitin carboxyl-terminal hydrolases family 2
 [PFAM] Ubiquitin carboxyl-terminal hydrolases family 2
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 4.92 %

SEQ MLAMDTCKHVGQLQLAQDHSSLPQKWHCVCNTTESIWACLSCSHVACGRYIEEHALKH
 SEG
 PRD cccccccccchhhhhhhccccccccccceccccccccccccccccccccchhhhhhhhhhh

SEQ FQESSHPVALEVNEMYVFCYLCDDYVLNDNATGDLKLLRRTLSAIKSQNYHCTTRSGRFL
 SEG
 PRD hhhhhccccccccccccccccccccccccccccchhhhhhhhhhhhhcccccccccccc

SEQ RSMGTGDDSYFLHDGAQSLLQSEDQLYTALWHRRRILMGKIFRTWFEQSPIGRKKQEEPF
 SEG
 PRD cccccccccccccccccchhh

SEQ QEKIVVKREVKKRRQLEYQVKAELSMPPRKSLRLQGLAQSTIIIEIVSVQVPAQTPASP
 SEG xxxxxxxxxxxxxxxxxxxx.....
 PRD hheeehh

SEQ AKDKVLSTSENEISQKVSDDSVKRRPIVTPGVGTGLRNLGNTCYMNSVLQVLSHLIFROC
 SEG
 PRD cchhhhhhhhhhhhhhhhh

SEQ FLKLDLNQWLAMTASEKTRSCKHPPVTDVTVYQMNCEQEKDTGFVCSRQSSLSGLSGGA
 SEGxxxxxxxxxxxxxxxx
 PRD hhhhhhhchhh

SEQ SKGRKMELIQKPTSQYISLCHELHTLFQVMWSGKWALVSPFAMLHSVWRLIPAFRGYA
 SEG xxxxx.....
 PRD cccccccccccccccccchhh

SEQ QQDAQEFLCELLDKIQRELETTGTSLPALIPTSQRKLIKQVLNVNNIFHGQLLSQVTCL
 SEG
 PRD hhh

SEQ ACDNKSNTIEPFDLSLEFFERYQCSGKDIASQPCLVTEMLAKFTETEALLEGKIYVCDQC
 SEG
 PRD cchhhhhhhhhhhhhhhhhhhhhhh

SEQ NSKRRRFSSKPVVLTEAQKQLMICHLPQVLRHLKRFWRSGRNNREKIGVHVGFEEILNM
 SEG
 PRD cccccccccchhh

SEQ EPYCCRETLKSLRPECFIYDLSAVVMHHGKGFSGHYTAYCYNSEGGFWVHCNDSKLSMC
 SEG
 PRD ccc

SEQ TMDEVCKAQAYILFYTORVTENGHSLKLLPPELLLGSQHPNEDADTSSNEILS
 SEG
 PRD cchhh

Prosites for DKFZphtes3_27d1.2

PS00001	33->37	ASN_GLYCOSYLATION	PDOC00001
PS00001	90->94	ASN_GLYCOSYLATION	PDOC00001
PS00001	484->488	ASN_GLYCOSYLATION	PDOC00001
PS00001	653->657	ASN_GLYCOSYLATION	PDOC00001
PS00004	545->549	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	113->116	PKC_PHOSPHO_SITE	PDOC00005
PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00005	213->216	PKC_PHOSPHO_SITE	PDOC00005
PS00005	254->257	PKC_PHOSPHO_SITE	PDOC00005
PS00005	261->264	PKC_PHOSPHO_SITE	PDOC00005
PS00005	315->318	PKC_PHOSPHO_SITE	PDOC00005
PS00005	320->323	PKC_PHOSPHO_SITE	PDOC00005
PS00005	394->397	PKC_PHOSPHO_SITE	PDOC00005
PS00005	453->456	PKC_PHOSPHO_SITE	PDOC00005
PS00005	506->509	PKC_PHOSPHO_SITE	PDOC00005
PS00005	542->545	PKC_PHOSPHO_SITE	PDOC00005
PS00005	548->551	PKC_PHOSPHO_SITE	PDOC00005
PS00005	580->583	PKC_PHOSPHO_SITE	PDOC00005
PS00005	608->611	PKC_PHOSPHO_SITE	PDOC00005
PS00005	611->614	PKC_PHOSPHO_SITE	PDOC00005
PS00005	676->679	PKC_PHOSPHO_SITE	PDOC00005
PS00006	125->129	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00006	223->227	CK2_PHOSPHO_SITE	PDOC00006
PS00006	247->251	CK2_PHOSPHO_SITE	PDOC00006
PS00006	249->253	CK2_PHOSPHO_SITE	PDOC00006
PS00006	313->317	CK2_PHOSPHO_SITE	PDOC00006
PS00006	506->510	CK2_PHOSPHO_SITE	PDOC00006
PS00006	525->529	CK2_PHOSPHO_SITE	PDOC00006
PS00006	661->665	CK2_PHOSPHO_SITE	PDOC00006
PS00006	706->710	CK2_PHOSPHO_SITE	PDOC00006
PS00007	193->200	TYR_PHOSPHO_SITE	PDOC00007
PS00007	192->200	TYR_PHOSPHO_SITE	PDOC00007
PS00008	218->224	MYRISTYL	PDOC00008
PS00008	355->361	MYRISTYL	PDOC00008
PS00008	359->365	MYRISTYL	PDOC00008
PS00008	471->477	MYRISTYL	PDOC00008
PS00008	589->595	MYRISTYL	PDOC00008
PS00009	171->175	AMIDATION	PDOC00009
PS00009	362->366	AMIDATION	PDOC00009
PS00972	274->290	UCH_2_1	PDOC00750
PS00973	619->639	UCH_2_2	PDOC00750

Pfam for DKFZphtes3_27d1.2

HMM_NAME	Ubiquitin carboxyl-terminal hydrolases family 2		
HMM	*GIqNlGNTCYMNSIIQCL*		
	G++NLGNTCYMNS++Q+L		
Query	274	GLRNLGNTCYMNSVLQVL	291
HMM_NAME	Ubiquitin carboxyl-terminal hydrolases family 2		
HMM	*YdLYgVICHYGntldyGHYWayVKNenhHRWkWYYFDEtV*		
	YDL +V+ H+G + ++GHY+AY++N + ++W+ +D++		
Query	619	YDLSAVVMHHGKGFGSGHYTAYCYNSE--GGFWVHCNDSKL	657

DKF2phtes3_27k4

group: transmembrane protein

Summary DKF2phtes3_27k4 encodes a novel 490 amino acid protein with similarity to two hypothetical *C.elegans* proteins.

The novel protein contains 10 transmembrane regions and a leucine zipper. It is a member of the new 10 trans-membrane domain containing protein family which is specific for multicellular eukariotes.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

strong similarity to *C.elegans* K07H8.2/ZK185.2
membrane regions: 10

complete cDNA, complete cds potential start at Bp 109, few EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1901 bp

Poly A stretch at pos. 1866, no polyadenylation signal found

```
1 GTGATTTACC AGAAAAACCA AGAAGACAGC CACAAAAAAG CAAACGGCAT
51 TTGGCAAGAT GGATTATCAA CTGCAGTACA GACTTTTAGT AATAGATCTG
101 AGCAACACAT GGAGTATCAC AGTTTCTCAG AGCAGTCTTT TCATGCCAAT
151 AATGGGCACG CATCATCAAG CTGCAGCCAA AAGTATGATG ACTATGCCAA
201 TTATAATTAC TGTGATGGAA GGGAGACTTC AGAAACCACT GCCATGTTAC
251 AAGATGAAGA TATATCTAGT GATGGTGATG AAGATGCTAT TGTAGAAGTG
301 ACCCCAAAAT TACCAAAGGA ATCCAGTGGC ATCATGGCAT TGCAAATACT
351 TGTGCCCTTT TTGCTAGCTG GTTTTGGAAAC AGTTTCAGCT GGCATGGTAC
401 TGGATATAGT ACAGCACTGG GAGGTGTTCA GAAAAGTTAC AGAAGTTTTT
451 ATTTTAGTCC CTGCACTTCT TGGTCTCAAA GGGAACTTGG AAATGACATT
501 GGCATCCAGA TTATCCACTG CAGTAAATAT TGGGAAGATG GATTCAACCA
551 TTGAAAAGTG GAACCTAATA ATTGGCAACT TGGCTTTAAA GCAGGTTCAG
601 GCAACAGTAG TGGGTTTTCT AGCAGCTGTG GCAGCAATTA TATTGGGCTG
651 GATTCCAGAA GGAAATATTT ACCTTGATCA TTCCATACTT CTGTGCTCTA
701 GCAGTGTGGC AACTGCCTTC ATTGCATCTC TTCTGCAGGG AATAATAATG
751 GTTGGGGTTA TCGTTGGTTC AAAGAAGACT GGTATAAATC CTGATAATGT
801 TGCTACACCC ATTGCTGCTA GTTTTGGCGA CCTTATAACT CTTGCCATAT
851 TGGCTTGGAT AAGTCAGGGC TTATACTCCT GTCTTGAGAC CTATTACTAC
901 ATTTCTCCAT TAGTTGGTGT ATTTTCTTTG GCTCTAACCC CTATTGGAT
951 TATAATAGCT GCCAAACATC CAGCCACAAG AACAGTTCTC CACTCAGGCT
1001 GAGAGCCTGT CATAACAGCT ATGGTTATAA GTAGCATTGG GGGCCTTATT
1051 CTGGACACAA CTGTATCAGA CCCAAACTTG GTTGGGATTG TTGTTTACAC
1101 GCCAGTTATT AATGGTATTG GTGGTAATTT GGTGGCCATT CAGGCTAGCA
1151 GGATTCTTAC CTACCTCCAT TTACATAGCA TTCCAGGAGA ATTGCCTGAT
1201 GAACCCAAAG GTTGTTACTA CCCATTTAGA ACTTCTTTG GTCCAGGAGT
1251 AAATAATAAG TCTGCTCAAG TTCTACTGCT TTTAGTGATT CCTGGACATT
1301 TAATTTTCTT CTACACTATT CATTTGATGA AAAGTGGTCA TACTTCTTTA
1351 ACTATAATCT TCATAGTAGT GTATTTATTT GGCCTGTGT TACAGGTATT
1401 TACCTTCTCT TGGATTGCTC ACTGGATGCT CCATCACTTC TCGAGGAAAG
1451 GAAAGGACCC GGATAGTTTC TCCATCCCCT ACCTAACAGC ATTGGGTGAT
1501 CTGCTCGGGA CAGCTCTGTT AGCCTTAAGT TTTCAATTTT TTTGGCTTAT
1551 TGGAGATCGA GATGGAGATG TTGGAGACTA ATAAATTCTA CAAACTGCTC
1601 TCAAGTTACC AAGGAAGAAA ATACACGACA ACCACTTATG GCTCTTTTTC
1651 AAAACTCTTA AATCAGTAGT TTGACTTTTG CCAGGGTAAT CTTCAAGTTGG
1701 CCCTGATTCA ATTAATGGC CTTAATTTTT TTTAAGGAA TTTGTGTCAA
1751 AACCAAGTAT AAGAGTATTC GTGCTGCTTT TCATAGAATA AATGATAATT
1801 TGACATAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1851 AAAAAAAAAA AAGGGGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAGGG
1901 G
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 109 bp to 1578 bp; peptide length: 490
 Category: similarity to unknown protein

```

1 MEYHSFSEQS FHANNHGASS SCSQKYDDYA NYNYCDGRET SETTAMLODE
51 DISSDGDDEDA IVEVTPKLPK ESSGIMALQI LVPFLLAGFG TVSAGMVLDI
101 VQHWEVERKV TEVFILVPAL LGLKGNLEMT LASRLSTAVN IGKMDSPIEK
151 WNLIIGNLAL KOVQATVVGFLA AAVAAIILG WIPEGKYLD HSILLCSSSV
201 ATAFIASLLQ GIIMVGIVVG SKKTGINPDN VATPIAASFG DLITLAILAW
251 ISQGLYSCLT TYYYISPLVG VFFLALTPIW IIAAKHPAT RTVLHSGWEP
301 VITAMVISSI GGLILDITVS DPNLVGIVVY TPVINGIGGN LVAIQASRIS
351 TYLHLHSIPG ELPDEPKGCY YPFRTFFGPG VNNKSAQVLL LLVIPGHLIF
401 LYTIHLMKSG HTSLTIIFIV VYLFGAFLQV FTLLWIADWM VHHFWRKGD
451 PDSFSIPYLT ALGDLGTAL LALSFHFLWL IGD RDGDVG
  
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_27k4, frame 1

TREMBL:AF036704_2 gene: "ZK185.2"; Caenorhabditis elegans cosmid
 ZK185., N = 1, Score = 730, P = 3.1e-72

TREMBL:AF047659_9 gene: "K07H8.2"; Caenorhabditis elegans cosmid
 K07H8., N = 1, Score = 940, P = 1.7e-94

>TREMBL:AF047659_9 gene: "K07H8.2"; Caenorhabditis elegans cosmid K07H8.
 Length = 507

HSPs:

Score = 940 (141.0 bits), Expect = 1.7e-94, P = 1.7e-94
 Identities = 204/412 (49%), Positives = 271/412 (65%)

```

Query:   68 LPKESSGIMALQILVPFLLAGFGTVSAGMVLDIQHWEEVERKVTEVFILVPALLGLKGNL 127
          +P ESS ++ Q+L PF +AG G V AG+VL IV W +F ++ E+ ILVPALLGLKGNL
Sbjct:   82 IPAESSYVLFQVLFPPFAVAGLGMVFAGLVLSIVVTWPLFEEIPEILILVPALLGLKGNL 141

Query:   128 EMTLASRLSTAVNIGKMDSPIEKWNLIIGNLALKQVQATVVGFLA AAVAAIILGWIPEGKY 187
          EMTLASRLST N+G MDS ++ +++I NLAL QVQATVV FLA+ A L +IP G +
Sbjct:   142 EMTLASRLSTLANLGHMDSSKQKRDVVIANLALVQVQATVVAFLASAFAAALAFIPSGDF 201

Query:   188 YLDHSILLCSSSVATAFIASLLQGIIMVGIVGSKKTGINPDNVATPIAASFGDLITLAI 247
          H L+C+SS+ATA ASL+ ++MV VIV S+K INPDNVATPIAAS GDL TL +
Sbjct:   202 DWAHGALMCASSLATAACSASLVLSLLMVVIVTSRKYNINPDNVATPIAASLGDLTTLTV 261

Query:   248 LAWISQGLYSCLTYYYISPLVG VFFLALTPIWIIIAAKHPATRTVLHSGWEPVITAMVI 307
          LA+ T +++ +V V FL L P WI IA ++ T+ L++GW PVI +M+I
Sbjct:   262 LAFFGSVFLKAHNTESWLNIVIVVLFLLLPFWIKIANENEGTQETLYNGWTPVIMSMLI 321

Query:   308 SSIGGLILDITVSDPNLVGIVVYTPVINGIGGNLVAIQASRISTYLHLHSIPGELPDEPK 367
          SS GG IL+T V + + Y PV+NG+GGNL A+QASR+STY H G LP+E
Sbjct:   322 SSAGGFILETAVRRYH--SLSTYGPVLNGVGGNLAAVQASRLSTYFHKAGTVGVLPNEWT 379

Query:   368 GCYYPF--RTFFGPGVNNKSAQVLLLVIPGHLIFLYTIHLM----KSGHTSLTIIFIVV 421
          + R FF +++SA+VLLLLV+PGH+ F + I L K+ T +F +
Sbjct:   380 VSRFTSVQRAFFSKEDWSRSARVLLLLLVVPGHICFNFLIQLFTLTSKNNVTPHGPLEFTSL 439

Query:   422 YLFGAFLQVFTLLWIADWMVHHFWRKGD PDSFSIPYLTALGDLLGTALLALS F 475
          Y+ A++QV LL++ +V W+ DPD+ IPYLTALGDLLGT LL + F
Sbjct:   440 YMIAAIQVVILLFVCQLLVALLWKWKIDPDNSVIPYLTALGDLLGTGLLFIV F 493
  
```

Pedant information for DKFZphtes3_27k4, frame 1

Report for DKFZphtes3_27k4.1

[LENGTH] 490
 [MW] 53266.39

[pI] 5.29
 [HOMOL] TREMBL:AF047659_9 gene: "K07H8.2"; Caenorhabditis elegans cosmid K07H8. 4e-94

[PROSITE] LEUCINE ZIPPER 1
 [PROSITE] MYRISTYL 7
 [PROSITE] CAMP_PHOSPHO_SITE 1
 [PROSITE] CK2_PHOSPHO_SITE 7
 [PROSITE] PROKAR_LIPOPROTEIN 2
 [PROSITE] TYR_PHOSPHO_SITE 1
 [PROSITE] PKC_PHOSPHO_SITE 3
 [PROSITE] ASN_GLYCOSYLATION 1
 [KW] TRANSMEMBRANE 10
 [KW] LOW_COMPLEXITY 3.06 %

SEQ MEYHSFSEQSFHANNGHASSSCSQKYDDYANYNYCDGRETSETTAMLQDEDISSDGEDA
 SEG
 PRD ccc
 MEM

SEQ IVEVTPKLPKESSGIMALQILVPFLLAGFGTVSAGMVLDIVQHWVFRKVTEVFILVPAL
 SEG
 PRD eeeeecc
 MEMMM

SEQ LGLKGNLEMTLASRLSTAVNIGKMDSPIEKWNLIIGNLALKQVQATVVGFLLAAVAAILG
 SEG
 PRD ccc
 MEM MMM

SEQ WIPEGKYYLDHSILLCSSSVATAFIASLLQGIIMVGVI VGSKKTGINPDNVATPIAASFG
 SEG
 PRD hcc
 MEMMM

SEQ DLITLAILAWISQGLYSCLETYYYISPLVGVFLLALTPIWIIIAAKHPATRTVLHSGWEP
 SEG
 PRD ccc
 MEM MMM

SEQ VITAMVISSIGGLILDTTVSDPNLVGIVVYTPVINGIGGNLVAIQASRISTYLHLHSIPG
 SEG
 PRD hcchhhhhhhcc
 MEM MMM

SEQ ELPDEPKGCYYPFRFTFFGPGVNNKSAQVLLLLVIPGHLIFLYTIHLMKSGHTSLTIIFIV
 SEG
 PRD ccc
 MEMMM

SEQ VYLFGAVLQVFTLLWIADWMVHHFWRKGDPSFSIPYLTALGDLLGTALLALSFLWL
 SEG
 PRD hhh
 MEM MMM

SEQ IGDRDGDVGD
 SEG
 PRD ecccccccccc
 MEM MM.....

Prosite for DKFZphtes3_27k4.1

PS00001	383->387	ASN_GLYCOSYLATION	PDOC00001
PS00004	108->112	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	23->26	PKC_PHOSPHO_SITE	PDOC00005
PS00005	65->68	PKC_PHOSPHO_SITE	PDOC00005
PS00005	221->224	PKC_PHOSPHO_SITE	PDOC00005
PS00006	5->9	CK2_PHOSPHO_SITE	PDOC00006
PS00006	54->58	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	238->242	CK2_PHOSPHO_SITE	PDOC00006
PS00006	257->261	CK2_PHOSPHO_SITE	PDOC00006
PS00006	296->300	CK2_PHOSPHO_SITE	PDOC00006
PS00006	318->322	CK2_PHOSPHO_SITE	PDOC00006
PS00007	25->33	TYR_PHOSPHO_SITE	PDOC00007
PS00008	90->96	MYRISTYL	PDOC00008
PS00008	122->128	MYRISTYL	PDOC00008
PS00008	216->222	MYRISTYL	PDOC00008
PS00008	220->226	MYRISTYL	PDOC00008

PS00008	254->260	MYRISTYL	PDOC00008
PS00008	336->342	MYRISTYL	PDOC00008
PS00008	339->345	MYRISTYL	PDOC00008
PS00013	12->23	PROKAR_LIPOPROTEIN	PDOC00013
PS00013	248->259	PROKAR_LIPOPROTEIN	PDOC00013
PS00029	459->481	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphtes3_27k4.1)

DKFZphtes3_27o14

group: testes derived

DKFZphtes3_27o14 encodes a novel 358 amino acid protein with similarity to *C. elegans* cosmid C55A6.

The new protein contains a C3HC4 zinc finger (RING finger) signature. The ring finger structure binds two atoms of zinc, and is involved in mediating protein-protein interactions. No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to *C.elegans* C55A6.1

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: /map="6"

Insert length: 2158 bp

Poly A stretch at pos. 2137, polyadenylation signal at pos. 2120

```
1 CCGAGGCCAG AGAGAAAAGA CTGCGAGGTG GCCGCAGCTG TGGCCGGAGA
51 GCACAAAGAA TGAACCAGCA GTGGAAGAGA AAATACTGTA AGCTGGCTGA
101 CTGCTGGTGA AGAAAATGCT TTATTTTGTG GGCAGGCATC TGTGGGATCT
151 GTAATAGAAA TATATTGGAG TAATTCAAGA TTCTGTGGTT GGCCCTTTTG
201 ACTGCTCTCT CTACAGGTTT AATTTGGGCA TTTACTCATT TTCATGGCTC
251 CAAGGACCAT GTATGTGTTG GGGATCTTCA ATATTCATGT TATTTTCTCC
301 TTGGTCTTAT TATGATTGTT ACCTTTATGA AGCTTTAGTG ATTACAAAGC
351 ACTTTTTTTG TCCATTTTTA CCTGAGCTTT GTAAACTCTG ATTTGCAGGA
401 TGGCTGGCTG TGGTGAAATT GATCATTCAA TAAACATGCT TCCTACAAAC
451 AGGAAAGCGA ACGAGTCCTG TTCTAATACT GCACCTTCTT TAACCGTCCC
501 TGAATGTGCC ATTTGTCTGC AAACATGTGT TCATCCAGTC AGTCTGCCCT
551 GTAAGCACGT TTTCTGCTAT CTATGTGTAA AAGGAGCTTC ATGGCTTGGA
601 AAGCGGTCTG CTCTTTGTCG ACAAGAAATT CCCGAGGATT TCCTTGACAA
651 GCCAACCTTG TTGTCAACAG AAGAACTCAA GGCAGCAAGT AGAGGAAATG
701 GTGAATATGC ATGGTATTAT GAAGGAAGAA ATGGGTGGTG GCAGTACGAT
751 GAGCGCACTA GTAGAGAGCT GGAAGATGCT TTTCCAAAG GTAAAAAGAA
801 CACTGAAATG TTAATTGCTG GCTTTCTGTA TGTCGCTGAT CTTGAAAACA
851 TGGTTCAATA TAGGAGAAAT GAACATGGAC GTCGCAGGAA GATTAAAGCGA
901 GATATAATAG ATATACCAAA GAAGGGAGTA GCTGGACTTA GGCTAGACTG
951 TGATGCTAAT ACCGTAAACC TAGCAAGAGA GAGCTCTGCT GACGGAGCGG
1001 ACAGTGTATC AGCACAGAGT GGAGCTTCTG TTCAGCCCTT AGTGTCTTCT
1051 GTAAGGCCCC TAACATCAGT AGATGGTCAG TTAACAAGCC CTGCAACACC
1101 ATCCCCTGAT GCAAGCACTT CTCTGGAAGA CTCTTTTGCT CATTTACAAC
1151 TCAGTGGAGA CAACACAGCT GAAAGGAGTC ATAGGGGAGA AGGAGAAGAA
1201 GATCATGAAT CACCATCTTC AGGCAGGGTA CCAGCACCAG ACACCTCCAT
1251 TGAAGAAACT GAATCAGATG CCAGTAGTGA TAGTGAGGAT GTATCTGCAG
1301 TTGTTGCACA GCACTCCTTG ACCCAACAGA GACTTTTGGT TTCTAATGCA
1351 AACCAGACAG TACCCGATCG ATCAGATCGA TCGGGAAGCT ATCGATCAGT
1401 AGCAGGGGGT GGAACAGTGA GTGTCAAGTG CAGATCTAGA AGGCCTGATG
1451 GACAGTGCAC AGTAACTGAA GTTTAAATAA AAATGTCTTC AGCTCCATGC
1501 TCAAGGTTGA AAGGGTTACC TGTAATTTTC TGCCACATA ACATTATACT
1551 CATCCCTAGT AGTGCATTTT GGGAGTTGGG GTGGGAAGGG GTATGGGAAG
1601 GATAGACTCA TAATTAAATG GTCTAACATG TCTCTGTTGA GAAATTTATT
1651 TAATGTAAGG AACTTGGGTG TTAATAGTTG AGAGCTGTTT AGTAATAACC
1701 CAGTTTTCTT GAGGTCTGTT TACTTTTATC TTTTAAAAA CTTCTGTAGT
1751 TCTTTTGGCC AGTGTGTTTG TATTATCTGT GCATTAATGG TCCTCATCTG
1801 ACTCCTGCAT TGTGTCTTAT TTTTCTGCAT GGATTGGCAT AAGACCATTA
1851 CTAAAAATTTG GCACCTGTGA GATGTTTGAT ATTATGAACA GGAACATAAA
1901 TTTAATGTAT GAATAGATGT GAATTTGGGA TTCAAATAA GATGAATAAC
1951 AACTATTTTA TAGTAAAGTT ATTGAAATGG AAATGAAAC AGCCAGTAAC
2001 TTATGTTTCA GAATGTTTGT AACACACTTC ATGGGTGTCC CATAGGCTTT
2051 GCTGTCTAGT CTTATAGTTT GAGGTTTTTT TGGTCTGCAT TTTTCTTTT
2101 GATTACAAAA TTTATAATTT AATAAATACT AGAGTTTATC AAAAAAAAAA
2151 AAAAAAAG
```

BLAST Results

Entry HSG117 from database EMBL:
human STS SHGC-36270.
Score = 1148, P = 8.9e-45, identities = 240/250

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 400 bp to 1473 bp; peptide length: 358
 Category: similarity to unknown protein
 Prosite motifs: ZINC_FINGER_C3HC4 (51-61)

```

1 MAGCGEIDHS INMLPTNRKA NESCSNTAPS LTVPECAICL QTCVHPVSLP
51 CKHVFCYLCV KGASWLGKRC ALCRQEIPED FLDKPTLLSP EELKAASRGN
101 GEYAWYYEGR NGWWQYDERT SRELEDAFSK GKKNTLEMLIA GFLYVADLEN
151 MVQYRRNEHG RRRKIKRDI DIPKKGAVAGL RLDCDANTVN LARESSADGA
201 DSVSAQSGAS VQPLVSSVRP LTSVDGQLTS PATPSPDAST SLEDSFAHLQ
251 LSGDNTAERS HRGEGEEDHE SPSSGRVPAP DTSIEETESD ASSDSEDVSA
301 VVAQHSLTQQ RLLVSNANQT VPDRSDRSRG DRSVAGGGTV SVSVRSRRRP
351 GQCTVTEV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_27o14, frame 1

TREMBL:CEC55A6_1 gene: "C55A6.1"; Caenorhabditis elegans cosmid C55A6,
 N = 2, Score = 165, P = 4.2e-15

SWISSPROT:YWZ6_CAEEL HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME
 X., N = 2, Score = 136, P = 3.1e-11

>TREMBL:CEC55A6_1 gene: "C55A6.1"; Caenorhabditis elegans cosmid C55A6
 Length = 484

HSPs:

Score = 165 (24.8 bits), Expect = 4.2e-15, Sum P(2) = 4.2e-15
 Identities = 42/106 (39%), Positives = 61/106 (57%)

Query: 75 QEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRN-GWWQYDERTSRELEDAFSKGGK 133
 Q +P LD ++ PEE K Y W Y G+N GWW+++ R RE+E+A++ GK
 Sbjct: 93 QNVFALDLDA-SICDPEERK-----Y-WIYSGKNQGGWRFEPNREREIEEAYNAGKC 142

Query: 134 NTEMLIAGFLYVADLENMVQYRRNEHGRRRRIKR---DIID-IPKKGAVAGL 180
 + E++I G YV D +QY R + R +KR D D I KG+AG+
 Sbjct: 143 HCEVVICGRPYVIDFHQFLQYPRGVNQRHVKRVSADDFDGGIGVKGLAGI 193

Score = 96 (14.4 bits), Expect = 4.2e-15; Sum P(2) = 4.2e-15
 Identities = 19/54 (35%), Positives = 30/54 (55%)

Query: 35 ECAICLQTCVHPVSLP-CKHVFCYLCVKGASW--LGKRCALCRQEIPEDFLDKPT 86
 EC IC + P ++P C H FC++C+KG +G C +CR I + +P+
 Sbjct: 11 ECPICQCKMIVPTTIPACGHKFCFICLKGVMNDMGG-CPMCRGPIDSNIFAQPS 64

Pedant information for DKFZphtes3_27o14, frame 1

Report for DKFZphtes3_27o14.1

[LENGTH]	358
[MW]	38818.90
[pI]	5.17
[HOMOL]	TREMBL:CEC55A6_1 gene: "C55A6.1"; Caenorhabditis elegans cosmid C55A6 2e-12
[FUNCAT]	11.04 dna repair (direct repair, base excision repair and nucleotide excision repair)
	[S. cerevisiae, YCR066w] 3e-04
[FUNCAT]	03.19 recombination and dna repair
	[S. cerevisiae, YCR066w] 3e-04
[FUNCAT]	30.10 nuclear organization
	[S. cerevisiae, YCR066w] 3e-04

[FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YCR066w] 3e-04
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YDR265w] 4e-04
 [FUNCAT] 30.19 peroxisomal organization [S. cerevisiae, YDR265w] 4e-04
 [BLOCKS] BL00518 Zinc finger, C3HC4 type, proteins
 [PROSITE] MYRISTYL 2
 [PROSITE] AMIDATION 3
 [PROSITE] CAMP_PHOSPHO_SITE 1
 [PROSITE] CK2_PHOSPHO_SITE 12
 [PROSITE] TYR_PHOSPHO_SITE 1
 [PROSITE] ZINC_FINGER_C3HC4 1
 [PROSITE] PKC_PHOSPHO_SITE 9
 [PROSITE] ASN_GLYCOSYLATION 2
 [PFAM] Zinc finger, C3HC4 type (RING finger)
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 19.83 %

SEQ MAGCGEIDHSINMLPTNRKANESCSNTAPSLTVPECAICLQTCVHPVSLPCKHVFCYLCV
 SEG
 lrmnd-TTTTTEETTTEEEETTTEEEHHHH
 SEQ KGASWLGRKRCALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRNGWQYDERT
 SEG
 lrmnd- HHHHHHCCBTTTTTCBCGGG-CBCC.....
 SEQ SRELEDAFSKGGKNTTEMLIAGFLYVADLENMVQYRRNEHGRRRKIKRDIIDI PKKGVAGL
 SEGxxxxxxxxxxxxxxxx.....
 lrmnd-
 SEQ RLDCDANTVNLARESSADGADSVSAQSGASVQPLVSSVRPLTSVDGQLTSPATPSPDAST
 SEGxxxxxxxxxxxxxxxx.....
 lrmnd-
 SEQ SLEDSFAHLQLSGDNTAERSHRGEGEEDHESPSSGRVPAPDTSIEETESDASSDSEDVSA
 SEG x.....xxxxxxxxxxxxxxxx.....
 lrmnd-
 SEQ VVAQHSLTQQRLLVSNANQTVDPDRSDRGTDRSVAGGGTVSVSVRSRRPDGQCTVTEV
 SEG xxx.....xxxxxxxxxxxxxxxx.....
 lrmnd-

Prosites for DKFZphtes3_27o14.1

PS00001	21->25	ASN_GLYCOSYLATION	PDOC00001
PS00001	318->322	ASN_GLYCOSYLATION	PDOC00001
PS00004	132->136	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	16->19	PKC_PHOSPHO_SITE	PDOC00005
PS00005	120->123	PKC_PHOSPHO_SITE	PDOC00005
PS00005	217->220	PKC_PHOSPHO_SITE	PDOC00005
PS00005	260->263	PKC_PHOSPHO_SITE	PDOC00005
PS00005	274->277	PKC_PHOSPHO_SITE	PDOC00005
PS00005	325->328	PKC_PHOSPHO_SITE	PDOC00005
PS00005	330->333	PKC_PHOSPHO_SITE	PDOC00005
PS00005	343->346	PKC_PHOSPHO_SITE	PDOC00005
PS00005	346->349	PKC_PHOSPHO_SITE	PDOC00005
PS00006	32->36	CK2_PHOSPHO_SITE	PDOC00006
PS00006	89->93	CK2_PHOSPHO_SITE	PDOC00006
PS00006	120->124	CK2_PHOSPHO_SITE	PDOC00006
PS00006	195->199	CK2_PHOSPHO_SITE	PDOC00006
PS00006	222->226	CK2_PHOSPHO_SITE	PDOC00006
PS00006	240->244	CK2_PHOSPHO_SITE	PDOC00006
PS00006	282->286	CK2_PHOSPHO_SITE	PDOC00006
PS00006	287->291	CK2_PHOSPHO_SITE	PDOC00006
PS00006	293->297	CK2_PHOSPHO_SITE	PDOC00006
PS00006	320->324	CK2_PHOSPHO_SITE	PDOC00006
PS00006	328->332	CK2_PHOSPHO_SITE	PDOC00006
PS00006	354->358	CK2_PHOSPHO_SITE	PDOC00006
PS00007	98->107	TYR_PHOSPHO_SITE	PDOC00007
PS00008	329->335	MYRISTYL	PDOC00008
PS00008	337->343	MYRISTYL	PDOC00008
PS00009	66->70	AMIDATION	PDOC00009
PS00009	130->134	AMIDATION	PDOC00009
PS00009	159->163	AMIDATION	PDOC00009
PS00518	51->61	ZINC_FINGER_C3HC4	PDOC00449

Pfam for DKFZphtes3_27o14.1

HMM_NAME Zinc finger, C3HC4 type (RING finger)
HMM *CPICFctFQlDyPWPFdePmMlPCgHsFCypCIrrW.....CPmC*
C+IC L + P++LPC+H+FCY C++ C +C
Query 36 CAIC-----LQT---CVHPVSLPCKHVFCYLCVKGASWLGRKCALC 73

DKFZphtes3_28d14

group: testes derived

DKFZphtes3_28d14 encodes a novel 97 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1279 bp

Poly A stretch at pos. 1232, no polyadenylation signal found

```
1 GGAGCTCAGA AGTTGGGCAA AGGTCACAGC AGACTTCCTG AAAAGCAGAC
51 ACTGAGGAAC ACAGTGGAGA GCGGGAGTTC ACAGCGACGC AGCTGAGGAC
101 GACGCAGGAC CTCTCCCAAA GGTGCTGCAG CTCCAGCACC AGGGGCCAGG
151 GCTGCGGCGA CAGCAGCTCA GCAACCCTTG CTGTGCTCAA GTTCTTGGGG
201 ATTGAGAGCT AAGTTCAAAA TTTAGAAACA GTGCCTTAAA GACGGGCAAG
251 AAAACCCCGT GTGGGAGTCT GCTCATCTAT GGTGTGTTAC TGCTCTCGCT
301 TTGATATTCT TAAATTCCCTA GGTACCAATG AAAAAGCCAA GTGAACGTGG
351 CAGACTGAGG AGGACACAGG ACCGTGTGCA CCTTCCATCT GTGAGAGGCA
401 CACTTCAGTC TGGGTTCAAG ATGCAGAATG GTGCCTACAG CAAAAAATAA
451 AAAAACACCC TCCTCCCTTC TTTACCATTT GAATGGACAT TTTCCTTACC
501 TGTGATCCCA ACAGAAACAG ATCCAGACCT ATCATGTGAA GTCCACGTTC
551 CAGGATCAGA AGTAACCAGT TTATGGACTG AGCTTACACG GGAAAGTCTA
601 CCCCCGACTC CTTCTGGATA GTAACATACA CAGCTGCATA AAAACGTCTC
651 CAAGGGGACA TACGATGCAT TTGCTTGGTG TCCCAGCCAA GCTCCCCACC
701 GCGGACCTCA CTGTTCCCTTA GAGCTCGAGA GCTCGTCTCC TATCAATCAG
751 AGAACCCCAT CAGCTGTGAC CAACAGAGCT GGAGCCCTCT GTGGAGGGAG
801 CTGACCCAC ACACAGGACA GAGCAGAATC CTGATTATTT TACAACTGTC
851 AAACCTTCTG AGTAAGAAGA CAAAAATATA CATTCCAAGG TATCTGTAAA
901 GTGCTTGGAA GATGCAGACA GCTGCACCGA GGGGCTCTGA TCCATCCACA
951 CGCTGCGGTT TGCTGCGGTC ACACACACGG TCTCAGTCAC GTGATGGTTT
1001 TGCTTTTATT TCTTAAACGG CTGAGTGATA ATCCAGTAG TGTGCAGTCA
1051 TTTATACCTT TTCAATGGGC GTCACCGCAG TGACGCTGCC CCAGCCCAT
1101 GCTGAGGGCC GACACAATTC ACGGAACAGA TTCATCATAT TTGGTCTTTA
1151 TGTAATAAAT AAATGTTTAA AAATTGCCTA AATATAAAAA AAAAAAAAAA
1201 AAAAAAAAAA AAAAAAAAAA AAAGGGCGGC CGAAAAAAAA AAAAAAAAAA
1251 AAAAAAAAAA AAAAAAAAAA GGGCGGCCG
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 328 bp to 618 bp; peptide length: 97
Category: putative protein

```
1 MKKPSEGRV RRRQERVHLP SVRGTLQSGF KMONGAYSKK KNTLLPSLP
51 FEWTFSLPVI PTETDPLDSC EVHVPGESEV SLWELTRES LPPTPSG
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_28d14, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_28d14, frame 1

Report for DKFZphtes3_28d14.1

[LENGTH] 97
[MW] 10945.56
[pI] 9.80
[PROSITE] MYRISTYL 2
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] CK2_PHOSPHO_SITE 2
[PROSITE] PKC_PHOSPHO_SITE 3
[KW] All_Alpha
[KW] LOW_COMPLEXITY 12.37 %

SEQ MKKPSEGRVRRRQERVHLPVSRGTLSQSGFKMQNGAYSKKKKNTLLPSLPFEWTFSLPVI
SEGXX
PRD cccccchhhhhhhhhhhcc

SEQ PTETDPDLSCEVHVPVPGSEVTSLSWTELTRESLPPTPSG
SEG
PRD cccccccceeeccccccchhhhhhhhhhhcccccccc

Prosites for DKFZphtes3_28d14.1

PS00004	2->6	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	41->45	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	5->8	PKC_PHOSPHO_SITE	PDOC00005
PS00005	21->24	PKC_PHOSPHO_SITE	PDOC00005
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00006	62->66	CK2_PHOSPHO_SITE	PDOC00006
PS00006	64->68	CK2_PHOSPHO_SITE	PDOC00006
PS00008	24->30	MYRISTYL	PDOC00008
PS00008	76->82	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_28d14.1)

DKFZphtes3_2a11

group: testes derived

DKFZphtes3_2a11 encodes a novel 1048 amino acid protein with very weak similarity to mucins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to mucin

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 4082 bp

Poly A stretch at pos. 4060, polyadenylation signal at pos. 4034

```
1 GAGGACTGCG AGCACAGCGG CGGCCGGGTG GCGGGGGTGA GTGGGGCCAG
51 CCGGGGCTGGA CAGCAGCGGG CCGCGGGCGC CGCGGCCGCG ATCCCTCCCC
101 CCGCCCGCCG AGCACATCGC CGCCGCGGAG ATGGGCGCCTC CGCGGCACCC
151 CCAGGCCGCG GAGATAGAAG CGGGCGGTGC GGGCGGCGGG CGGCGGCTAC
201 AGGTGGAAT GAGTTCTCAA CAGTTTCCTC GGTTAGGAGC CCCTTCTACC
251 GGGCTGAGCC AGGCCCTTC TCAGATTGCA AACAGTGGT CTGCTGGATT
301 GATAAACCCA GCTGCTACAG TCAATGATGA ATCTGGTCGA GATTCTGAAG
351 TCAGTGCCAG GGAGCACATG AGTTCAGCA GCTCCCTCCA GTCCCGGGAG
401 GAGAAGCAAG AGCCTGTTGT GGTAAGGCC TATCCACAGG TGCAGATGTT
451 GTCGACACAC CATGCTGTCG CATCAGCCAC ACCTGTTGCA GTGACAGCCC
501 CGCCAGCACA CCTGACGCCA GCAGTGCCAC TTTCATTTTC GGAGGGACTT
551 ATGAAGCCGC CCGGAAGGCC CACCATGCCT AGCCGTCCCA TTGCTCCTGC
601 TCCACCTTCT ACCCTGTCAC TTCCCCCAA GGTTCAGGG CAGGTTACCG
651 TTACCATGGA GAGTAGCATC CCTCAAGCTT CAGCCATTCC TGTGGCAACA
701 ATCAGTGGAC AACAGGGCCA TCCCAGTAAC CTGCATCACA TCATGACTAC
751 AAATGTGCAA ATGTCTATCA TCCGACGCAA TGCTCCTGGG CCCCCTCTTC
801 ACATTGGAGC TTCTCATTTA CCTCGAGGTG CAGTGTCTGC TGCTGTGATG
851 TCCAGTTCTA AAGTAACAC AGTCCTGAGG CCGACCTCAC AGCTGCCAAA
901 TGCTGCTACT GCTCAGCCAG CAGTACAGCA CATCATTCAC CAACCAATCC
951 AGTCTCGGGC ACCTGTGACC ACCTCCAATG CCATCCCTCC TGCTGTGGTA
1001 GCAACTGTCT CAGCCACCAG AGCTCAGTCT CAGTCATCA CTACGACAGC
1051 GCGCGATGCT ACTGATTCAG CACTTAGTAG GCCAACCTTG TCTATCCAGC
1101 ATCCTCCATC TGCAGCAATC AGTATTCAGC GTCCTGCCCA GTCACGAGAT
1151 GTCACAAACA GAATCACACT ACCATCTCAC CCTGCATTAG GGACGCCAAA
1201 ACAGCAGCTT CATACATGG CACAGAAAAC AATCTCAGT ACTGGCAGCG
1251 CAGTGGCTGC AGCCACAGTA GCACCTATTT TGGCAACCAA CACCATTCCT
1301 TCAGCGACCA CAGCTGGATC TGTGTACAC ACGCAAGCTC CCACAAGTAC
1351 CATTGTTACC ATGACAGTAC CCTCCCATTC CTCCCATGCT ACTGCTGTGA
1401 CCACCTCAAA CATCCAGTC GCCAAGGTGG TGGCCAGCA GATCAGGCAC
1451 ACTTCTCTCT GGATCCAGCC AGACTACCCT GCCGAGAGGA GTAGCCTGAT
1501 TCCCATCTCC GGACATCGGG CCTCTCCCAA TCCTGTGGCC ATGGAAACCC
1551 GAAGTGACAA CAGACCGTCT GTTCCGTTT AGTTCCAATA TTTTGTGCCA
1601 ACTTACCCCT CTTCTGCATA CCCACTGGCG GCACATACCT ACACCCCAAT
1651 CACCAGTTCC GTGTCCACTA TCCGACAGTA TCCAGTTTCA GCTCAGGCTC
1701 CAAACTCTGC CATCACAGCT CAGACTGGTG TTGGGTTAGC GTCTACCGTC
1751 CACCTAAACC CCATGCAGTT GATGACAGTG GATGCATCCG ATGCTCGACA
1801 TATTCAAGGG ATCCAGCCAG CACCCATCAG TACCCAGGGT ATCCAGCCGG
1851 CCCCCATTGG GACCCAGGG ATACAGCCTG CACCACTTGG CACACAGGGA
1901 ATTCACTCAG CAACCCCAAT CAACACACAA GGGCTTCAGC CTGCACCTAT
1951 GGGTACTCAG CAGCCTCAGC CTGAAGGAAA GACTTCAGCA GTGGTGTGG
2001 CAGATGGAGC CACAATTGTG GCCAACCCTA TTAGCAATCC ATTCAGTGCT
2051 GCTCCAGCAG CAACAACCGT GGTGCAGACC CACAGCCAGA GTGCTAGCAC
2101 CAACGCTCCC GCCCAGGGCT CATGCCACG GCCAAGCATA CTCGGAAGA
2151 AACCTGCCAC AGATGGTGCC AAACCCAAGT CTGAAATCCA CGTGTCTATG
2201 GCCACTCCGG TCACTGTGTC CATGGAGACT GTATCCAATC AAAATAATGA
2251 TCAGCCTACC ATTGCGCTCC CTCCAATGCT CCAGCAGCCC CCACCGACCA
2301 TTTCAACTAT GATTGCAGCA GCCAGTCCCC CGTCACAACC AGCGTTTGGC
2351 TTTTCAACCA TTCTGGAGC GGTCCCCATC ACTCCACCCA TCACCACCAT
2401 TGCAGCTGCA CCACCTCCAT CAGTCACTGT GGGTGGCAGT CTTTCTCCG
2451 TCTTGGGCCC TCCCGTTTCT GAAATTAAAG TGAAAGAAGA AGTAGAACCA
2501 ATGGATATCA TGAGGCCAGT TTCTGCAGTT CCTCCACTGG CTACCAACAC
2551 TGTGTCTCCA TCTCTTGCA TGCTGGCAAA CAACTTGTC ATGCCTACAA
2601 GTGACCTACC ACCTGGTGCC TCCCCAAGGA AAAAGCCTCG AAAGCAACAG
2651 CATGTGATCT CAACAGAAGA AGGTGACATG ATGGAGACAA ACAGCACTGA
2701 TGATGAGAAG TCCACTGCCA AGAGTCTTCT GGTGAAGGCT GAGAAGCGCA
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2751 AGTCTCCTCC CAAGGAGTAT ATTGATGAGG AAGGTGTGAG ATATGTCCCA
2801 GTGCGTCCAA GACCCCCCAT TACTTTGCTT CGTCACTATC GGAACCCCTG
2851 GAAAGCTGCT TACCACCACT TTCAGAGGTA CAGTGACGTC CGGGTCAAAG
2901 AGGAGAAGAA AGCTATGCTG CAGGAAATAG CTAATCAGAA AGGAGTATCC
2951 TGTGCTGCTC AAGGCTGGAA AGTCCACCTC TGTGCTGCCC AGTTACTACA
3001 GCTGACGAAT CTAGAACATG ATGTCTATGA AAGACTTACT AACCTGCAGG
3051 AAGGGATTAT CCCAAAGAAA AAAGCAGCAA CAGATGATGA TCTCCACCGA
3101 ATAAACGAAC TGATACAGGG AAATATGCAG AGGTGTAAAC TTGTGATGGA
3151 TCAAATCAGT GAAGCCAGAG ACTCCATGCT TAAGGTTTAA GATCATAAAG
3201 ACCGTGTCCT GAAGCTGCTT AACAGAAGCG GGACTGTCAA AAAAGTGTCC
3251 AAATTGAAGC GAAAGGAAAA AGTCTAGACC CAGAACAATC AGGAGATTGG
3301 AAGCAAATTT ATGAAGAATG ATGGTGGGGG TGGGGGGAGG GTTTTGGTTT
3351 TTCCAAAGT GGAACATTGA AATAAAGGAA GTGTTCTTAA GTTCCCGTGT
3401 GAAAGCAGAG GAACCCATGA CATCCAAGGG CGTGAAGGA TCAGAGCTGA
3451 CTGGACATAG TGAGCTGCCT TCTTGCGTTC GGGTGCACCC CTGTTAAACC
3501 TGATCTGTGT CATAAGTGAC TCCGGATGCA TCAGTGTCCA CCAGTTGGAA
3551 GCAATGACAA GGATGGCTGG CTGGTGTITT TCAGCCTTCC GGTTTATAGA
3601 CTGTATTATC CTAGTGGATT CCTGCAGGCC CCATACTGAG CCTGGACTGA
3651 AAGTATCCAC TCGGACCATC TGTTATCTCT CTACACTGAA AATAAAACCT
3701 CTTCCACCCA CCCCATTGGG TTCTTCTGCC TGACCTTCAA ATGCCCATGT
3751 TGGCCTTTTA CAGCAGTGCC ACGGCACCAA GCGAGCTGCC ACATCTCACA
3801 CTCTAAAGGG TTGAACTAT TAGTTCTTGT CATTTTTTAA AAAAAACCAT
3851 TCCCAAGTGA AATTGTTATA TCGTCTGTCT TCGGTGTGTC AGAACTGGGT
3901 TTTTGTGGAG GTTCAGAGCA GGCAACACCA TAAGTTGCTC TCAGATCCTT
3951 GTTCTGAAGT ACATTCTTGG TTATCTGTAC TTCTGTAGCT GGTGTGATGC
4001 TGTTAATTGT ATGTACCACA CATCTCCAGA CGTTAATAAA GGACTCAAAG
4051 AGGTTTTTGT AAAAAAAAAA AAAAAAAAAA AA

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BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 131 bp to 3274 bp; peptide length: 1048
 Category: similarity to known protein

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1 MGPPRHPOAG EIEAGGAGGG RRLOVEMSSO QFPRLGAPST GLSQAPSQIA
51 NSGSAGLINP AATVNDESGR DSEVSAREHM SSSSSLQSRE EKQEPVVVRP
101 YPQVQMLSTH HAVASATPVA VTAPPAHLTP AVPLSFSEGL MKPPPKPTMP
151 SRPIAPAPPS TSLPPKVPV QVTVTMESSI PQASAI PVAT ISGQQGHPSN
201 LHHIMTTNVQ MSIIRSNAPG PPLHIGASHL PRGAAAAAVM SSSKVTTVLR
251 PTSQLPNAAT AQPAVQHIIH QPIQSRPPVT TSNAIPPAVV ATVSATRAQS
301 PVITTTAAHA TDSALSRPTL SIQHPPSAAI SIQRPAQSRD VTTRITLPSH
351 PALGTPKQQL HTMAQKTIFS TGT PVAAATV APILATNTIP SATTAGSVSH
401 TQAPTSTIVT MTVPSSHSSHA TAVTTSNIPV AKVVPQOITH TSPRIQPDYP
451 AERSSSLIPIS GHRASPNPVA METRSDNRPS VPVQFYFLP TYPPSAYPLA
501 AHTYTPITSS VSTIRQYPVS AQAPNSAITA QTGVGVASTV HLNPMQLMTV
551 DASHARHIQG IQPAPISTQG IQPAPICTPG IQAPPLGTQG IHSATPINTQ
601 GLQAPPMGTQ QPQPEGKTSV VVLADGATIV ANPISNPFSA APAATTVVQT
651 HSQSASTNAP AQGSSPRPSI LRKKPATDGA KPKSEIHVSM ATPVTVSMET
701 VSNQNNQDPT IAVPPTAQPP PPTIPTMIAA ASPPSQPAVA LSTIPGAVPI
751 TPITTTIAAA PPPSVTVGGS LSSVLGPPVP EIKVKEEVEP MDIMRPVSAV
801 PPLATNTVSP SLALLANNLS MPTSDLPFGA SPRKKPRKQQ HVISTEEGDM
851 METNSTDDEK STAKSLLVKA EKRKSPKEY IDEEGVRYVP VRPRPPITLL
901 RHYRNPWKAA YHHFQRYSDV RVKEEKKAML QEIANQKGVs CRAQGWKVHL
951 CAAQLQLTN LEHDVYERLT NLQEGII PKK KAATDDDLHR INELIQGNMQ
1001 RCKLVMQDIS EARDSMLKVL DHKDRVLKLL NKNGTVKKVS KLKRKEKV

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2a11, frame 2

SWISSPROT:MUC2_HUMAN MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)., N = 1,
 Score = 334, P = 2.4e-25

PIR:A43932 mucin 2 precursor, intestinal - human (fragments), N = 1,
Score = 321, P = 3.2e-24

TREMBL:D88440_1 product: "high molecular mass nuclear antigen"; Gallus
gallus mRNA for high molecular mass nuclear antigen, partial cds., N =
1, Score = 312, P = 8.3e-24

PIR:S48478 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast
(Saccharomyces cerevisiae), N = 1, Score = 300, P = 2.1e-22

>SWISSPROT:MUC2_HUMAN MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
Length = 5,179

HSPs:

Score = 334 (50.1 bits), Expect = 2.4e-25, P = 2.4e-25
Identities = 184/770 (23%), Positives = 263/770 (34%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + T V T P TP + + P P PT P
Sbjct: 3471 VTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPT 3530

Query: 155 A-PAPPSTLSLPPKVP-GQVTVMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
P +T P P G T T + P T +G Q P+ TT V +
Sbjct: 3531 TTPITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQT-PTTPIITTTTIVTPT 3589

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTVLRPTSQLPNAATAQPAVQHI 268
+ P P+ + P +++ +TT T T P I
Sbjct: 3590 PTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPI 3649

Query: 269 IHQPIQSRPPVTTSNAI PPAVVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
+ P T P T + T +P T T T + T++ P
Sbjct: 3650 TTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVT---PTPT 3706

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI
Sbjct: 3707 PTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIIT 3766

Query: 386 TNTI-PSATTAGSVSHQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPOQIHTSP 443
T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
Sbjct: 3767 TTTVTPPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTPTGT 3825

Query: 444 RIQPDYPAERSSLIPISGHRASPNP VAMETRSNRPSPVQFQYFL-PTYPPSAYPLAAH 502
+ P ++ + +P P +T + + P+ + PT P+
Sbjct: 3826 QTPTTTPIITTTTIVT----PTPTPTGTQTPT----TTPITTTTIVTPTPTPTG--TQTP 3874

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
T TPIT++ + T P Q P + IT T V T Q T
Sbjct: 3875 TTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTPTG--TGTQTPTTTPIITTTTIVT 3932

Query: 561 IQPAPISTQGIQPAPIGTPI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPQ- 613
P P TQ PI T P P GTQ + TPI T P P GTQ P
Sbjct: 3933 PTPTPTGTQTPTTTPIITTTTIVTPTPTGTQ-TPTTPIITTTTIVTPTPTGTQTPTT 3991

Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSIL 671
P T+ V T P + P + T T T +Q+ +T ++ P+
Sbjct: 3992 TPITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPT 4051

Query: 672 RKKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNQDPTIAVP---PTAQPPPTIPTMI 728
T P + TP +T + T P PT Q P T P
Sbjct: 4052 PTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIIT 4111

Query: 729 AAASPPSQPAVALSTIPGAVPITPPITTTIAAAPPSP-----VTVGSLSSVLGP-PVPEI 782
P+ T P PIT TT+ P P+ T + ++ + P P P
Sbjct: 4112 TTTVTPPTPTGTQT-PTTPIITTT-TTVTPTPTPTGTQTPTTPIITTTTIVTPTPTPTG 4169

Query: 783 KVKEEVEPMDIMRPVSAVP-PLATNTVSPSLALLANNLSMPTSDLPFGASPRKKPRKQ 841
P+ V+ P P T T P+ A + TS+ PP +S + R
Sbjct: 4170 TQTPTTPIITTTTIVTPTPTGTQTGPPHTHTSTAPIAELTTSNPPPESSSTPQTSRSTSS 4229

Query: 842 VISTEEGDMMET 853
+ TE ++ T
Sbjct: 4230 PL-TESTTLLST-4240

Score = 328 (49.2 bits), Expect = 1.0e-24, P = 1.0e-24
Identities = 180/745 (24%), Positives = 254/745 (34%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + T V T P TP + + P P PT P
Sbjct: 3540 VTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPTGTQTPT 3599

Query: 155 A-PAPPSTLSLPPKVP-GQVTVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
 P +T P P G T T + P T +G Q P+ TT V +
 Sbjct: 3600 TTPITTTTTVTPPTPTGTQTPTTPIITTTTTVTPTPTGTQT-PTTPIITTTTTVTPT 3658

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLPNAATAQPAVQHI 268
 + P P+ + P +++ +TT T T P I
 Sbjct: 3659 PTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPI 3718

Query: 269 IHQPIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
 + P T P T + T +P T T T + T++ P
 Sbjct: 3719 TTTTTPPTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVT---PTPT 3775

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
 Q P + TT P+ GT + T + T TP T PI
 Sbjct: 3776 PTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIIT 3835

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQIHTSP 443
 T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
 Sbjct: 3836 TTTVTPTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTP-TPTGT 3894

Query: 444 RIQPDYPAERSSSLIPISGHRASPNPVMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 502
 + P ++ + +P P +T + + P+ + PT P+
 Sbjct: 3895 QTPTTPIITTTTTVT-----PTPTPTGTQTPT-----TTPITTTTTVTPTPTPTG--TQTP 3943

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
 T TPIT++ + T P Q P + IT T V T Q T
 Sbjct: 3944 TTPITTTTTVTPTPTPTGTQTPTTPIITTTTTVTPTPTPT--TGTQTPTTPIITTTTTVT 4001

Query: 561 IQPAPISTQGIQAPIGTPIG---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQFQ- 613
 P P TQ PI T P P GTQ + TPI T P P GTQ P
 Sbjct: 4002 PTPTPTGTQTPTTPIITTTTTVTPTPTGTQT-PTTPIITTTTTVTPTPTGTQTPTT 4060

Query: 614 -PECKTSAVVADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSIL 671
 P T+ V T P + P + T T T +Q+ +T ++ P+
 Sbjct: 4061 TPITTTTTVTPTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTPT 4120

Query: 672 RKKPATDGAAPKSEIHVSMATPVTVSMETVSNQNNDOPTIAVP---PTAQPPPTPTPTMI 728
 T P + TP +T + T P PT Q P T P
 Sbjct: 4121 PTGTQTPTTPIITTTTTVTPTPTPTGTQTPTTPIITTTTTVTPTPTPTGTQTPTTPIIT 4180

Query: 729 AAASPPSQPAVALSTIPGAVPITPPITIAAA-PPPSVTVGSLSSVLGPVPVEIKVKEE 787
 P+ T P T PI + + PPP + + S P +
 Sbjct: 4181 TTTVTPTPTPTGTQTGPPTHTSTAPIAELTTSNPPESSTPQTSRSTSSPLTESTTLLST 4240

Query: 788 VEPMDIMRPVSAVPLATNTVSPSLALLANNLSMP--TSDLPFGASPR 833
 + P M S PP +T T +P+ + LS P T+ PPG R
 Sbjct: 4241 LPFAIEM--TSTAPP-STPT-APTTTSGGHTLSPPPSTTSPPGTPT 4284

Score = 325 (48.8 bits), Expect = 2.2e-24, P = 2.2e-24
 Identities = 186/782 (23%), Positives = 261/782 (33%)

Query: 96 VVVRPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
 V P P T + + T V T P TP + + P P PT P
 Sbjct: 3494 VTPTPTPTGTQTPTTPIITTTTTVTPTPTPTGTQTPTTPIITTTTTVTPTPTPTGTQTPT 3553

Query: 155 A-PAPPSTLSLPPKVP-GQVTVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
 P +T P P G T T + P T +G Q P+ TT V +
 Sbjct: 3554 TTPITTTTTVTPPTPTGTQTPTTPIITTTTTVTPTPTGTQT-PTTPIITTTTTVTPT 3612

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLPNAATAQPAVQHI 268
 + P P+ + P +++ +TT T T P I
 Sbjct: 3613 PTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPI 3672

Query: 269 IHQPIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
 + P T P T + T +P T T T + T++ P
 Sbjct: 3673 TTTTTPPTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVT---PTPT 3729

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
 Q P + TT P+ GT + T + T TP T PI
 Sbjct: 3730 PTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIIT 3789

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQIHTSP 443
 T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
 Sbjct: 3790 TTTVTPTPTPTGTQTPTTPIITTTTTVTPTPTGTQTPTTPIITTTTTVTPTP-TPTGT 3848

Query: 444 RIQPDYPAERSSSLIPISGHRASPNPVMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 502
 + P ++ + +P P +T + + P+ + PT P+
 Sbjct: 3849 QTPTTPIITTTTTVT-----PTPTPTGTQTPT-----TTPITTTTTVTPTPTPTG--TQTP 3897

Query: 503 TYTPITSSVS-TIRQYPVSAOAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560

T TPIT++ + T P Q P + IT T V T Q T
 Sbjct: 3898 TTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTP--TGTQTPTTPIITTTTIVT 3955
 Query: 561 IQPAPISTQGIQAPIGTPIG---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPQ- 613
 P P TQ P I T P P GTQ + TPI T P P GTQ P
 Sbjct: 3956 PTPTPTGTPTTTTPIITTTTIVTPTPTPTGTQ-TPTTPIITTTTIVTPTPTPTGTQTPTT 4014
 Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSIL 671
 P T+ V T P + P + T T T +Q+ +T ++ P+
 Sbjct: 4015 TPITTTTIVTPTPTPTGTQTPTTPIITTTTIVTPTPTPTGTQTPTTPIITTTTIVTPTPT 4074
 Query: 672 RKKPATDGAAPKSEIHVSMATPVTVSMETVSNQNNQDPTIAPV---PTAQPPPTIPTMI 728
 T P + TP +T + T P PT Q P T P
 Sbjct: 4075 PTGTQTPTTPIITTTTIVTPTPTPTGTQTPTTPIITTTTIVTPTPTPTGTQTPTTPIIT 4134
 Query: 729 AAASPPSQPAVALSTIPGAVPITPITTTIAAAPPSPVTVGGSLSVVGPPVPEIKVKEEV 788
 P+ T P PIT TT P P+ T G+ + P I V
 Sbjct: 4135 TTTVPTPTPTGTQT-PTTTPIT---TTTTVPTPTPT--GTQT---PTTTPITTTTIV 4184
 Query: 789 EPMDIMRPVSAVPLATNTVSPSLALLANNLSMPTSDLPFGASPRKKPRKQOHVISTEEG 848
 P PP T+T +P L +N P S P + P + + +
 Sbjct: 4185 TPTPTPTGTQTGPPTHTST-APIAELTTSN-PPESSTPQTSRSTSSPLTESTTLLSTLP 4242
 Query: 849 DMMETNSTDDEKSTAKSLLVKAERKRSPP 877
 +E ST + SPP
 Sbjct: 4243 PAIEMTSTAPPSTPTAPTTTSGGHTLSPP 4271
 Score = 324 (48.6 bits), Expect = 2.8e-24, P = 2.8e-24
 Identities = 170/717 (23%), Positives = 248/717 (34%)
 Query: 95 PVVVRYPYQVQMLSTHHAVASATP--VAVTAPPAHLTPAVPLSFSEGLMKPPPKPTMPSR 152
 P P P +T + +P T PP TP+ P++ + + P P+ P
 Sbjct: 1401 PPTTTPSPPTTTTTLPTTTPSPPTTTTTPPTTTPSPPTTTTTPPL-PTTTPSPPTIS 1459
 Query: 153 PIAPAPPSTLSLPPKVPGQVTVTMESIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
 PP+T PP T S + P T + P I +
 Sbjct: 1460 TTTTTPPTTTPSPPTTTPSPPTTTPSPPTTTPPTTTPPTTTPS---PPMTTPITPPASTTT 1516
 Query: 213 IIRSNAPGPELHIGASHLPGRGAAAAVMSSSKVTTLRPTSQ--LPNAAQAQPAVQHIIH 270
 + + P PP + P S T + PTS LP T P
 Sbjct: 1517 LPPTTTPSPPTTTTTPPP---TTTTPSPPTTTPITPPTSTTLPTTTPSPPTTTTTP 1571
 Query: 271 QPIQSRP-EVTTSNAPPAVAVTVSA-TRAQSEVITTTAAHATDSALSREPTLSIQHPFSA 328
 P + P P TT+ PP + T T SP TTT + S PT + PP++
 Sbjct: 1572 PPPTTTPSPPTTTPSPPTTTPPTTTPPTTTPSPPTTTPPTTTPPTTTPPTTTPITPPTS 1631
 Query: 329 AISIORPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKTIESTGTPVAAATVAPILATNT 388
 ++ T T P P TP T I +T TP T + +T
 Sbjct: 1632 TTTTLPPTTTPSPPTTTTTP--PPTTTPSPPTTTPPTTTPSPPTTTPPTTTPPTTTP 1689
 Query: 389 IPSATTAGSVSHTQAPTSTIVTMTVPSSHSHATAV-TTSNIPVAKVVPQQIHTSPRIQP 447
 P TT + S T P+S I T T PS ++ + TT P P T T + P
 Sbjct: 1690 SPPTTMTTPSPPTTTPSSPITTTTTPSSTTTPSPPTTMTTPSPPTTTPSPPTTMTTLPP 1749
 Query: 448 DYPAERSSLIPISGHRASPNPVAMETRSDNRPSVPV-QFQYFLPTYPPSAY-P-----LA 500
 + + P+ P T + P VP+ + +L + P+ + P L
 Sbjct: 1750 TTTSSPLTTTLPSPITPPTFSPFSTTTPTTTPCVPLCNWTGWLDGKPNFHKPGGDTELI 1809
 Query: 501 AHTYTPITSSVSTIR--QYP-VSAQAPNSAITAQTGVG-VASTVHLNPMQLMTVDASHAR 556
 P ++ + R YP V + VG + P ++ + A
 Sbjct: 1810 GDVCGPGWAANISCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQKPGGVIPM-AFCLN 1868
 Query: 557 HIQGIQAPAPISTQGIQAPIGTPIGQ-PAPLGTQGIHSATPINTQGLQAPAPMGTOQPQ-- 613
 + +Q TQ P + T + P P T I + T + P P GTQ P
 Sbjct: 1869 YEINVQCCECVTQ---PTTMTTTTENPTPTTPIITTTTIVTPT---PTPTGTQTPTTT 1922
 Query: 614 PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSILR 672
 P T+ V T P + P + T T T +Q+ +T ++ P+
 Sbjct: 1923 PIITTTTIVTPTPTPTGTQTPTTPIITTTTIVTPTPTPTGTQTPTTPIITTTTIVTPTPT 1982
 Query: 673 KKKPATDGAAPKSEIHVSMATPVTVSMETVSNQNNQDPTIAPV---PTAQPPPTIPTMIA 729
 T P + TP +T + T P PT Q P T P
 Sbjct: 1983 TGTQTPTTPIITTTTIVTPTPTPTGTQTPTTPIITTTTIVTPTPTPTGTQTPTTPIITTT 2042
 Query: 730 AASPPSQPAVALSTIPGAVPITPITTTIAAAPPSPVTVGGSLSVVGPPVPEIKVKEEVE 789
 P+ T P PIT TT P P+ T G+ + P V
 Sbjct: 2043 TTVPTPTPTGTQT-PTTTPIT---TTTTVPTPTPT--GTQTPTTPIITTTTIVTPTPT 2096
 Query: 790 PMDIMRPVSAVPLATNTVSPS 811
 P P + P T TV+P+
 Sbjct: 2097 PTGTQTPTT-PITTTTIVTPT 2117

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + T V T P TP + + P P PT P
Sbjct: 2068 VTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPT 2127

Query: 155 A-PAPPSTLSLPKVP-GQVVTMESSIPQASAI PVATISGQOGHPNLHHIMTTNVQMS 212
P + T P P G T T + P T + G Q P + TT V +
Sbjct: 2128 TTPITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQT-PTTTPITTTTPTPT 2186

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLPNAATAQPAVQHI 268
+ P P+ + P +++ +TT T T P I
Sbjct: 2187 PTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPI 2246

Query: 269 IHQPIQSRPPVTTNSAIPPAVVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
+ P T P T + T + P T T T + T++ P
Sbjct: 2247 TTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPT 2303

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAOKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI
Sbjct: 2304 PTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIIT 2363

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQITHTSP 443
T T+ P+ T G+ + T P + T T+ T P+ + T TT V P T T
Sbjct: 2364 TTTVTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPT 2422

Query: 444 RIQPDYPAERSSLIPISGHRASPNP VAMETRSNRPSPVPVQFYFL-PTYPPSAYPLAAH 502
+ P ++ + + P P + T + + P+ + PT P+
Sbjct: 2423 QTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPT 2471

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
T TPIT++ + T P Q P + IT T V T Q T
Sbjct: 2472 TTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPT--TGTQTPTTTPIITTTTPT 2529

Query: 561 IQPAPISTQGIQPAPIGTPIG---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPQ- 613
P P TQ PI T P P GTQ + TPI T P P GTQ P
Sbjct: 2530 PTPTPTGTQTPTTTPIITTTTPTPTPTGTQ-TPTTPIITTTTPTPTPTGTQTPTT 2588

Query: 614 -PEGKTSAVVLADGATIVANFISNPFSAAPAAAT-TVVQTHSQSASTNAPAQGSPPRPSIL 671
P T V T P + P + T T T + Q+ + T ++ P+
Sbjct: 2589 TPITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPT 2648

Query: 672 RKKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNQPTIAVP---PTAQPPPTIPTMI 728
T P + TP + T + T P PT Q P T P
Sbjct: 2649 PTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIIT 2708

Query: 729 AAASPPSOPAVALSTIPGAVPITPPIITIAAAPPSVTVGSSLSSVLGPPVPEIKVKEEV 788
P+ T P PIT TT P P+ T G+ + P V
Sbjct: 2709 TTTVTPTPTPTGTQT-PTTTPIT---TTTPTPTPTPT--GTQTPTTTPIITTTTPTPT 2762

Query: 789 EPMDIMRPVS AVPPLATNTVSPS 811
P P + P T TV+P+
Sbjct: 2763 TPTGTQTPTTT-PIITTTTPTPT 2784

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + T V T P TP + + P P PT P
Sbjct: 2206 VTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPT 2265

Query: 155 A-PAPPSTLSLPKVP-GQVVTMESSIPQASAI PVATISGQOGHPNLHHIMTTNVQMS 212
P + T P P G T T + P T + G Q P + TT V +
Sbjct: 2266 TTPITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQT-PTTTPITTTTPTPT 2324

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLPNAATAQPAVQHI 268
+ P P+ + P +++ +TT T T P I
Sbjct: 2325 PTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPI 2384

Query: 269 IHQPIQSRPPVTTNSAIPPAVVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
+ P T P T + T + P T T T + T++ P
Sbjct: 2385 TTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPT 2441

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAOKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI
Sbjct: 2442 PTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIITTTTPTPTPTGTQTPTTTPIIT 2501

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQITHTSP 443
T T+ P+ T G+ + T P + T T+ T P+ + T TT V P T T

Sbjct: 2502 TTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGT 2560

Query: 444 RIQPDYPAERSSLIPISGHRASPNPVMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 502
+ P ++ + +P P +T + + P+ + PT P+

Sbjct: 2561 QTPTTTPITTTTTVT-----PTPTPTGTQTPT-----TTPITTTTTVTPTPTPTG--TQTP 2609

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
T TPIT++ + T P Q P + IT T V T Q T

Sbjct: 2610 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPT--TGTQTPTTTPITTTTTVT 2667

Query: 561 IQPAPISTQGIQAPIGTPTGI---QPAPLGTQGIHSATPINTOGL---QPAPMGTOQPQ- 613
P P TQ PI T P P GTQ + TPI T P P GTQ P

Sbjct: 2668 PTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQ-TPTTTPITTTTTVTPTPTPTGTQTPTT 2726

Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSIL 671
P T+ V T P + P + T T T +Q+ +T ++ P+

Sbjct: 2727 TPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPT 2786

Query: 672 RKKPATDGA KPKSEIHVSMATPVTVSMETVSNQNDQPTIAVP---PTAQPPPTIPTMI 728
T P + TP +T + T P PT Q P T P

Sbjct: 2787 PTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITT 2846

Query: 729 AAASPPSQPAVALSTIPGAVPITPPIITIAAAPPSVTVGSSLSSVLGPPVPEIKVKEEV 788
P+ T P PIT TT P P+ T G+ + P V

Sbjct: 2847 TTTVTPTPTPTGTQT-PTTTPIT---TTTTVTPTPTPT--GTQTPTTTPITTTTTVTPTP 2900

Query: 789 EPMDIMRPVSAVPLATNTVSPS 811
P P + P T TV+P+

Sbjct: 2901 TPTGTQTPTTT-PITTTTTVTPT 2922

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRPYQVQMLSTHHAASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + T V T P TP + + P P PT P

Sbjct: 2321 VTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPT 2380

Query: 155 A-PAPPSTLSLPPKVP-QQVTVTMESIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
P +T P P G T T + P T +G Q P+ TT V +

Sbjct: 2381 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQT-PTTTPITTTTTVTPT 2439

Query: 213 IIRSNAPGP---PLHIGASHLRGAAAAA-VMSSSKVTTVLRPTSQLPNAATAQPAVQHI 268
+ P P+ + P +++ +T T T P I

Sbjct: 2440 PTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTP 2499

Query: 269 IHQPIQSRPPVTTNAIPPAVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
+ P T P T + T +P T T T + T++ P

Sbjct: 2500 TTTTPTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVT---PTPT 2556

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI

Sbjct: 2557 PTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITT 2616

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPPQIHTSP 443
T T+ P+ T G+ + T P +T T P+ + T TT V P T T

Sbjct: 2617 TTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGT 2675

Query: 444 RIQPDYPAERSSLIPISGHRASPNPVMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 502
+ P ++ + +P P +T + + P+ + PT P+

Sbjct: 2676 QTPTTTPITTTTTVT-----PTPTPTGTQTPT-----TTPITTTTTVTPTPTPTG--TQTP 2724

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
T TPIT++ + T P Q P + IT T V T Q T

Sbjct: 2725 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPT--TGTQTPTTTPITTTTTVT 2782

Query: 561 IQPAPISTQGIQAPIGTPTGI---QPAPLGTQGIHSATPINTOGL---QPAPMGTOQPQ- 613
P P TQ PI T P P GTQ + TPI T P P GTQ P

Sbjct: 2783 PTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQ-TPTTTPITTTTTVTPTPTPTGTQTPTT 2841

Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSIL 671
P T+ V T P + P + T T T +Q+ +T ++ P+

Sbjct: 2842 TPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPT 2901

Query: 672 RKKPATDGA KPKSEIHVSMATPVTVSMETVSNQNDQPTIAVP---PTAQPPPTIPTMI 728
T P + TP +T + T P PT Q P T P

Sbjct: 2902 PTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITT 2961

Query: 729 AAASPPSQPAVALSTIPGAVPITPPIITIAAAPPSVTVGSSLSSVLGPPVPEIKVKEEV 788
P+ T P PIT TT P P+ T G+ + P V

Sbjct: 2962 TTTVTPTPTPTGTQT-PTTTPIT---TTTTVTPTPTPT--GTQTPTTTPITTTTTVTPTP 3015

Query: 789 EPMDIMRPVSAVPPLATNTVSPS 811
P P + P T TV+P+
Sbjct: 3016 TPTGTQTPTTT-PITTTTTVTPT 3037

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + TV T P TP + + P P PT P
Sbjct: 2390 VTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPT 2449

Query: 155 A-PAPPSTLSLPPKVP-GQVTVMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
P +T P P G T T + P T +G Q P+ TT V +
Sbjct: 2450 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQT-PTTPITTTTVTPT 2508

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLENAATAQPAVQHI 268
+ P P+ + P +++ -TT T T P I
Sbjct: 2509 PTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPI 2568

Query: 269 IHQPIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRLTSLIQHPPSA 328
+ P T P T + T +P T T T + T++ P
Sbjct: 2569 TTTTIVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVT---PTPT 2625

Query: 329 AISIORPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI
Sbjct: 2626 PTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPIIT 2685

Query: 386 TNTI-PSATTAGSVSHQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQITHTSP 443
T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
Sbjct: 2686 TTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGT 2744

Query: 444 RIQPDYFAERSSSLIPISGHRASPNPVAMETRSNRPSPVPVQFYFL-PTYPPSAYPLAAH 502
+ P ++ + +P P +T + + P+ + PT P+
Sbjct: 2745 QTPTTTPITTTTVT----PTPTPTGTQTPT---TTPITTTTTVTPTPTPTG--TQTP 2793

Query: 503 TYTPITSSVS-TIRQYPVSAOAPNSA-ITAQTGVGVASTVHLNPMOLMTVDASHARHIOG 560
T TPIT++ + T P Q P + IT TV T Q T
Sbjct: 2794 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPT--TGTQTPTTTPITTTTVT 2851

Query: 561 IQPAPISTQGIQPAPIGTPI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPQ- 613
P P TQ PI T P P GTQ + TPI T P P GTQ P
Sbjct: 2852 PTPTPTGTQTPTTTPITTTTVTPTPTPTGTQ-TPITTTPITTTTVTPTPTPTGTQTPTT 2910

Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSRPSPIL 671
P T+ V T P + P+ T T T+Q+ T ++ P+
Sbjct: 2911 TPITTTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPT 2970

Query: 672 RKKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNDOPTIAVP---PTAQQPPTIPTMI 728
T P + TP +T + T P PT Q P T P
Sbjct: 2971 PTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPIIT 3030

Query: 729 AAASPPSQPAVALSTIPGAVPITPPITTTIAAAPPSPVTVGGSLSVLGPPVPEIKVKEEV 788
P+ T P PIT TT P P+ T G+ + P V
Sbjct: 3031 TTTVTPTPTPTGTQT-PTTPIIT---TTTTVTPTPTPT--GTQTPTTTPITTTTVTPTPT 3084

Query: 789 EPMDIMRPVSAVPPLATNTVSPS 811
P P + P T TV+P+
Sbjct: 3085 TPTGTQTPTTT-PITTTTTVTPT 3106

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P T + + TV T P TP + + P P PT P
Sbjct: 2459 VTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPT 2518

Query: 155 A-PAPPSTLSLPPKVP-GQVTVMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
P +T P P G T T + P T +G Q P+ TT V +
Sbjct: 2519 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQT-PTTPITTTTVTPT 2577

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLENAATAQPAVQHI 268
+ P P+ + P +++ +TT T T P I
Sbjct: 2578 PTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPI 2637

Query: 269 IHQPIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRLTSLIQHPPSA 328
+ P T P T + T +P T T T + T++ P
Sbjct: 2638 TTTTIVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVT---PTPT 2694

Query: 329 AISIORPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI
Sbjct: 2695 PTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPIIT 2754

Query: 386 TNIT-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQITHTSP 443
 T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
 Sbjct: 2755 TTTVTPTPTPTGTQTPTTTTPIITTTTIVTPTPTGTQTPTTTPIITTTTIVTPTPT-TPTGT 2813

Query: 444 RIQPDYPAERSSLIPISGHRASPNPVMETRSDNRPSVPVQFQYFL-PTYPPSAYPLAAH 502
 + P ++ + +P P +T + + P+ + PT P+
 Sbjct: 2814 QTPTTTPITTTTIVT-----PTPTPTGTQTPT----TTPITTTTIVTPTPTPTG--TQTP 2862

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
 T TPIT++ + T P Q P + IT TV T Q T
 Sbjct: 2863 TTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPT--TGTQTPTTTPIITTTTIVT 2920

Query: 561 IQPAPISTQGIQAPIGTPTGI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPO- 613
 P P TQ PI T P P GTQ + TPI T P P GTQ P
 Sbjct: 2921 PTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQ-TPTTTPIITTTTIVTPTPTPTGTQTPTT 2979

Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSPPRSIL 671
 P T+ V T P + P + T T T +Q+ +T ++ P+
 Sbjct: 2980 TPITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPT 3039

Query: 672 RKKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNQPTIAVP---PTAQPPPTIPTMI 728
 T P + TP +T + T P PT Q P T P
 Sbjct: 3040 PTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIIT 3099

Query: 729 AAASPPSQPAVALSTIPGAVPITPPIITIAAAPPSVTVGGSLSVLPVPEIKVKEEV 788
 P+ T P PIT TT P P+ T G+ + P V
 Sbjct: 3100 TTTVTPTPTPTGTQT-PTTTPIT---TTTTVTPTPTPT--GTQTPTTTPIITTTTIVTPTPT 3153

Query: 789 EPMDIMRPVSAVPLATNTVSPS 811
 P P + P T TV+P+
 Sbjct: 3154 TPTGTQTPTTT-PIITTTTIVTPT 3175

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
 Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
 V P P T + + TV T P TP + + P P PT P
 Sbjct: 2528 VTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPT 2587

Query: 155 A-PAPPSTLSLPPKVP-GQVTVMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
 P +T P P G T T + P T +G Q P+ TT V +
 Sbjct: 2588 TTPITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQT-PTTTPITTTTIVTPT 2646

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTVLVRPTSQLPNAATAQPAVQHI 268
 + P P+ + P +++ +TT T T P I
 Sbjct: 2647 PTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPI 2706

Query: 269 IHQPIQSRPPVTTSNAPPAVVATVSATRAQSPVITTTAAHATDSALSRPTLSIQHPPSA 328
 + P T P T + T +P T T T + T++ P
 Sbjct: 2707 TTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVT---PTPT 2763

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
 Q P + TT P+ GT + T + T TP T PI
 Sbjct: 2764 PTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIIT 2823

Query: 386 TNIT-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQITHTSP 443
 T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
 Sbjct: 2824 TTTVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPT-TPTGT 2882

Query: 444 RIQPDYPAERSSLIPISGHRASPNPVMETRSDNRPSVPVQFQYFL-PTYPPSAYPLAAH 502
 + P ++ + +P P +T + + P+ + PT P+
 Sbjct: 2883 QTPTTTPITTTTIVT-----PTPTPTGTQTPT----TTPITTTTIVTPTPTPTG--TQTP 2931

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
 T TPIT++ + T P Q P + IT TV T Q T
 Sbjct: 2932 TTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPT--TGTQTPTTTPIITTTTIVT 2989

Query: 561 IQPAPISTQGIQAPIGTPTGI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPO- 613
 P P TQ PI T P P GTQ + TPI T P P GTQ P
 Sbjct: 2990 PTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQ-TPTTTPIITTTTIVTPTPTPTGTQTPTT 3048

Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSPPRSIL 671
 P T+ V T P + P + T T T +Q+ +T ++ P+
 Sbjct: 3049 TPITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPT 3108

Query: 672 RKKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNQPTIAVP---PTAQPPPTIPTMI 728
 T P + TP +T + T P PT Q P T P
 Sbjct: 3109 PTGTOTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIITTTTIVTPTPTPTGTQTPTTTPIIT 3168

Query: 729 AAASPPSQPAVALSTIPGAVPITPPIITIAAAPPSVTVGGSLSVLPVPEIKVKEEV 788

P+ T P PIT TT P P+ T G+ + P V
Sbjct: 3169 TTTVTPTPTPTGTQT-PTTTPIT---TTTTVTPTPTPT--GTQTPTTTPITTTTTVTPTP 3222
Query: 789 EPMDIMRPVSAVPPLATNTVSPS 811
P P + P T TV+P+
Sbjct: 3223 TPTGTQTPTTT-PITTTTTVTPT 3244

Score = 318 (47.7 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 174/717 (24%), Positives = 243/717 (33%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P P T + + T V T P TP + + P P PT P
Sbjct: 3080 VTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPT 3139
Query: 155 A-PAPPSTLSLPPKVP-GQVVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
P +T P P G T T + P T +G Q P+ TT V +
Sbjct: 3140 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQT-PTTTPITTTTTVTPT 3198
Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTVLRPTSQLPNAATAQPAVQHI 268
+ P P+ + P +++ +TT T T P I
Sbjct: 3199 PTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTP I 3258
Query: 269 IHQIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRLPSIQHPSPA 328
+ P T P T + T +P T T T + T++ P
Sbjct: 3259 TTTTPTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVT---PTPT 3315
Query: 329 AISIQRPQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
Q P + TT P+ GT + T + T TP T PI
Sbjct: 3316 PTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITT 3375
Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQITHTSPT 443
T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
Sbjct: 3376 TTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGT 3434
Query: 444 RIQPDYPAERSSLIPISGHRASPNPVMETRSDNRPSVPVQFQYFL-PTYPPSAYPLAAH 502
+ P ++ + +P P -T + + P+ + PT P+
Sbjct: 3435 QTPTTTPITTTTTVT-----PTPTPTGTQTPT----TTPITTTTTVTPTPTPTG--TQTP 3483
Query: 503 TYTPITSSVS-TIRQYFVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
T TPIT++ + T P Q P + IT T V T Q T
Sbjct: 3484 TTTPTTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPT--TGTQTPTTTPITTTTTVT 3541
Query: 561 IQPAPISTQGIQAPIGTPTGI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPO- 613
P P TQ PI T P P GTQ + TPI T P P GTQ P
Sbjct: 3542 PTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQ-TPTTTPITTTTTVTPTPTPTGTQTPTT 3600
Query: 614 -PEGKTSAVVLADGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSPPRESIL 671
P T+ V T P + P + T T T +Q+ +T ++ P+
Sbjct: 3601 TPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPT 3660
Query: 672 RKKPATDGA PKSEIHVSMATPVTVSMETVSNQNDQPTIAMP---PTAQPPPTIPTMI 728
T P + TP +T + T P PT Q P T P
Sbjct: 3661 PTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITT 3720
Query: 729 AAASPPSQPAVALSTIPGAVPITPPTITIAAAPPSVTVGGSLSVLGPPVPEIKVKEEV 788
P T P PIT TT P P+ T G+ + P V
Sbjct: 3721 TTTVTPTPTPTGTQT-PTTTPIT---TTTTVTPTPTPT--GTQTPTTTPITTTTTVTPTPT 3774
Query: 789 EPMDIMRPVSAVPPLATNTVSPS 811
P P + P T TV+P+
Sbjct: 3775 TPTGTQTPTTT-PITTTTTVTPT 3796

Score = 313 (47.0 bits), Expect = 4.2e-23, P = 4.2e-23
Identities = 169/695 (24%), Positives = 245/695 (35%)

Query: 96 VVVRYPYQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
V P P P T + + T V T P TP + + P P PT P
Sbjct: 3655 VTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPT 3714
Query: 155 A-PAPPSTLSLPPKVP-GQVVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
P +T P P G T T + P T +G Q P+ TT V +
Sbjct: 3715 TTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQT-PTTTPITTTTTVTPT 3773
Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTVLRPTSQLPNAATAQPAVQHI 268
+ P P+ + P +++ +TT T T P I
Sbjct: 3774 PTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTP I 3833
Query: 269 IHQIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRLPSIQHPSPA 328
+ P T P T + T +P T T T + T++ P
Sbjct: 3834 TTTTPTPTPTPTGTQTPTTTPITTTTTVTPTPTPTGTQTPTTTPITTTTTVT---PTPT 3890

Query: 329 AISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
 Q P + TT P+ GT + T + T TP T PI
 Sbjct: 3891 PTGTQPTTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIIT 3950

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQIHTHTSP 443
 T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
 Sbjct: 3951 TTTVTPPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTPTGT 4009

Query: 444 RIQPDYPAERSSSLIPISGHRASPNPVMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 502
 + P ++ + +P P +T + + P+ + PT P+
 Sbjct: 4010 QTPTTTPITTTTIVT-----PTPTPTGTQPT-----TTPITTTTIVTPTPTPTG--TQTP 4058

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQ 560
 T TPIT++ + T P Q P + IT T V T Q T
 Sbjct: 4059 TTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTP--TGTQPTTTPIITTTTIVT 4116

Query: 561 IQPAPISTQGIQAPIGTPGI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPQP 614
 P P TQ PI T P P GTQ + TPI T P P GTQ P
 Sbjct: 4117 PTPTPTGTQPTTTPIITTTTIVTPTPTGTQ-TPTTPIITTTTIVTPTPTPTGTQPT- 4174

Query: 615 EGKTSAVVLADGATIVANPISNPFSAAPAAATTVVQTHSQSASTNAPAQSSPRPSILRKK 674
 T+ + T+ P P T ++ ++N P + S+P+ S
 Sbjct: 4175 ---TTPITTT--TTVTPPTPTGTQTPHTSTAPIAELTTSNPPESSTPQTSRSTSS 4229

Query: 675 PATDGAKPKSEIH--VSMATPVTVSMETVSNQNNDOPTIAVPP-TAQOPP--PTIPTMIA 729
 P T+ S + + M + S T + T++ PP T PP PT T
 Sbjct: 4230 PLTESTLLSLPPAIEMTSTAPPSTPTAPTTTSGGHTLSPPPSTTTSPPGTPTRGTTTG 4289

Query: 730 AASPPSQPAVALSTI----PGAVPITPP--ITTIAAAP-PPSVTVGGSLSVLGPPVPEI 782
 ++S P+ V +T P P++ P I T P P SV + L+ P E+
 Sbjct: 4290 SSSAPTSTVQTTTTSAWTPPTPLSTPSIIRTGLRYPSSVLICCVLNDTYYPAGEEV 4349

Score = 279 (41.9 bits), Expect = 1.8e-19, P = 1.8e-19
 Identities = 138/540 (25%), Positives = 194/540 (35%)

Query: 278 PVTTSNAIPPAVVATVSATRAQSPVITTTAAH-----ATDSALSRP--TLSIOHPPSAA 329
 P+TT+ + P T + T +P+ TTT T + + P T + P
 Sbjct: 1946 BITTTTIVTPTPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTP 2005

Query: 330 ISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILAT 386
 Q P + TT P+ GT + T + T TP T PI T
 Sbjct: 2006 TGTQPTTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTT 2065

Query: 387 NTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQIHTHTSPR 444
 T+ P+ T G+ + T P +T T+T P+ + T TT V P T T +
 Sbjct: 2066 TTVTPPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTPTGTQ 2124

Query: 445 IQPDYPAERSSSLIPISGHRASPNPVMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 503
 P ++ + +P P +T + + P+ + PT P+ T
 Sbjct: 2125 TPTTTPITTTTIVT-----PTPTPTGTQPT-----TTPITTTTIVTPTPTPTG--TQTP 2173

Query: 504 YTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQGI 561
 TPIT++ + T P Q P + IT T V T Q T
 Sbjct: 2174 TTPITTTTIVTPTPTPTGTQPTTTPIITTTTIVTPTPTP--TGTQPTTTPIITTTTIVTPT 2231

Query: 562 QPAPISTQGIQAPIGTPGI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPQP-- 613
 P P TQ PI T P P GTQ + TPI T P P GTQ P
 Sbjct: 2232 TPTPTGTQPTTTPIITTTTIVTPTPTGTQ-TPTTPIITTTTIVTPTPTPTGTQPTTT 2290

Query: 614 PEGKTSAVVLADGATIVANPISNPFSAAPAAAT-TVVQTHSQSASTNAPAQSSPRPSILR 672
 P T+ V T P + P + T T T +Q+ +T ++ P+
 Sbjct: 2291 PITTITTTIVTPTPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTP 2350

Query: 673 KKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNDOPTIAVP---PTAQOPPPTIPTMIA 729
 T P + TP +T + T P PT Q P T P
 Sbjct: 2351 TGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTPTGTQPTTTPIITTT 2410

Query: 730 AASPPSQPAVALSTIPGAVPITPPITTIAAAPPSVTVGGSLSVLGPPVPEIKVKEEVE 789
 P+ T P PIT TT P P+ T G+ + P V
 Sbjct: 2411 TTVTPPTPTGTQPTTTPIITTTTIVTPTPT--GTQPTTTPIITTTTIVTPTPT 2464

Query: 790 PMDIMRPVSAVPLATNTVSPS 811
 P P + P T TV+P+
 Sbjct: 2465 PTGTQPTTT-PITTTTIVTPT 2485

Score = 265 (39.8 bits), Expect = 5.8e-18, P = 5.8e-18
 Identities = 179/746 (23%), Positives = 257/746 (34%)

Query: 96 VVVRYPVQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
 V P P T + + T V T P TP + + P P PT P
 Sbjct: 3678 VTPTPTPTGTQPTTTPIITTTTIVTPTPTGTQPTTTPIITTTTIVTPTPTGTQPTPT 3737

Query: 155 A-PAPPSTLSLPPKVP-GQVTVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
 P +T P P G T T + P T +G Q P+ TT V +
 Sbjct: 3738 TTPITTTTTPPTPTPTGTQTPTTTTITTTTTPPTPTPTGTQT-PTTTPITTTTTPPT 3796

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTTVLRPTSQLPNAATAQPAVOHI 268
 + P P+ + P +++ +TT T T P I
 Sbjct: 3797 PTPTGTQTPTTTTITTTTTPPTPTPTGTQTPTTTTITTTTTPPTPTPTGTQTPTTTPI 3856

Query: 269 IHQIQSRPPVTTSSNAIPPAVVATVSATRAQSPVITTTAAHATDSALSRTLSIQHPPSA 328
 + P T P T + T +P T T T + T++ P
 Sbjct: 3857 TTTTTPPTPTPTGTQTPTTTTITTTTTPPTPTPTGTQTPTTTTITTTTTP---PTPT 3913

Query: 329 AISIQRPQSRDVTTRITLPSHPALGTPKQQLHTMAQKT-IFSTGTPVAAAT--VAPILA 385
 Q P + TT P+ GT + T + T P T P I
 Sbjct: 3914 PTGTPTTTTITTTTTPPTPTPTGTQTPTTTTITTTTTPPTPTPTGTQTPTTTPIIT 3973

Query: 386 TNTI-PSATTAGSVSHTQAPTSTIVTMT-VPSHSSHATAVTTSNIPVAKVVPQQIHTTSP 443
 T T+ P+ T G+ + T P +T T+T P+ + T TT V P T T
 Sbjct: 3974 TTTVTPPTPTGTQTPTTTTITTTTTPPTPTPTGTQTPTTTTITTTTTPPTPTPTGT 4032

Query: 444 RIQPDYPAERSSSLIPISGHRASPNPVAMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAH 502
 + P ++ + +P P +T + + P+ + P T P+
 Sbjct: 4033 QTPTTTTITTTTTP---PTPTPTGTQTPT---TTPITTTTTPPTPTPTG--TQTP 4081

Query: 503 TYTPITSSVS-TIRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQG 560
 T TPIT++ + T P Q P + IT T V T Q T
 Sbjct: 4082 TTPITTTTTPPTPTPTGTQTPTTTTITTTTTPPTPTPTG--TGTQTPTTTTITTTTTP 4139

Query: 561 IQPAPISTOGIQPAPIGTPIG---QPAPLGTQGIHSATPINTOGL---QPAPMGTTQQQP 614
 P P TQ P I T P P GTQ + TPI T P P GTQ P
 Sbjct: 4140 PTPTPTGTQTPTTTTITTTTTPPTPTPTGTQ-TPTTTTITTTTTPPTPTPTGTQTGPP 4198

Query: 615 ECKTSAVVADGATIVANPISNPFSAAPA---ATTVVQTHSQSA-STNAPA---QGSSRP 668
 TS +A+ T +NP P S+ P +T+ T S + ST PA S+ P
 Sbjct: 4199 T-HTSTAPIAELT--SNP--PPESTPQTSRSTSSPLTESTTLLSTLPPAEMTSTAPP 4253

Query: 669 SILRKKPATDGA PKSEIHVSMATPVTVSMETVSNQNDQPTIAVPPTAQPPPTIPTMI 728
 S T G S + +P + ++ PT + T T PT
 Sbjct: 4254 STPTAPTSTSGGHTLSPPSTTTSPPGTPTRGTTTGSSAPTSTVQTTTSAWT-PTPT 4312

Query: 729 AAASPPSQPAVALSTIPGAVPITPPITIAAAPPSPVTVGSSLSSVLGPPVPEIKVKEEV 788
 ++P L P +V I + AP V G+ + E
 Sbjct: 4313 PLSTPSIIRTGLRPYPSSVLICCVLNDTYAPGEEV-YNGTYGDTCYFVNCSLSCTLEF 4371

Query: 789 EPMDIMRPVSAVPELATNTVSPSLALLANNLSMPTSDLPFGASPRKKPRKQOH 841
 S P + +T +PS ++ S PT P P P +Q++
 Sbjct: 4372 YNWSCPSTPSTPTPSKPTPSKP--SSTPSKPTPGTKPECPDFDPPEQEN 4422

Score = 254 (38.1 bits), Expect = 8.7e-17, P = 8.7e-17
 Identities = 167/697 (23%), Positives = 245/697 (35%)

Query: 115 SATPVAVTAPPAHLTPAVPLSFSEGLMKPPPK--PTMPSP-PIAPAPPSTLSLPPKV-PG 170
 S + T PP TP+ P + + PPP P+ P+ P I P P ST +LPP P
 Sbjct: 1587 SPPTITTTTPPTTTTPSPPTTTT---TPPTTTTPPTTTTPTP-PTSTTTPPTTTPS 1642

Query: 171 QVTVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMSIIRSNAPGPPLHIGASHL 230
 T + P + P T + + TT I + P PP +
 Sbjct: 1643 PPPTTTTTPPTTTTPSPPTTTTPSPITTTTTPPTTTTPSSPI--TTTPSPPTTMTTTPS 1700

Query: 231 PRGAAAAVMSSSKVTTVLRPTSQLPNAATAQPAVOHIHQIQS-RPPVTTSSNAIPPAV 289
 P SS +TT P+S + P P + PP TT +PP
 Sbjct: 1701 P-----TTTPSSPITTTTTPSS---TTTPSPPTTMTTTPSPPTTTMTTLPPT 1751

Query: 290 VATVSATRAQSPVITT-TAAHATDSALSRTLSIQH---PPSAAISIQRPQSRDVTTR 344
 ++ T P IT T + + + + P + + + S + +P ++
 Sbjct: 1752 TSSPLTTTLPPTSITPPTFSPTTTTPTTPCVPLCNWTGWLDGKPNFHKPGGDTLIGD 1811

Query: 345 ITLPSHPALGTPKQQLHTMAQKTIFSTGTPVAAATVAPILATN-----TIPSATTAGS 397
 + P A + + ++ I G V ++ N IP A
 Sbjct: 1812 VCGPGWAANISCRATMYP--DVPIQGLGQTVVCDVSVGLICKNEDQKPGGVIPMAFCLNY 1869

Query: 398 VSHTQAPTSTI--VTMTVPSHSSHATAVTTSNIPVAKVVPQQIHTTSPRIQPDYPAERSS 455
 + Q TMT + + + T TT+ I V T T + P ++
 Sbjct: 1870 EINVCCECVTQPTTMTTTT-TENPTPTTTTITTTTTPPTPTPTGTQTPTTTTITTTT 1928

Query: 456 LIPISGHRASPNPVAMETRSDNRPSVPVQFYFL-PTYPPSAYPLAAHTYTPITSSVS-T 513
 + +P P +T + + P+ + P T P+ T TPIT++ + T
 Sbjct: 1929 TVT-----PTPTPTGTQTPT---TTPITTTTTPPTPTPTG--TQPTTTTITTTTTP 1977

Query: 514 IRQYPVSAQAPNSA-ITAQTGVGVASTVHLNPMQLMTVDASHARHIQIQPAPISTQGIQ 572

P Q P + IT T V T Q T P P TQ
 Sbjct: 1978 PTPPTGTQTPTTTTPIITTTTTVTPTPTPT--TGTQTPTTTPIITTTTTVTPTPTPTGTQTPT 2035
 Query: 573 PAPIGTPGI---QPAPLGTQGIHSATPINTQGL---QPAPMGTOQPO--PEGKTSAVVLA 624
 PI T P P GTQ + TPI T P P GTQ P P T+ V
 Sbjct: 2036 TTPITTTTTVTPTPTPTGTQ-TPTTTPITTTTTVTPTPTPTGTQTPTTTPIITTTTTVTPTPT 2094
 Query: 625 DGATIVANPISNPFSAAPAAT-TVVQTHSQSASTNAPAQGSSPRPSILRKKPATDGAKPK 683
 T P + P + T T T +Q+ +T ++ P+ T P
 Sbjct: 2095 PTPGTQTPTTTPIITTTTTVTPTPTPTGTQTPTTTPIITTTTTVTPTPTPTGTQTPTTTPI 2154
 Query: 684 SEIHVSMATPVTVMETVSNQNDQPTIAVP---PTAQQPPPTIPTMIAAASPPSQPAVA 740
 + TP +T + T P PT Q P T P P+
 Sbjct: 2155 TTTTPTPTPTPTGTQTPTTTPIITTTTTVTPTPTPTGTQTPTTTPIITTTTTVTPTPTPTG 2214
 Query: 741 LSTIPGAVPITPPITIAAAPPSSVTVGSSLSVLGPPVPEIKVKEEVEPMDIMRPVSAV 800
 T P PIT TT P P+ T G+ + P V P T P P+
 Sbjct: 2215 TQT-PTTTPIT---TTTTVTPTPTPT--GTQTPTTTPITTTTTVTPTPTPTGTQTPTTT- 2267
 Query: 801 PPLATNTVSPS 811
 P T TV+P+
 Sbjct: 2268 PITTTTTVTPT 2278

Score = 243 (36.5 bits), Expect = 1.3e-15, P = 1.3e-15
 Identities = 110/406 (27%), Positives = 154/406 (37%)

Query: 121 VTAP-PAHLTPAVPLSFSEGLMKPPPKPTMPSRPIAPAPPSTLSLPPKVPGQVVTMESS 179
 +T P P TP+ P + + L P P+ P+ PP+T PP T + ++
 Sbjct: 1396 ITTPSPPTTTPSPPTTTTTL-PTTTPSPPTTTTTPPTTTPSPPTTTPSPPTT--TTTLPPT 1452
 Query: 180 IPQASAI PVATISGQQGHPSNLHHIMTTNVQMSIIRSNA GPPLHIGASHLPRGAAAAAV 239
 P P++T + P+ TT + P PP + P
 Sbjct: 1453 TPSP---PISTTTTTP--PTTTPSPPTTTPSP--TTTTPSPPTTTTTPPP-----TT 1498
 Query: 240 MSSSKVTTVLRP---TSQLPNAATAQPAVQHIIHQPIQSRP-PVTTSNAI PPAVVATVSA 295
 S +TT + P T+ LP T P P + P P TT+ PP T+
 Sbjct: 1499 TPSPMTTPTTPASTTTLPPTTTPSPPTTTTTPPTTTPSPPTTTPITPTSTTTLP 1558
 Query: 296 TRAQSPVITTTAAHATDSALSRPTLSIQHPPSA AISIQRPAQSRDV-TTRITLPSHPALG 354
 T SP TTT + S PT + PP+ + P + TT T P P
 Sbjct: 1559 TTTTPSPPTTTTTPPTTTPSPPTTTPSPPTTTPPTTTPPTTTPSPPTTTPPTTTP--PPTT 1616
 Query: 355 TPKQQLHTMAQKTIESTGTAVAAATVAPILATNTIPSATTAGSVSHTQAPTSTIVTMTVP 414
 TP T +T P T +P T T P TT S T P+ I T T P
 Sbjct: 1617 TPSPPTTTPITPTSTTTLP-PTTTPSPPTTTPPTTTPSPPTTTPSPPTTTPSPPTTTPPTTTP 1675
 Query: 415 SHSSHATA-VTTSNIPVAKVVPQQITHTSPIQPDYPAERSSLIPISGHRASPNPVAMET 473
 ++ ++ +TT+ P + T SP P P ++ P S SP P M T
 Sbjct: 1676 PPTTTPSSPITTTTPSPPTTMM---TTPSPPTTTPSSPITTTT-PSSTTTPSPPTTMTT 1730
 Query: 474 RSDNR-PSVPVQFQYFLPTYPPSAYPLAHTYTPITSSVSTIRQYPVSAQAPNS 526
 S PS P LP S+ PL T TP+ S++ P S P +
 Sbjct: 1731 PSPTTTPSPPTTMTTLPPTTSS-PL---TTPLPSPITPPTSPFSTTTPTT 1780

Score = 189 (28.4 bits), Expect = 8.0e-09, P = 8.0e-09
 Identities = 92/374 (24%), Positives = 133/374 (35%)

Query: 439 THTSPRIQPDYPAERSSLIPISGHRASPNPVAMETRSDNRPSVPVQFQYF-LPTYPPSAY 497
 T + P P P ++ +P + + P PS P+ LPT PS
 Sbjct: 1398 TPSPPTTTPSPPTTTLPTTTPSPPTTTPPTTTPSPPTTTPPTTTPPTTTPPTTTPPTTTPSP- 1456
 Query: 498 PLAHTYTPITSSVSTIRQYPVSAQAPNSAITAQTGVGVASTVHLNPMQL-MTVDASHAR 556
 P++ T P T++ S P S T T +T PM +T AS
 Sbjct: 1457 PISTTTTTPTTTPSPPTTTPSPPTTTPSPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 1516
 Query: 557 HIQGIQAPISTQGIQAPIGTQGIQAPLGTQGIHSATPINTQGLQAPMGTOQPOPEG 616
 P+P +T P P TP +P T I P +T L P T P P
 Sbjct: 1517 LPPTTTPSPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 1566
 Query: 617 KTSAVVLADGATIVANPISNPFSAAPAATTVVQTHSQSASTNAP--AQGSSPRPSILRKK 674
 T+ T +P P + P+ T+ T +T +P ++P P+
 Sbjct: 1567 TTTTT---PPPTTTPSP---PTTTPSPPTTTPPTTTPPTTTPSPPTTTPPTTTPPTTTPPTTTPSP 1620
 Query: 675 PATDGAKPKSEIHVSMATPVTVMETVSNQNDQPTIAV-PPTAQPPPTIPTMIAA--A 731
 P T P + + P T + PT PPT P P I T
 Sbjct: 1621 PTTTPTPTPTT--TTTLPPTTTPSPPTTTPPTTTPPTTTPSPPTTTPPTTTPPTTTPPTTTPPT 1678
 Query: 732 SPSPQPAVALSTIPGAVPITPPITIAAAPPSSVTVGSSLSVLGPPV-----PEIKVK 785
 + PS P + P TP TT ++P + T S ++ PP P
 Sbjct: 1679 TTPSSPITTTTPSPPTTMTTTPSPPTTTPSSPITTTTTPSSTTTPSPPTTMTTTPSPTTTPS 1738

Query: 786 EEVEPMDIMRPVSAVPPLATNTVSPSL 812
 M + P + PL T + PS+
 Sbjct: 1739 PPTTTMTTLPPTTTSSPLTTPLPPSI 1765

Score = 185 (27.8 bits), Expect = 1.6e-09, P = 1.6e-09
 Identities = 71/270 (26%), Positives = 99/270 (36%)

Query: 563 PAPISTOGIQPAPIGTPGIQAPALGTQGIHSATP---INTQGLQPAPMGTOQPQ---PEG 616
 P+P +T P P TP P T + + TP I+T P P T P P
 Sbjct: 1422 PSPPTTTTTPPTTTTPS-PPITTTTTLPTTTSPPISTT-TTPPTTTTPSPPTTTTSP 1479

Query: 617 KTSAVVLADGATIVANPISNPFSAAPAATTVVQTHSQSASTNAPAQSSPRPSILRKKPA 676
 T+ T P + P +P TT + T S +T P SP + P
 Sbjct: 1480 PTTTSPPTTTTTPPTTTTP---SPPMTTPI-TPPASTTTLPPTTTTPSPPTTTTTPPP 1535

Query: 677 TDGAKPKSEIHVSMATPVTVMETVSNQNNDOPTIAVPPTAQPPPTIPTMIAAASPPSQ 736
 T P + TP+T T + P+ P T PPPT + PS
 Sbjct: 1536 TTTSPPT-----TTPITPTSTTTLPPTTTTPS-PPPTTTTTPPTTTTPSPPTTTTTPSP 1588

Query: 737 PAVALSTIPGAVPITPPITTIAAAPPSVTVGGSLSSVLGPPVPEIKVKEEVEPMDIMRP 796
 P + +T P +PP TT PPP+ T ++ + PP + P P
 Sbjct: 1589 PTITTTTTPPTTTTPSPPTTT-TTTPPTTTTPSPPTTTITPTTSTTTLPPTTTTPSP--PP 1645

Query: 797 VSAVPLATNTVSPSLALLANNLSMPTSDLPFGASP 832
 + P T T SP + T+ PP +P
 Sbjct: 1646 TTTTTPPTTTTPSPPTTTTPSPPTTTTTPPTTTTP 1681

Score = 183 (27.5 bits), Expect = 3.4e-09, P = 3.4e-09
 Identities = 91/390 (23%), Positives = 139/390 (35%)

Query: 326 PSAAISIQRPQAQSRDVTTR-ITLPSHPALGTPKQQLHTMAQKTIFFSTGTPVAAATVAPIL 384
 PS + P + T T PS P T T I +T TP+ T +P +
 Sbjct: 1399 PSPPTTTSPPTTTTTLPTTTTPSPPTTTTTPPTTTTPSPPTTTTTLPTTTTPSPPI 1458

Query: 385 ATNTIPSATTAGSVSHTQAPTSTIVMTVPSSHSHATAVTTSNIP--VAKVVPQQITHTS 442
 +T T P TT S T P+ T + P+ ++ TT+ P + P T T
 Sbjct: 1459 STTTTPPTTTTPSPPT-TTTPSPPTTTTPSPPTTTTTPPTTTTPSPPTTTTTPPTTTTTP 1517

Query: 443 PRIQPDYPAERSSLIPISGHRASP---NPVAMETRSDNR--SVPVQFQYFLPTYPPSAY 497
 P P ++ P SP P+ T + P + P T PP+
 Sbjct: 1518 PPTTTPSPPTTTTTPPTTTTPSPPTTTTTPITPTSTTTLPPTTTTPSPPTTTTTPPTTT 1577

Query: 498 PLAATYTPITSSVSTIRQYVPSAQAPNSAITAQTVGVGASTVHLNPMQL-MTVDASHAR 556
 P T TP +++T P + +P T T +T P +T S
 Sbjct: 1578 PSPPTTTTPSPPTTTTTPPTTTTPSPPTTTTTPPTTTTTPPTTTTTPPTTTTTPPTTTTTP 1634

Query: 557 HIQGIQAPAPISTOGIQPAPIGTPGIQAPALGTQGIHSATPINTQGLQPAPMGTOQPQPEG 616
 P+P T P P TP P P T T T P P
 Sbjct: 1635 LPPTTTTPSPPTTTTTPPTTTTPS--P-PTTTTPSPPTTTTTPPTTTTPSPPTTTTTPSP 1691

Query: 617 KTSAVVLADGATIVANPISNPFSAAPAATTVVQTHSQSASTNAPAQSSPRPSILRKKPA 676
 T+ + T ++PI+ + P+TT + +T +P SP + + P
 Sbjct: 1692 PTTMTTTPSPTTTTPSPPTTT-TTTPSSTTTTPSPPTTTTTPSPTTTTPSPPTTTTMTLPP 1749

Query: 677 TDGAKPKSEIHVSMATPVTVMETVSNQNNDOPTIAVPP 715
 T + P + + P +++ T S + PT P
 Sbjct: 1750 TTTSSPLT----TTLPPSITPPTFSPESTTTPTTPCVP 1784

Score = 176 (26.4 bits), Expect = 1.8e-07, P = 1.8e-07
 Identities = 101/402 (25%), Positives = 142/402 (35%)

Query: 345 ITLPSHPALGTPKQQLHTMAQKTIFFSTGTPVAAATVAPILATNTIPSATTAGSVSHTQAP 404
 IT PS P TP T +T +P T P T P TT + T P
 Sbjct: 1396 ITTTPSPPTT-TPSPPTTTTTLPTTTTPSPPTTTTTPPTTTTPSPPTTTTTLPTTTTP 1454

Query: 405 TSTIVMTVPSSHSHATAVTTNIPVAKVVPQQITHTSPIQPDYPAERSSLIPISGHR 463
 + I T T P ++ + TT+ + P P T TP+ P PI+
 Sbjct: 1455 SPPISTTTTTPPTTTTPSPPTTTTPSPPTTTTTPPTTTTTPPTTTTTPPTTTTTPPTTTTTP 1511

Query: 464 ASPNPVAMETRSDNRPSVPVQFQYFLPTYPPSAYPLAATYTPITSSVSTIRQYVPSAQ 523
 AS + T PS P T PP+ P + T TPIT ST P + +
 Sbjct: 1512 ASSTTLPTTT----PSPPTTTT---TTPPTTTTP-SPPTTTTTPPTTTTTLPTTTTPS 1563

Query: 524 PNSAITAQ----TGVGASTVHLNPMQLMTVDASHARHIQGIQAPAPISTOGIQPAPIGTP 579
 P T T +T +P +T P+P +T P P TP
 Sbjct: 1564 PPPTTTTTPPTTTTPSPPTTTTTPSPPTTTTTPPTTTTTPPTTTTTPPTTTTTPPTTTTTP 1618

Query: 580 G-----IQAPALGTQGIHSAT---PINTQGLQPAPMGTOQPQPEGKTSAVVLADGATIV 630
 I P P T + T P T P P T P S +
 Sbjct: 1619 SPPTTTTTPITP-PTSTTTLPPTTTTPSPPTTTTTPPTTTTPSPPTTTTTPSPPTTTTTPPT 1677

Query: 631 ANPISNPFSAAPAA-TTVVQTHSQSASTNAP-AQGSSPRPSILRKKPATDGAKPKSEIHV 688
S+P + P+ TT + T S + + ++P ++P + P T P
Sbjct: 1678 TTTTSSPITTTTSPPTTTMTTTPSPPTTTTSSPITTTTTPSSTTTTSPPTTMTTTPSP---T 1734

Query: 689 SMATPVTVSMETVSNQNNDOPTIAVPPTAQPPPTIPTMIAAASPPSQPAVALSTIPG 746
+ +P T +M T+ P P PPT + + P+ P V L G
Sbjct: 1735 TTPSPPTTTMTTLPPTTTSSPLTTTLPSPITPPTFSPF--STTTPTTTPCVPLCNWTG 1790

Score = 168 (25.2 bits), Expect = 9.3e-08, P = 9.3e-08
Identities = 89/387 (22%), Positives = 133/387 (34%)

Query: 448 DYPAERSSLIPISGHRASPNPVAMETRSNDRPSVPVQFQYFLPTYPPSAYPLAAHTYTPI 507
DY + P+ +P+P T + + P P PT PS P T P
Sbjct: 1381 DYKIRVNCCWPMKCIITPSP---PTTTPSP--PTTTTTLPTTTPSP-PTTTTTPPP 1434

Query: 508 TSSVS---TIRQYPVSAQAPNSAITAQTGVGVASTVHLNPMQLMTVDASHARHIQGIQPA 564
T++ S T P+ P+ I+ T +T P T +
Sbjct: 1435 TTTTSPPTTTTTLPTTTPSPPTTTTTPPTTT---PSPPTTTPSPPTT-----TPS 1485

Query: 565 PISTQGIQPAPIGTPIG-QPAPLGTQGIHSATPINTQGLQPAPMGTQQPQ---PEGKTS 620
P +T P P TP P+ + P T P T P P T+
Sbjct: 1486 PPTTTTTPPTTTPSPPTTTPITPPASTTTLPPTTTPSPPTTTTTPPTTTPSPPTT 1545

Query: 621 VVLADGATIVANPISNPFSAAPAAATTVVQTHSQSA-STNAPAQGS---SPRPSILRKKP 675
+ +T P + P TT T + S +T P+ + +P P+ P
Sbjct: 1546 PITPTTSTTLPTTTPSPPTTTTTPPTTTPSPPTTTPSPPTTTTTPPTTTPSPPT 1605

Query: 676 ATDGAKPKSEIHVS--MATPVTVSMETVSNQNNDOPTIAVPPTAQPPPTIPTMIAAASP 733
T P S TP+T T + P+ P T PPPT +
Sbjct: 1606 TTTTTPPTTTPSPPTTTPITPPTSTTLPTTTPS-PPPTTTTTPPTTTPSPPTTTT 1664

Query: 734 PSQPAVALSTIPGAVPITPPITIAAAPPSPVTVGGSLSVLP---PVPEIKVKEEVE 789
PS P +T P + PITT + P ++T ++ P P
Sbjct: 1665 PSPPTTTTTPPTTTPSSPITTTTPSPPTTMTTTPSPPTTTPSSPITTTTTPSSTTTPSP 1724

Query: 790 PMDIRPVSAVPPLATNTVSPSLALLANLMSPTSDLPFGASP 832
P + P P T +L + + T+ LPP +P
Sbjct: 1725 PTTMTTTPSPPTTTPSPPTTMTTLPPTTSSPLTTTLPSPITP 1767

Score = 154 (23.1 bits), Expect = 2.7e-06, P = 2.7e-06
Identities = 70/277 (25%), Positives = 92/277 (33%)

Query: 565 PISTQGIQPAPIGTPIGQPAPLGTQGIHSATPINTQGLQPAPMGTQQPQPEGKTS 624
PIST P P TP P P T + TP P T P P T +
Sbjct: 1457 PISTT-TTPPTTTPS--P-PTTTPSPPTTTPSPPTTTTTPPTTTPSPPTTTP--ITP 1510

Query: 625 DGATIVANPISNPFSAAPAAATTVVQTHSQSASTNAP---AQGSSPRPSILRKKPATDGA 680
+T P + P TT T + S T P ++ P+ P T
Sbjct: 1511 PASTTTLPTTTPSPPTTTTTPPTTTPSPPTTTPITPPTSTTLPTTTPSPPTTTT 1570

Query: 681 KPKSEIHVSMATPVTVSMETVSNQNNDOPTIAVPPTAQ--PPPTIPTMIAAASPPSQPA 738
P S T T S T++ T PPT PPPT T + P P
Sbjct: 1571 TPTTTPSPPTTTTTPSPPTTTTTPPTTTPSPPTTTTTPPTT-TSPPTTTPITPP 1629

Query: 739 VALSTIPGAVPITPPITIAAAPPSPVTVGGSLSVLPVPEIKVKEEVEPMDIMRPVS 798
+ +T+P +PP TT PPP+ T ++ PP+ +
Sbjct: 1630 TSTTTLPTTTPSPPTT-TTTPPTTTPSPPTTTPSPPTTTTTPPTTTPSPPTT 1688

Query: 799 AVPPLATNTV----SPSLALLANL--SMPTSDLPFGASPRKKP 836
PP T T +PS + S T PP P
Sbjct: 1689 PSPPTTMTTTPSPPTTTPSPPTTTTTPSSTTTPSPPTTMTTTPSP 1733

Score = 148 (22.2 bits), Expect = 1.1e-05, P = 1.1e-05
Identities = 62/254 (24%), Positives = 89/254 (35%)

Query: 583 PAPLGTQGIHSATPINTQGLQPAPMGTQQPQPEGKTS 637
P+P T S P T L P T P P T+ + T P+
Sbjct: 1399 PSPTTTP--SPPTTTTTLPP---TTTTPSPPTTTTTPPTTTPSPPTTTTTLPTT 1452

Query: 638 FSAAPAAATTVVQTHSQSASTNAPAQGSSPRPSILRKKPATDGAKPKSEIHVS--MATPVT 695
+ P +TT T + + + P SP P+ P T P S M TP+T
Sbjct: 1453 TSPPISTTT--TPPTTTPSPPTTTPSP-PTTTPSPPTTTTTPPTTTPSPPTTTPIT 1509

Query: 696 VSMETVSNQNNDOPTIAVPPTAQPPPTIPTMIAAASPPSQPAVALSTIPGAVPITPPIT 755
T + P+ T PP T P+ + P P + +T+P +PP T
Sbjct: 1510 PPASTTTLPTTTPSPPTTTTTPPTTTPS--PPTTTPITPPTSTTLPTTTPSPPT 1567

Query: 756 TIAAAPPSPVTVGGSLSVLPVPEIKVKEEVEPMDIMRPVSAVPPLATNTVSPSLALL 815
T PPP+ T ++ PP + PP T P+ +
Sbjct: 1568 T-TTTPPTTTPSPPTTTTTPSPPTTTTTPPTTTPSPPTTTTTPPTTTPSPPTTTPIT 1626

Query: 816 ANNLSMPTSDLPFGASPRKKP 836
 S T+ LPP +P P
 Sbjct: 1627 TPPTS--TTTLPPPTTSPPPP 1645

Score = 131 (19.7 bits), Expect = 1.2e-03, P = 1.2e-03
 Identities = 112/492 (22%), Positives = 174/492 (35%)

Query: 96 VVVRPYPQVQMLSTHHAVASATPVAVTAPPAHL-TPAVPLSFSEGLMKPPPKPTMPSRPI 154
 V P P T + + T V T P TP + + P P PT P
 Sbjct: 3977 VTPTPTPTGTQTPTTTPITTTTIVTPTPTPTGTQTPTTTPITTTTIVTPTPTPTGTQTPT 4036

Query: 155 A-PAPPSTLSLPPKVP-GQVVTMESSIPQASAI PVATISGQQGHPSNLHHIMTTNVQMS 212
 P +T P P G T T + P T +G Q P+ TT V +
 Sbjct: 4037 TTPITTTTIVTPTPTPTGTQTPTTTPITTTTIVTPTPTPTGTQT-PTTTPITTTTIVTPT 4095

Query: 213 IIRSNAPGP---PLHIGASHLPRGAAAAA-VMSSSKVTVLRPTSQLPNAATAQPAVQHI 268
 + P P+ + P +++ +TT T T P I
 Sbjct: 4096 PTPTGTQTPTTTPITTTTIVTPTPTPTGTQTPTTTPITTTTIVTPTPTPTGTQTPTTTP 4155

Query: 269 IHQPIQSRPPVTTSSNAIPPA--VVATVSATRAQSPVITTA--AHATDSALSRLTSLIQH 324
 + P T P + T + T +P T T H + + ++ T S
 Sbjct: 4156 TTTTIVTPTPTPTGTQTPTTTPITTTTIVTPTPTPTGTQTGPPTHSTAPIAELTTSNPP 4215

Query: 325 PPSAAISIQRPQAS--RDVTTTRI-TLPSHPALGTPKQQLHTMAQKTIESTGTPVAAATVA 381
 P S+ R S + TT + TLP PA+ + T T + T T++
 Sbjct: 4216 PESSTPQTSRSTSSPLTESTTLLSTLP--PAI----EMTSTAPPSTPTAPTTS SGGHTLS 4269

Query: 382 PILATNTIPSAT-TAGSVS-HTQAPTSTIVTMTVPSHSSHATAVTTSNIPVAKVVPQQIT 439
 P +T T P T T G+ + + APT + V T S A T + P++ P I
 Sbjct: 4270 PPPSTTSPPGTPTRGTTTGSSSAPTPSTVQTTTS-----AWTPTPTPLS--TPSIIR 4321

Query: 440 HTSPRIQPDYPAERSSLIPIGHRASPNP-VAMETRSNDN----RPSVPVQFQYFLPTYP- 493
 T ++P YP+ ++ +P V T D S+ --+ + P
 Sbjct: 4322 TTG--LRP-YPSSVLICCVLNDTYYPAGEEVNGTYGDTCYFVNCSLSCTLEFYNWSCPS 4378

Query: 494 -PSAYPLAAHTYTPITSSSVSTIRQYPVSAOAPNSAITAQTGVGVASTVHLNPMQLMTVDA 552
 PS P + + TP S S+ P P T L + T
 Sbjct: 4379 TPSTPTPSKS-TPTPSKPSSTPSKPTPGTKPECPDFDPPRQENETWWLDCDFMATCKY 4437

Query: 553 SHARHIQGIQ---PAPISTQGIQPAPIGTP 579
 ++ I ++ P P + G+QP + P
 Sbjct: 4438 NNTVEIVKVECEPPMPPTCSNGLQPVVRVEDP 4468

Score = 117 (17.6 bits), Expect = 1.8e-02, P = 1.8e-02
 Identities = 41/156 (26%), Positives = 55/156 (35%)

Query: 710 TIAVPPTAQPPPTIPTMIAAASPPSQPAVALSTIPGAVPITPPITTIAAAPPSPVTVGG 769
 T + P T PPPT T + + PS P +T P +PPITT P P+ T
 Sbjct: 1398 TSPPTTTTSPPTTTTTLPTTTTSPPTTTTTPPTTTTSPPTITT-TTTLPTTTTSP 1456

Query: 770 SLSSVLGPPVPEIKVKEEVEPMDIMRPVSAVPLATNTVSPSLALLANNLSMPTSDLPFG 829
 +S+ PP P P + P T T SP T+ PP
 Sbjct: 1457 PISTTTTTP-----PTTTPSPPTTTPSPPTTTPSPPTTTTTP-PPTTTPSPPM 1504

Query: 830 ASPRKKPRKQOHVISTEEGDMMETNSTDDEKSTAKS 865
 +P P + T +T +T S
 Sbjct: 1505 TTITPPASTTTLPPTTTTSPPTTTTTPPTTTTTPS 1540

Score = 61 (9.2 bits), Expect = 1.6e-09, P = 1.6e-09
 Identities = 23/93 (24%), Positives = 41/93 (44%)

Query: 397 SVSHTQAPTSTIVTMTVPSHSSHATAVTTSNIPVAKVV----PQOITHTSPRIQPDYPAE 452
 S++ + +T T+T+P+ + T TT+ P + V P+ S I D+P+
 Sbjct: 1257 SITTRPSTLTFTTTITLPTTPTSFTTTTTPSTSVLSTTPKLCLLWSDWINEHDHPS 1316

Query: 453 RSS---LIPISGHRASPNPVAMETRSNDNRPSVPVQ 484
 S P G +P + E RS P + ++
 Sbjct: 1317 GSDGDGDRPFDFGVCAPEDI--ECRSVKDPHLSLE 1349

Score = 50 (7.5 bits), Expect = 8.0e-09, P = 8.0e-09
 Identities = 16/41 (39%), Positives = 19/41 (46%)

Query: 334 RPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKTIESTGTP 374
 RP+ TT ITLP+ P T T T+ ST TP
 Sbjct: 1261 RPSTLTFTT-ITLPTTPTSFTTTTTPSTSVLST-TP 1299

Score = 46 (6.9 bits), Expect = 5.4e-08, P = 5.4e-08
 Identities = 24/106 (22%), Positives = 37/106 (34%)

Query: 324 HPPSAAISIQRPQASRDVTTRITLPSHPALGTPKQQLHTMAQKTIESTGTPVAAATVAPI 383
 +PP A++ + +S T + P G Q A G I

Sbjct: 1196 YPPGASVPTEETCKSCVCTNSSQVVCREEGKILNQTQDGAFCYWEICGPNGTVEKHENI 1255

Query: 384 LATNTIPSA-TTAGSVSHTQAPTSTIVTMTVPSSHSHATAVTTSNI 428

+ T PS TT +++ PTS T T + +S TT +

Sbjct: 1256 CSITTRPSTLTFTTITLPTTPTSTFTTTTTTTTTTPTSTVLSTTPKL 1301

Score = 44 (6.6 bits), Expect = 8.7e-08, P = 8.7e-08
Identities = 14/34 (41%), Positives = 17/34 (50%)

Query: 478 RPSVPVQFQYF-LPTYPPSAAYPLAAHTYTPITSSV 511

RPS F LPT P S + T TP +S+V

Sbjct: 1261 RPSTLTFTTITLPTTPTS-FTTTTTTTTTPTSSTV 1294

Pedant information for DKFZphtes3_2all, frame 2

Report for DKFZphtes3_2all.2

[LENGTH] 1048
[MW] 110324.04
[pI] 9.83
[HOMOL] PIR:147141 gastric mucin (clone PGM-2A) - pig (fragment) 8e-15
[FUNCAT] 30.90 extracellular/secretion proteins [S. cerevisiae, YIR019c] 1e-09
[FUNCAT] 30.01 organization of cell wall [S. cerevisiae, YIR019c] 1e-09
[FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae, YIR019c] 1e-09
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YDR420w] 4e-09
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDR420w] 4e-09
[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR151c] 4e-06
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YGR014w] 1e-05
[FUNCAT] 11.01 stress response [S. cerevisiae, YHL028w] 1e-04
[FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YHL028w] 1e-04
[EC] 3.2.1.3 Glucan 1,4-alpha-glucosidase 3e-08
[PIRKW] glycosidase 3e-08
[PIRKW] transmembrane protein 3e-08
[PIRKW] polysaccharide degradation 3e-08
[PIRKW] glycoprotein 9e-08
[PIRKW] calcium binding 9e-08
[PIRKW] hydrolase 3e-08
[PIRKW] cytoskeleton 7e-08
[SUPFAM] equine herpesvirus glycoprotein X 2e-07
[SUPFAM] yeast glucan 1,4-alpha-glucosidase homolog 3e-08
[SUPFAM] polymorphic epithelial mucin 7e-08
[SUPFAM] glucan 1,4-alpha-glucosidase homology 3e-08
[SUPFAM] equine herpesvirus 1 glycoprotein homology 2e-07
[PROSITE] MYRISTYL 9
[PROSITE] AMIDATION 1
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] CK2_PHOSPHO_SITE 10
[PROSITE] PKC_PHOSPHO_SITE 12
[PROSITE] ASN_GLYCOSYLATION 3
[KW] Irregular
[KW] LOW_COMPLEXITY 20.04 %

SEQ MGPPRHPQAGEIEAGGAGGRRRLQVEMSSQFRLGAPSTGLSQAPSIANSQSAGLINP
SEGxxxxxxxxxxxxx.....
PRD ccc

SEQ AATVNDESGRDSEVSAREHMSSSSLQSREEKQEPVVVRYPVQVQMLSTHHAVASATPVA
SEGxxxxx.....xxxxxxxxxxxxx
PRD ccc

SEQ VTAPPAHLTPAVPLSFSEGLMKPPPKPTMPSRPIAPAPPSTLSLPPKVPQVTVTMESSI
SEG xxxxxxxxxxxxxxxx.....xxxxxxxxxxxxx.....xxxxxxxxxxxxx
PRD ccc

SEQ PQASAI PVATISGQQGHPSNLHHIMTTNVQMSIIRSNA GPPLHIGASHLPRGAAAAAVM
SEGxxxxxxxxx.....
PRD ccc

SEQ SSSKVTTVLRPTSQLPNAATAQPAVQHIIHQPIQSRPPVTTSNAI PPAVVATVSATRAQS
SEG
PRD ccc

SEQ PVITTTAAHATDSALSRPTLSIQHPPSA AISIQRPAQSRDVTTRITLPSHPALGTPKQQL
SEG
PRD ccc


```

SEQ HTMAQKTI FSTGT PVAAATVAPILATNTIP SATTAGSVSHTQAPTSTIVTMTVP SHSSHA
SEG .....XXXXXXXXX.....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ TAVTTSNIPVAKVVPQQITH TSPRIQPDYPAERSSLIPI SGHRASPNPVAMETRS DNRPS
SEG XXXXXX.....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ VPVQFYFLPTYP PSAYPLAAHTYTPITSSVSTIRQY PVSQAQAPNSAITAQ TGVGVASTV
SEG .....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ HLNPMQLMTVDASHARHIQGIQ PAPISTQGIQ PAPIGTPGIQ PAPILGTQGIHSATPINTQ
SEG .....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ GLQPAPMG TQQPQPEGKTS AVVLADGATIVANPISNPFSAAPAATT VVQTHSQSASTNAP
SEG .....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ AQGSSPRPSILRK KPATDGAKPKSEIHVSMATPVTVSMETVSNQNN DQPTIAVPPTAQQP
SEG .....XXXXXXXXX.....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ PPTIPTMIAAASPPSQPAVALSTIPG AVPI TPPITTIAAAPPSVTVG GSSLSSVLGPPVP
SEG XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ EIKVKEEVEPMDIMRPV SAVPPLATNTVSPSLALLANNLSMPTSDLP PGASPRKKPRKQQ
SEG XXXXXXXXXXXX.....XXXXXXXXXX.....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ HVISTEEGDMMETNSTDDEKSTAKSL LVKAEKRKSPKKEYIDEEGVRYVPVRPRPPITLL
SEG .....XXXXXXXXXX.....
PRD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ RHYRNPWKAA YHHFQRYSDVRVKEEKAMLQEI ANQKGVSCRAQGWK VHLCAAQLQLLTN
SEG .....
PRD ECCCCCHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCC

SEQ LEHDVYERLTNLQEG IIPKKKAATDDDLHRINELIQGNMQRCKLVMDQISEARD SMLKVL
SEG .....
PRD CCHHHHHHHHHHHCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

SEQ DHKDRVLKLLNKN GTVKKVSKLKRKEKV
SEG .....XXXXXXXXXX.....
PRD HHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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Prosites for DKFzphes3_2all.2

PS00001	818->822	ASN_GLYCOSYLATION	PDOC00001
PS00001	854->858	ASN_GLYCOSYLATION	PDOC00001
PS00001	1033->1037	ASN_GLYCOSYLATION	PDOC00001
PS00004	872->876	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	1037->1041	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	68->71	PKC_PHOSPHO_SITE	PDOC00005
PS00005	75->78	PKC_PHOSPHO_SITE	PDOC00005
PS00005	242->245	PKC_PHOSPHO_SITE	PDOC00005
PS00005	342->345	PKC_PHOSPHO_SITE	PDOC00005
PS00005	355->358	PKC_PHOSPHO_SITE	PDOC00005
PS00005	442->445	PKC_PHOSPHO_SITE	PDOC00005
PS00005	513->516	PKC_PHOSPHO_SITE	PDOC00005
PS00005	665->668	PKC_PHOSPHO_SITE	PDOC00005
PS00005	831->834	PKC_PHOSPHO_SITE	PDOC00005
PS00005	862->865	PKC_PHOSPHO_SITE	PDOC00005
PS00005	940->943	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1035->1038	PKC_PHOSPHO_SITE	PDOC00005
PS00006	63->67	CK2_PHOSPHO_SITE	PDOC00006
PS00006	68->72	CK2_PHOSPHO_SITE	PDOC00006
PS00006	75->79	CK2_PHOSPHO_SITE	PDOC00006
PS00006	88->92	CK2_PHOSPHO_SITE	PDOC00006
PS00006	135->139	CK2_PHOSPHO_SITE	PDOC00006
PS00006	473->477	CK2_PHOSPHO_SITE	PDOC00006
PS00006	844->848	CK2_PHOSPHO_SITE	PDOC00006
PS00006	855->859	CK2_PHOSPHO_SITE	PDOC00006
PS00006	959->963	CK2_PHOSPHO_SITE	PDOC00006
PS00006	984->988	CK2_PHOSPHO_SITE	PDOC00006
PS00008	15->21	MYRISTYL	PDOC00008

PS00008	16->22	MYRISTYL	PDOC00008
PS00008	36->42	MYRISTYL	PDOC00008
PS00008	233->239	MYRISTYL	PDOC00008
PS00008	372->378	MYRISTYL	PDOC00008
PS00008	533->539	MYRISTYL	PDOC00008
PS00008	535->541	MYRISTYL	PDOC00008
PS00008	590->596	MYRISTYL	PDOC00008
PS00008	768->774	MYRISTYL	PDOC00008
PS00009	19->23	AMIDATION	PDOC00009

(No Pfam data available for DKF2phtes3_2all.2)

DKFZphtes3_2a17

group: metabolism

DKFZphtes3_2a17 encodes a novel 574 amino acid protein without similarity to known proteins.

The novel protein contains a thiol protease cys pattern. Eukaryotic thiol proteases (EC 3.4.22.-) are a family of proteolytic enzymes containing an active site cysteine. Cathepsins belong to this protease family.

The new protein can find application in modulation of proteolytic processes and as a new enzyme for proteomic analysis and biotechnologic production processes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 2312 bp

Poly A stretch at pos. 2300, polyadenylation signal at pos. 2273

```
1  GTTTTCACCT  GATCATTAGA  AACTAATGAA  ACACCTTTTA  AGTCTTATGA
51  ATTCAGGTTA  CACTGTTTTC  CAGATGCCTT  GGCAGCTGGT  ACAGGGCCTC
101  TGAAAAATGG  AACCAAATTC  TCTGAGGACT  AAAGTCCCAG  CTTTCTTATC
151  TGATTTGGGG  AAGGCCACAT  TGAGGGGAAT  CAGAAAGTGT  CCCCAGATGTG
201  GCACATACAA  TGGAACCCGG  GGACTGAGCT  GTAAGAACAA  GACATGTGGA
251  ACCATATTCC  GCTACGGTGC  ACGCAAGCAG  CCTAGTGTTG  AAGCTGTCAA
301  AATCATTACA  GGCTCTGATC  TTCAGGTCTA  CTCAGTGCGG  CAAAGAGACC
351  GGGGCCCTGA  TTACCGATGC  TTTGTGGAGC  TCGGGGTTTC  AGAGACAACA
401  ATCCAGACAG  TGGATGGGAC  GATCATCACT  CAGCTGAGCT  CTGGACGGTG
451  TTATGTCCCC  TCATGCCTGA  AAGCTGCCAC  TCAAGGCCTT  GTGGAAAACC
501  AGTGCCAGCA  CATCAAGCTG  GCGGTGAACT  GCCAGGCAGA  GGCCACCCCT
551  CTGACCCCTGA  AGAGCTCGGT  CCTGAATGCA  ATGCAGGCCT  CCCCAGAAAC
601  CAAACAGACC  ATCTGGCAGT  TGGCCACGGA  ACCCACAGGT  CCTCTGGTGC
651  AGAGAATTAC  TAAAAACATC  TTGGTGGTGA  AATGCAAGGC  AAGCCAGAAG
701  CACAGTTTGG  GGTATTTGCA  TACATCTTTT  GTGCAGAAAG  TCAGTGGCAA
751  AAGCTTGCCCT  GAGCGCCGCT  TCTTCTGCTC  CTGTCAGACT  CTGAAATCGC
801  ACAAGTCAAA  TGCTCCAAAG  GATGAGACAG  CCCAGAGATG  CATTCATTTT
851  TTTGCTTGA  TCTGTGCCCT  TGCCAGTGAT  GAGACACTGG  CTCAGGAATT
901  CTCAGACTTC  TAAATTTTG  ATTCCAGCGG  TCTTAAAGAG  ATTATTGTAC
951  CCCAGTTAGG  TTGCCATTCA  GAATCAACAG  TATCTGCTTG  TGAGTCTACT
1001  GCCTCTAAGT  CAAAGAAGAG  GAGAAAGGAT  GAAGTATCTG  GTGCACAGAT
1051  GAACAGTTCA  CTACTGCCTC  AAGATGCAGT  GAGCAGTAAT  CTAAGGAAAA
1101  GTGGCCTGAA  AAAGCCTGTG  GTTGCTTCCT  CGTTAAAAAG  GCAGGCCTGT
1151  GGTCAGCTGT  TAGATGAGGC  ACAAGTGACT  TTATCCTTCC  AAGACTGGCT
1201  GGCCAGTGTC  ACAGAACGCA  TCCATCAAAC  CATGCACTAT  CAGTTTGATG
1251  GCAAACCAGA  ACCATTGGTG  TTCCACATTC  CTCAGTCATT  TTTTGATGCC
1301  CTGCAACAAA  GAATATCTAT  AGGAAGTGCA  AAAAAACGGC  TCCCCAACTC
1351  CACCCAGACT  TTTGTTTCGA  AAGATGCCTT  GCCACTGGGA  ACCTTTTCCA
1401  AGTATACTTG  GCATATCACT  AATATCCTGC  AAGTTAAACA  AATCTTAGAT
1451  ACCCCAGAGA  TGCCCTTGGA  AATCACCCGT  AGCTTTATCC  AGAACCGAGA
1501  TGGGACTTAT  GAGCTATTTA  AATGCCCTAA  AGTGGAAGTA  GAAAGCATAG
1551  CAGAAACCTA  CGGTCGTATA  GAAAAACAAC  CAGTGTCTGC  ACCCTTGGAA
1601  CTAATAACTT  TTCTCAAAGT  TGGCAACACT  TCCCAGATC  AAAAGGAGCC
1651  AACACCTTTC  ATCATCGAGT  GGATCCCAGA  TATCCTTCCC  CAATCTAAGA
1701  TTGGCGAGCT  GCGGATCAAG  TTTGAGTATG  GCCACCACCG  GAATGGGCAT
1751  GTGGCGGAGT  ACCAAGACCA  GCGGCCCCCT  TTGGACCAGC  CCTTGGAAC
1801  GGCCCTCTG  ACCACTATTA  CTTTCCCTTA  AAGCAAAACA  AGATAATAAT
1851  CTTTGTGCTG  TTAATTTGCA  CATCCCCACC  CCTTGACAAC  TTTAAATGCT
1901  AGTTAGGCAC  TTAGATGGCC  CTGTTCCCTG  GTAACTGCT  CTTAGCTAAG
1951  ATGCAAAATC  CAGTGCTTT  CAAGTGGATT  CTGTGAAGA  AAATCTCTTG
2001  TAAATAGCCT  TTTTGATGCT  GCTGTGTACA  GTCTTCATTA  TGCATTGGGC
2051  AGTATTTCTG  GCTAGAGTTT  TAAAAGGAAC  AGAAAGAAAA  CCAGCTTATT
2101  TTCCTTCTTA  CGGACTCATC  TTTAGCGTTT  ATTTCAACCT  TTTGCTAATT
2151  CTCTGAGAAA  TCTGCAGCAC  TCAGCCATAC  ACCAACAGTG  TTGGAAGTT
2201  AACACCCCTG  TTAGGGCAGA  ATGTTAAAGA  CCATCTTGGC  AGAGTTCCAG
2251  CCACGCTCTT  TATCTGTTC  TCAAATAAAG  CAGTGTCACT  AGTTTTCTCT
2301  AAAAAAAAAA  AA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 107 bp to 1828 bp; peptide length: 574
 Category: putative protein

```

1 MEPNSLR TKV PAF LSDLGKA TLRGIRK CPR CGTYNGTRGL SCKNKTCGTI
51 FRYGARKQPS VEAVKIITGS DLQVYSVRQR DRGPDYRCFV ELGVSETTIQ
101 TVDGTIIITQL SSGRCYVPSC LKAATQGVVE NQCQHIKLAV NCQAEATPLT
151 LKSSVLNAMQ ASPETKQTIW QLATEPTGPL VQRITKNILV VKCKASQKHS
201 LGYLHTSFVQ KVSCKSLPER RFFCSCQTLK SHKSNASKDE TAQRCIHFFA
251 CICAFADET LAQEFSDFLN FDSSGLKEII VPQLGCHSES TVSACESTAS
301 KSKRRKDEV SGAQMNSSLL PQDAVSSNLR KSGLKPPVVA SSLKRQACGQ
351 LLDEAQVTL S FQDWLASVTE RIHQTMHYQF DGKPEPLVFH IPQSFFDALQ
401 QRISIGSAK RLPNSTTAFV RKDALPLGTF SKYTWHITNI LQVKQILDTP
451 EMPLAITRSF IQNRDGTIEL FKCPKVEVES IAETYGRIEK QPVLRLPELEK
501 TFLKVGNTSP DQKEPTPFII EWIPDILPQS KIGELRIKFE YGHRNRGHVA
551 EYQDQRPPLD QPLELAPLTT ITFP

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2a17, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3_2a17, frame 2

Report for DKFZphtes3_2a17.2

[LENGTH]	574
[MW]	64076.89
[pI]	9.15
[PROSITE]	MYRISTYL 5
[PROSITE]	CK2_PHOSPHO_SITE 9
[PROSITE]	PKC_PHOSPHO_SITE 14
[PROSITE]	ASN_GLYCOSYLATION 5
[PROSITE]	THIOL_PROTEASE_CYS 1
[KW]	Alpha_Beta

```

SEQ  MEPNSLR TKVPAFLSDLGKATLRGIRK CPRCGTYNGTRGLSCKNKTCGTIFRYGARKQPS
PRD  cccccccccchhhhhccccchhhhhcccccccccccccccccccccccccccccccccccccc

SEQ  VEAVKIITGSDLQVYSVRQRDRGPDYRCFVELGVSETTIQTVDGTIIITQLSSGRCYVPSC
PRD  ceeeeeeccccceeeccccccccccccccccccccccccccccccccccccccccccccchh

SEQ  LKAATQGVVENQCQHIKLAVNCQAEATPLTLKSSVLNAMQASPETKQTIWQLATEPTGPL
PRD  hhhhhhhcchhhhhheehhhhhhhccccchhhhhhhhhccccchhhhhhhhhccccchh

SEQ  VQRITKNILVVKCKASQKHS LGYLHTSFVQKVSCKSLPERRFFCSCQTLKSHKSNASKDE
PRD  hhhhhhhheeecccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  TAQRCIHFFACICAFASETLAQEFSDFLNFDSSGLKEIIVPQLGCHSESTVSACESTAS
PRD  hhhhhhhhhhhhhhhhhchhhhhhhhhhhcccccccccccccccccccccccccccccccccc

SEQ  KSKRRKDEVSGAQMNSSLLPQDAVSSNLRKSGLKPPVVASSLKRQACGQLLDEAQVTL S
PRD  ccchhhhhccccccccccccccccccccchhhhhhhccccceehhhhhhhhhchhhhhhhhhhh

SEQ  FQDWLASVTERI HQTMHYQFDGKPEPLVFHI PQSFFDALQQRISIGSAKKRLPNSTTAFV
PRD  hhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccc

SEQ  RKDALPLGTF SKYTWHITNILQVKQILDTP E M P L E I T R S F I Q N R D G T Y E L F K C P K V E V E S
PRD  ecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  IAETYGRIEKQPVLRLPELEK TFLKVGNTSPDQKEPTPFII EWIPDILPQSKIGELRIKFE
PRD  hhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccc

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SEQ YGHRNGHVAEYQDQRPLDQPLELAPLTTITFP
 PRD eccccceeeccccccccccccccccceeeccc

Prosites for DKFZphtes3_2a17.2

PS00001	35->39	ASN_GLYCOSYLATION	PDOC00001
PS00001	44->48	ASN_GLYCOSYLATION	PDOC00001
PS00001	235->239	ASN_GLYCOSYLATION	PDOC00001
PS00001	316->320	ASN_GLYCOSYLATION	PDOC00001
PS00001	414->418	ASN_GLYCOSYLATION	PDOC00001
PS00005	5->8	PKC_PHOSPHO_SITE	PDOC00005
PS00005	21->24	PKC_PHOSPHO_SITE	PDOC00005
PS00005	41->44	PKC_PHOSPHO_SITE	PDOC00005
PS00005	76->79	PKC_PHOSPHO_SITE	PDOC00005
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	150->153	PKC_PHOSPHO_SITE	PDOC00005
PS00005	196->199	PKC_PHOSPHO_SITE	PDOC00005
PS00005	213->216	PKC_PHOSPHO_SITE	PDOC00005
PS00005	228->231	PKC_PHOSPHO_SITE	PDOC00005
PS00005	231->234	PKC_PHOSPHO_SITE	PDOC00005
PS00005	302->305	PKC_PHOSPHO_SITE	PDOC00005
PS00005	342->345	PKC_PHOSPHO_SITE	PDOC00005
PS00005	369->372	PKC_PHOSPHO_SITE	PDOC00005
PS00005	407->410	PKC_PHOSPHO_SITE	PDOC00005
PS00006	68->72	CK2_PHOSPHO_SITE	PDOC00006
PS00006	216->220	CK2_PHOSPHO_SITE	PDOC00006
PS00006	237->241	CK2_PHOSPHO_SITE	PDOC00006
PS00006	293->297	CK2_PHOSPHO_SITE	PDOC00006
PS00006	360->364	CK2_PHOSPHO_SITE	PDOC00006
PS00006	367->371	CK2_PHOSPHO_SITE	PDOC00006
PS00006	394->398	CK2_PHOSPHO_SITE	PDOC00006
PS00006	480->484	CK2_PHOSPHO_SITE	PDOC00006
PS00006	508->512	CK2_PHOSPHO_SITE	PDOC00006
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	93->99	MYRISTYL	PDOC00008
PS00008	104->110	MYRISTYL	PDOC00008
PS00008	127->133	MYRISTYL	PDOC00008
PS00008	312->318	MYRISTYL	PDOC00008
PS00139	109->121	THIOL_PROTEASE_CYS	PDOC00126

(No Pfam data available for DKFZphtes3_2a17.2)

DKFZphtes3_2d15

group: testes derived

DKFZphtes3_2d15 encodes a novel 274 amino acid protein with similarity to *C.elegans* cosmid F25H2.1.

The novel protein contains a Pfam predicted C2-domain.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to *C.elegans* F25H2.1

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 3615 bp

Poly A stretch at pos. 3603, polyadenylation signal at pos. 3578

```
1 GCGGCGGCCCT CGAGGTGACA ACTGTCTCCG TCCAGGCTC CGGCGGGGGC
51 GCAGGAGGTC GCCCGGCGCG TCACTGTCCG GTCGGCGAGC CACGGGGGCC
101 GCCGCAGCAC CATGGCGACC ACCGTCAGCA CTCAGCGCGG GCCGGTGTAC
151 ATCGGTGAGC TCCCGCAGGA CTTCTCTCCG ATCAGGCCCC CACAGCAGCA
201 GCGGCAGGTC CAGCTGGACG CCCAGGCGGC CCAGCAGCTG CAGTACGGAG
251 GCGCAGTGGG CACCGTGGGC CGACTGAACA TCACGGTGGT ACAGGCAAAG
301 TTGGCCAAGA ATTACGGCAT GACCCGCATG GACCCCTACT GCCGACTGCG
351 CCTGGGCTAC GCGGTGTACG AGACGCCAC GGCACACAAT GGCGCCAAGA
401 ATCCCCGCTG GAATAAGGTC ATCCACTGCA CGGTGCCCCC AGGCGTGGAC
451 TCTTTCTATC TCGAGATCTT CGATGAGAGA GCCTTCTCCA TGGACGACCG
501 CATTGCCTGG ACCACATCA CCATCCCGGA GTCCCTGAGG CAGGGCAAGG
551 TCGAGGACAA GTGGTACAGC CTGAGCGGGA GGCAGGGGGA CGACAAGGAG
601 GGCATGATCA ACCTCGTCAT GTCCTACGCG CTGCTTCCAG CTGCCATGGT
651 GATGCCACCC CAGCCCGTGG TCCTGATGCC AACAGTGTAG CAGCAGGGCG
701 TTGGCTATGT GCCATCACA GGGATGCCCG CTGTCTGTAG CCCCGGCATG
751 GTGCCGTGGG CCCTGCCCCC GGCCGCCGTG AACGCCAGC CCCGCTGTAG
801 CGAGGAGGAC CTGAAAGCCA TCCAGGACAT GTTCCCCAAC ATGGACCAGG
851 AGGTGATCCG CTCCTGTCTG GAAGCCAGC GAGGGAACAA GGATGCCGCC
901 ATCAACTCCC TGCTGCAGAT GGGGGAGGAG CCATAGAGCC TCTGCCTCGA
951 TGCCGTTTTG CCCCCTCTCT TTGGACACGC CGACCCGGCG CTCGCCAAGG
1001 AATGCTGTCC CAACAAGATT CCCGTGAAAG AGCACCCGTG TCGCCCCCTC
1051 CCGTGGACTT CTGTGCCGCC CCGTCCACAC CTGTTCTTGG GTGCATGTGG
1101 GTTTTCGGTT CCTGGCGGTC CAGGACGGGG CGGGGGCTCC CCTCCCATCT
1151 CGTGTGGGGA GGTCTCAGCG CGCTCTCTCT TCCCTGGGAC GTGCGTCTCT
1201 CCTTCTCATG CCGTTCTGGA AAATGCTCTT GCTGTAGAGA GCAGCTGCTT
1251 CTGCCAGGTT GTTGGAGGTG GTGGAGCGCC TTCCGATTCC ATTATGGCA
1301 TTTTGTGATG TGATGTAATT GGAATAGAGC TGTGATTTA AGGCACACAC
1351 AATCCCTCAC ACTGTGGGTT TTTTITAGAA CTTCCAGAC GAAAACTCAC
1401 GGCCTTGCCC TAACGCGCTT TGCTGTGAGC CTGGCCCTG CCCAGGGCTT
1451 GGGTCTGGTC AGCTGAGCAG CTTCTGTGG ATGGTGTGG GCCGGCTCT
1501 GGCCTGGCTC ACCTGGCCAC TGTCCAGCCA GCCTTGTGAC AGACTCCGGC
1551 CTGAAGGCAG AATGAACCCA CACCTGGAGT GAGGAAGGGG GCCTGGCAGC
1601 GTTGGCCAGG CTCTGCCTGA TTGCCAGCCA GCGGGCATCT GAAGCCGGGT
1651 CCTTCGCCCG CCGGAGGCTG CCGTCCGTCT CTCCTGCTGC GCTCGTGCCA
1701 GCTCCGTGGG TGTCTCCCA GGGAGCTTCT CTTCTCAACA GGCCTTGCGA
1751 GGCTGGGGTG AGAGGTGATA GAGGCAGCAC TGTGCATGAT TCCGAGAGGG
1801 TGTGGTGCCA CTGCCAGCCG ACTGTGACA GCTTGGGAGC TGCTGTGCCC
1851 AGGACGTGGG TTCAGCGTGG GCGAGGAAAG CCTGGCGAGC GTGGCCCTGT
1901 AAAAGCTTTC TGAGGCGGGA GGCGCTCACT TACCTCTGAC TGCTGGGCG
1951 CTGCGTGTAG CATCTTGGCC TACAGGACAG ATTTTAGGTG ACACCTGGTT
2001 ATGACAGTCA GAAATTGAG AAGCTTCTCA CAAGTATGAC ACTTTAAATA
2051 ATCTGCATGC CATTGAGACA CCTGCATGTC TGGTGTGTTG GGTTCAGTG
2101 TCTTGGCCGC GGCCTTCGGA TGTAACCCCA CTGATAACGG ACAGAAAGAG
2151 AATGCCACCA AGTGGTCTT CTGTGGAAGA TGCAGAAGGA GGAAGTTAGT
2201 GCTTACATTT TAGTCTTTT CTCCCTCAAA AAAATAGGTT AAGTTTCAGT
2251 CCGACCTAGA AAATACTGCT TTCTGCCATC GATTGGGGGT GGTTTTGTGC
2301 AAATACTACT TTGATAAATA TTTATTTTGG TAAACTTGAA GTGTGTGGTG
2351 GCCCTGGGGG AGGGACATGC TGGCAGCAGC CGCCTCTTTC AGCTGTGGGT
2401 CTTAAAGGCC TTTGATCCTT TGAAGAAGAA AGACATGGTA TTTGTTCAGC
2451 AGACGCCGAC CACTCAGACG GAGGGGCCCC TGGGATTCCC TGTCTCAGAT
2501 GGCCTGGTCT TACGCTGTG TAGATTCTT CTCCATTGGG AATGAAGGTG
2551 TCAGGCGGGA CTGGAACGTT CTAGATGGTA TGTTCCGTGA TATTAACAAC
2601 TCTAACCAG GACAGACCAC AAGCCACACT CAGAGGCCCT ACTGTGCTGG
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2651 GGGCTTCGGT GTCCAGGCGC CCAGGTGTGG CCACCAGCAC CGGTTTCTGC
2701 CTTCCGGTTG CTGGGGTGCA GTGAGACTGC CACACGCGTG CACATGTGGC
2751 TCTGTGGGTG TCTCCTAGAG AGGACGTGGC CCCTGCTGCC AGCCCTTGAG
2801 CAGCCCGTGT GGGGGCCCGA GGGACCCACA CAGTGGGGGC CAGCCTCGCT
2851 GGAGGGAGAG CAACCCTTTG CCGATGACCA CGCTTGCCGC CATCTCTTAG
2901 TTTTCTTTTT CACAAGCGCT TTATTTTTTT AATAGACAAA TCACATTTTG
2951 CAAGGCCTTT AATTAAATAA GATTCTTCTT TCCTTCATTT TATGCTTTAT
3001 TTCTGTTTTG AAGGCTTACT GTAGAAGTGG CTTACTGTAG AAGCAGCTTG
3051 CTGAGCCCTT CCGAGCGGTC CCCAGAATTA GCTGGTTCAC AACCCCCACC
3101 CTCCTCCGCC CCCGCCGTGT TCAGGTGTGG ATGAGGTCGT CACACTCAGA
3151 AGGACAGGCT TGTCTGCCAG CTCACAAGGG GAGGCTGCAG TGGGTTTGGG
3201 AGCTGGGTTT AGGCCCTTGG TGTCTGAGGG CCCAGGCTT GCCAGCCTCT
3251 GCTGCTCCTG CTCCTGGGTT TGAAGATGCA GGCCGATCGC CAGCTCCGTG
3301 GCAGCGGTCA CAGGACACAG CCGTACTGTG CCATCTTGGA GCCTCAGGCG
3351 GGGCTCCGGA GATAGAAGAC AGGTCGCCGG AGGCTCCCC TCCTCTCCTC
3401 TCCCTCTGCG AGATGCTCCC TGGGCGCTAC CCTGCAGGGT GCCAGGCAGG
3451 AGTGTCTCA GAACGTGCGC TTCTGATTAT TTTACTGGGG TCCATTGTCC
3501 AGATTTTCTT TTGATTGTAA AATATATTTT TACTTTTGTAG TCTTCTAATT
3551 TAATAAATGA TCCATATAAA AATAGAGAAA TAAAGTCCTT TAAGGGAAGG
3601 TTTAAAAAAA AAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 112 bp to 933 bp; peptide length: 274
 Category: similarity to unknown protein
 Classification: no clue

```

1 MATTVSTQRG PVYIGELPQD FLRITPTQQQ RQVQLDAQAA QQLQYGGAVG
51 TVGRLNITVV QAKLAKNYGM TRMDPYCRLR LGYAVYETPT AHNGAKNPRW
101 NKVIHCTVPP GVDSFYLEIF DERAFSMDDR IAWTHITPE SLRQGVKVEDK
151 WYSLSGRQGD DKEGMINLVM SYALLPAAMV MPPQPVVLMV TVYQQGVGYV
201 PITGMPAVCS PGMVVALPPP AAVNAQPRCS EEDLKAIQDM FPNMDQEVIR
251 SVLEAQRGNK DAAINSLLOM GEEP

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_2d15, frame 1

TREMBL:CEF25H2_1 gene: "F25H2.1"; Caenorhabditis elegans cosmid F25H2,
 N = 1, Score = 385, P = 1.1e-35

>TREMBL:CEF25H2_1 gene: "F25H2.1"; Caenorhabditis elegans cosmid F25H2
 Length = 457

HSPs:

Score = 385 (57.8 bits), Expect = 1.1e-35, P = 1.1e-35
 Identities = 77/182 (42%), Positives = 118/182 (64%)

```

Query:      4 TVSTQRGPVYIGELPQDFLRIT-PTQQQRQVQLDAQAAQQLQYGGAVGTVGRLNITVVQA 62
             TV+ +R V +GELP FLR+ P QQ + ++ Q + ++ T GRL++T+++A
Sbjct:      5 TVAERRRQVLVGELPPHFLRLAVPIQQTAEPEI-VQP-RMVSEFVPP-NTRGRLSVTILEA 61

Query:      63 KLAKNYGMTRMDPYCRLRLGYAVYETPTAHNGAKNPRWNKVIHCTVPPGVDSFYLEIFDE 122
             L KNYG+ RMDPYCR+R+G ++T A N + P WN+ ++ +P V+S Y++IFDE
Sbjct:      62 NLVKNYGLVRMDPYCRVRVGNVEFDTNVAANAGRAPTWNRTLNAYLPMNVESIYIQIFDE 121

Query:      123 RAFSMDDRIAWTHITIPESLRQGVKVEDKWYSLSGRQGDDEKGMINLVMSYAL--LPAAMV 180
             +AF D+ IAW HI +P ++ G D+++ LSG+QG+ KEGMI+L S+A LP
Sbjct:      122 KAFGPDEVIWAHIMLPLAIFNGDNIDEYFQLSGQQGEGKEGMIHLHFSFAPIDLPLQQA 181

```

Query: 181 MPPQP 185

P +P

Sbjct: 182 APAEP 186

Score = 92 (13.8 bits), Expect = 1.8e-01, P = 1.7e-01
 Identities = 26/68 (38%), Positives = 38/68 (55%)

Query: 194 QQGVGYVPITGMPAVCSGMPVPV--ALP--PAAVNAQPRCSEEDLKAIQDMFPNMDQEV 249

QQG G + + +P +P+ A P PA +EED K IQ+MFP +D+EVI
 Sbjct: 156 QQGEGKEGMIHLHFSFAPIDLPLQQAAPAPAPLPVEITEEDTKEIQEMFPIVDKEVI 215

Query: 250 RSVLEAQR 257

+ +LE +R

Sbjct: 216 KCILEERR 223

Pedant information for DKFZphtes3_2d15, frame 1

Report for DKFZphtes3_2d15.1

[LENGTH] 274
 [MW] 30281.97
 [pI] 5.68
 [HOMOL] TREMBL:CEF25H2_1 gene: "F25H2.1"; Caenorhabditis elegans cosmid F25H2 4e-36

[PFAM] C2 domain
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 16.42 %

SEQ MATTVSTQRGPVYIGELPQDFLRITPTQQQRQVQLDAQAAQQLQYGGAVGTVGRNLNITVV
 SEGXXXXXXXXXXXXXXXXX.....
 PRD cccccccccccccccccccccccccchhhhhhhhhhhhhhhcccccccccccccccc

SEQ QAKLAKNYGMTRMDPYCRLRLGYAVYETPTAHNGAKNPRWNKVIHCTVPPGVDSFYLEIF
 SEGXXXXXXXXX.....
 PRD hhhhhhhccccccccchhhhhheeeeecccccccccccccccccccccccccccccccc

SEQ DERAfSMDDRIAWTHITIPESLRQGVKVEDKWYSLSGRQGDKEGMINLVMSYALLPAAAMV
 SEGXXXXXXXXX.....
 PRD ccc

SEQ MPPQPVVLMPTVYQQGVGYVPITGMPAVCSGMPVPVALPAAVNAQPRCSEEDLKAIQDM
 SEG xxx
 PRD ccc

SEQ FPNMDQEVIRSVLEAQRGNKDAAINSLQMGEEP
 SEG
 PRD ccc

(No Prosite data available for DKFZphtes3_2d15.1)

Pfam for DKFZphtes3_2d15.1

HMM_NAME C2 domain
 HMM *LTVrIIcARNLWkMDMnGfSDPYVKVdMdPdPkDtkKWKtKtiWNNGLN
 L+++++A+ + + M+ DPY+++ + + + +T T +N N
 Query 55 LNITVVQAKLAKNYGMT-RMDPYCRLRLGYAVY-----ETPTAHNGAKN 97
 HMM PVWNEEeFvFedIPyPdlqrkMLRFaVWDWDRFSRBDFIGHCi*
 P+WN + +P + + ++++++ FS +D I+ +
 Query 98 PRWN-KVIHCT-VPPGVDSF---YLEIFDERAFSMDDDRIAWTH 135

DKFZphtes3_2e12

group: Transcription Factors

DKFZphtes3_2e12 encodes a novel 849 amino acid protein with similarity to Zinc finger proteins.

The new protein is a putative transcription factor with three C2H2 zinc fingers. Additionally, a cytochrome C family heme-binding site signature is present in the protein, which is only found in cytochrom C related proteins.

The new protein can find application in modulating/blocking the expression of genes controlled by this transcription factor.

similarity to finger proteins

complete cDNA, complete cds, 5 EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 3205 bp

Poly A stretch at pos. 3192, polyadenylation signal at pos. 3171

```
1 GGCACGGCCG GGTCTGGCT GGCCAAACGA GGCTCGCGGA AGCAGCAGCC
51 GCCGCTGAC CGCAGCTGGA TTTTGAAGAT TGATCCAAGG GACTGTATTA
101 ATTTTCAGGAA TTGATTTGAA AGACACTGGC TCTGCCACTT AACAGCCATG
151 TAACCTTGGA TATGGAAGAA AGTAGCAGTG TTGCCATGTT GGTGCCAGAT
201 ATTGGGGAAAC AGGAAGCTAT ACTGACTGCT GAAAGTATCA TCAGTCCTTC
251 ATTGGAAATT GATGAACAAA GAAAAACTAA ACCAGATCCA TTAATCCATG
301 TTATCCAGAA GTTAAGCAAG ATAGAAAAAT GAAAAGTCAC AAAAATGTCT
351 TTTAATTGGG AAGAAACGCC CACGTTCAAG TGCTGCAACA CACTCTCTTG
401 AAACCCAGAA ACTTTGTGAG ATTCCGGCTA AAGTAATCCA GTCACCTGCT
451 GCTGATACTA GAAGGGCTGA GATGTCACAA ACAAATTTTA CCCCTGACAC
501 TCTTGCCAG AATGAAGGGA AGGCTATGTC TTATCAGTGT AGCCTTTGTA
551 AGTTTCTATC ATCATCCTTT TCCGTGTTAA AAGATCATAT TAAGCAACAT
601 GGTCAGCAAA ATGAAGTGAT ACTGATGTGC TCAGAGTGCC ATATTACATC
651 TAGAAGCCAG GAGGAAGTTG AAGCCACGTT GGTGAATGAC CATGACAATG
701 ATGCCAATAT CCACACCCAA TCCAAAGCCC AACAGTGCCT AAGCCCTCC
751 AGCTCTTTGT GTCGGAAGAC CACAGAAAGA AATGAAACCA TTCCAGATAT
801 CCCAGTAAGT GTGGACAATC TACAGACTCA TACTGTCCAA ACTGCATCTG
851 TGGCAGAAAT GGTAGGAGG AAATGGTATG CATACGAACA GTACGGCATG
901 TATCGATGCT TGTTTTGTAG TTATACTTGT GGCCAGCAGA GAATGTGAA
951 AACACACGCT TGGAAACATG CTGGGGAGGT TGATTGCTCC TATCCAATCT
1001 TTGAAAATGA AATGAACCCC CTAGGCCTGC TGGATTCTTC AGCAGTGCT
1051 GCGCCTGGTG GGTGCGATGC AGTCGTCATT GCTATTGGAG ACAGTGAAGT
1101 GAGTATCCAC AATGGGCCAT CAGTGCAAGT GCAGATTGCG AGCTCAGAAC
1151 AGTTATCATC TTCATCTCCT TTAGAACAGA GTGCAGAAAG AGGAGTACAC
1201 CTAAGTCAGT CAGTTACCCT GGACCCCAAT GAGGAAGAAA TGCTAGAAGT
1251 GATTCTTGAT GCAGAGGAGA ATCTGATTCC TGATAGCCTG CTTACATCAG
1301 CACAGAAATAT CATCAGCAGC AGCCCCAATA AAAAAGGGCA TGTTAACGTG
1351 ATAGTGGAGC GATTGCCAAG TGCTGAAGAA ACCCTTTCAC AGAAGCGCTT
1401 CCTCATGAAC ACTGAAATGG AAGAAGGGAA GGACCTGAGC CTGACAGAAG
1451 CTCAGATTGG GCGCGAAGGA ATGGATGATG TTTATCGTGC TGATAAATGT
1501 ACTGTTGATA TTGGGGGATT GATCATAGGC TGGAGCAGTT CAGAGAAAAA
1551 AGACGAGTTA ATGAATAAAG GCCTGGCTAC TGATGAGAAAT GCCCCACCAG
1601 GCGGAGAGAG GACAAATTCT GAGTCTCTTC GATTACACTC ATTAGCTGCA
1651 GAAGCCCTTG TCACAATGCC TATAAGAGCT GCAGAGTTGA CAAGAGCCAA
1701 CCTGGGGCAC TATGGAGATA TAAACCTTTT AGATCCAGAT ACTAGTCAAA
1751 GGCAAGTAGA TAGTACATTG GCAGCGTACT CAAAAATGAT GTCGCCACTT
1801 AAAAATCTCT CAGATGGATT AACTAGTCTT AACCAAAGCA ACTCCACCTT
1851 GGTAGCACTC CCAGAGGGTA GGCAGGAATT GTCAGATGGG CAGGTTAAGA
1901 CAGGCATCAG CATGTCTCTT CTACCCGTCA TTGAAAAATT GAGAGAAAGG
1951 ACAGACCAAA ACGCTTCAGA CGATGACATT TTGAAAGAGT TGCAGGACAA
2001 CGCCAGTGC CAACCCAAAC GCGATACAAG TTTGTCCGGA AACAAATGTG
2051 TGCAATATAG CCGGAATGCT GAACGACCCT ACCGTTGCCG CCTGTGTAC
2101 TACACAAGTG GCAACAAGGG CTACATCAAG CAGCACTTAC GAGTCCATCG
2151 ACAGAGACAG CCTTATCAGT GTCCTATCTG CGAGCACATA GCGGACAACA
2201 GCAAGATTTT GGAGAGTCAC ATGATCCACC ACTGTAAGAC AAGAATATAC
2251 CAGTGCAAGC AGTGTGAAGA ATCCTTCCAT TATAAGAGTC AATTGAGGAA
2301 CCATGAGAGA GAACAGCACA GTCTTCCAGA TACCTTGTC AATAGCAACTT
2351 CTAATGAGCC AAGAATTTCC AGTGATACAG CTGATGGAAA ATGTGTCCAG
2401 GAAGGGAATA AGTCTTCAGT CCAGAAACAA TATAGATGTG ATGTGTGTGA
2451 TTATACAAGT ACACATATG TTGGTGTGAG AAACACAGG CGAATCCATA
2501 ACTCTGATAA CGCGTACAGA TGCTCTCTGT GTGGGTATGT GTGTAGCCAT
2551 CCTCCTTCTT TGAAGTCTCA TATGTGAAA CATGCAAGTG ACCAAAATTA
```

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2601 CAACTACGAA CAAGTAAACA AGGCTATTAA CGACGCGATT TCACAAAGTG
2651 GCAGAGTTCT GGGGAAATCC CCTGGAAAGA CTCAATTAAA GAGCAGTGAA
2701 GAGAGTGCAG ATCCCGTCAC TGGAAGTTCG GAAAATGCAG TGTCATCTTC
2751 AGAACTGATG TCCCAGACTC CCAGTGAAGT TCTGGGTACC AACGAGAATG
2801 AGAAACTGAG CCCTACAAGT AATACCTCAT ATAGTTTAGA AAAAATCTCC
2851 AGTCTGGCCC CTCCTAGCAT GGAGTACTGC GTTTTACTCT TCTGCTGTTG
2901 TATTTGTGGT TTTGAATCAA CCAGCAAAGA AAACCTCTTG GATCATATGA
2951 AAGAGCACGA GGGTGAAATT GTAAACATCA TCCTGAATAA GGACCACAAT
3001 ACAGCTCTAA ACACAAATTA GGTGGAATAA TGACTCGAGC AGGAAAGCAG
3051 TAGAAGAGGA TTCCTTCACC ACAGTTTCAC CTTTACGCTG TCAGACAACT
3101 TCCTGCCACA GAAGAAGTCG TTGATGTGAT TTTTGAGGAA ATGACAGATG
3151 TGACTTTGGA ACCAAACTTG TAATAAAAGG AATTCCAAAT GGAAAAAAA
3201 AAAAA

```

BLAST Results

No BLAST result

Medline entries

90301500:

Cloning and sequencing of a zinc finger cDNA expressed in mouse testis.

92310982:

Zfp-37, a new murine zinc finger encoding gene, is expressed in a developmentally regulated pattern in the male germ line.

Peptide information for frame 1

ORF from 472 bp to 3018 bp; peptide length: 849
Category: similarity to known protein

```

1 MSQTNFTPDT LAQNEGKAMS YQCSLCKFLS SSFVSLKDHI KQHGGQNEVI
51 LMCSECHITS RSQEELEAHV VNDHDNDANI HTQSKAQCV SPSSSLCRKT
101 TERNETIPDI PVSVDNLQTH TVQTASVAEM GRRKWAYEQ YGMYRCLFCS
151 YTCGQQRMLK THAWKHAGEV DCSYPIFENE NEPLGLLDSS AAAAPGGVDA
201 VVIAIGESSEL SIHNGPSVQV QICSSEQLSS SSPLEQSAER GVHLSQSVTL
251 DPNEEEMLEV ISDAEENLIP DSLTSAQKI ISSSPNKKGH VNVIVERLPS
301 AEETLSQKRF LMNTEEMEGK DLSLTEAQIG REGMDDVYRA DKCTVDIGGL
351 IIGWSSSEKK DELMNKGLAT DENAPPGRRR TNESLRLHS LAEALVTMP
401 IRAAELTRAN LGHYGDINLL DPOTSQRQVD STLAAYSKMM SPLKNSSDGL
451 TSLNQSNTSL VALPEGRQEL SDQVKTGIS MSLTVIEKL RERTDQNASD
501 DDILKELQDN AQCOPNSDTS LSGNNVVEYI PNAERP YRCR LCHYTSGNKG
551 YIKQHLRVHR QRQPYQCPIC EHIADNSKDL ESHMIHCKT RIYQCKQCEE
601 SFHYKSQLRN HEREQHS LPD TSLIATSNEP RISSDTADGK CVQEGNKSSV
651 QKQYRCVCD YSTTTYVGV NHRRIHNSDK PYRCSLCGYV CSHPPSLKSH
701 MWKHASDQNY NYEQVNKAIN DAISQSGRVL GKSPGKTQLK SSESADPVT
751 GSSENAVSSS ELMSQTPSEV LGTNEKLS PTSNTSYSLE KISSLAPPSM
801 EYCVLLFCCC ICGFESTSKE NLLDHMKHE GEIVNIILNK DHNTALNTN

```

BLASTP hits

Entry S10245 from database PIR:
finger protein, testis - mouse

Score = 265, P = 8.4e-23, identities = 61/205, positives = 91/205

Entry S22954 from database PIR:
finger protein zfp-37 - mouse

Score = 265, P = 9.1e-22, identities = 61/205, positives = 91/205

Entry AF031657_1 from database TREMBL:

gene: "Zfp94"; product: "zinc-finger protein 94"; Rattus norvegicus
zinc-finger protein 94 (Zfp94) gene, partial cds.

Score = 243, P = 1.6e-21, identities = 57/190, positives = 85/190

Alert BLASTP hits for DKFZphtes3_2e12, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_2el2, frame 1

Report for DKFZphtes3_2el2.1

[LENGTH] 849
 [MW] 94325.42
 [pI] 5.47
 [HOMOL] PIR:A54661 zinc finger protein ZNF41 - human (fragment) 2e-22
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YJL056c] 3e-09
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YJL056c] 3e-09
 [FUNCAT] 04.03.01 trna synthesis [S. cerevisiae, YPR186c PZF1 - TFIIIA] 1e-07
 [FUNCAT] 04.01.01 rrna synthesis [S. cerevisiae, YPR186c PZF1 - TFIIIA] 1e-07
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YOR113w] 4e-07
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YGL209w] 2e-04
 [FUNCAT] 13.04 homeostasis of other ions [S. cerevisiae, YNL027w] 2e-04
 [FUNCAT] 11.01 stress response [S. cerevisiae, YMR037c] 3e-04
 [BLOCKS] BL00028 Zinc finger, C2H2 type, domain proteins
 [SCOP] dlmeys_9.6.1.1.1 a designed zinc finger protein [syntheti 8e-06
 [PIRKW] nucleus 8e-18
 [PIRKW] RNA binding 5e-13
 [PIRKW] duplication 7e-13
 [PIRKW] tandem repeat 1e-21
 [PIRKW] spermatogenesis 6e-16
 [PIRKW] zinc 9e-21
 [PIRKW] zinc finger 1e-21
 [PIRKW] DNA binding 1e-21
 [PIRKW] metal binding 3e-15
 [PIRKW] phosphoprotein 5e-13
 [PIRKW] leucine zipper 1e-13
 [PIRKW] alternative splicing 6e-18
 [PIRKW] eye lens 2e-16
 [PIRKW] oocyte 1e-12
 [PIRKW] transcription factor 6e-18
 [PIRKW] segmentation 7e-13
 [PIRKW] embryo 1e-12
 [PIRKW] transcription regulation 2e-19
 [PIRKW] homeobox 2e-08
 [SUPFAM] POZ domain homology 7e-15
 [SUPFAM] transcription factor Krueppel 7e-13
 [SUPFAM] zinc finger protein ZFP-36 1e-21
 [SUPFAM] homeobox homology 2e-08
 [SUPFAM] unassigned homeobox proteins 2e-08
 [PROSITE] CYTOCHROME_C 1
 [PROSITE] MYRISTYL 10
 [PROSITE] ZINC_FINGER_C2H2 3
 [PROSITE] AMIDATION 2
 [PROSITE] CAMP_PHOSPHO_SITE 2
 [PROSITE] CK2_PHOSPHO_SITE 18
 [PROSITE] TYR_PHOSPHO_SITE 3
 [PROSITE] PKC_PHOSPHO_SITE 10
 [PROSITE] ASN_GLYCOSYLATION 7
 [PFAM] Zinc finger, C2H2 type
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 5.65 %

SEQ MSQTNFTPDTLAQNEGKAMSYQCSLCKFLSSSFVSKDHIKQHGQONEVILMCSECHITS
 SEGXXXXXXXXXXXXXXXXXXXX.....
 lmeyF
 SEQ RSQEELEAHVVNDHDNDANIHTQSKAQCVSPSSSLCRKKTTERNETIPDIPVSDNLQTH
 SEG
 lmeyF
 SEQ TVQTASVAEMGRRKQWYAYEQYGMRYCLFCSYTCGQQRMLKTHAWKHAGEVDCSYPIFENE
 SEG
 lmeyF
 SEQ NEPLGLLDSSAAAAPGGVDAVVIAIGESLSIHNGPSVQVQICSSEQLSSSSPLEQSAER
 SEGXXXXXXXXXXXXXXXXXXXX.....
 lmeyF
 SEQ GVHLSQSVTLDPNEEEMLEVISDAEENLIPDSLLTSAQKIISPPNKKGHVNVVIVERLPS
 SEG
 lmeyF

```

SEQ      AEETLSQKRFLMNTMEMEGKDLSLTEAQIGREGMDDVYRADKCTVDIGGLIIGWSSSEKK
SEG      .....
ImeyF    .....

SEQ      DELMNKGLATDENAPPGRRRRTNSESRLRLHSLAAEALVTMPIRAAELTRANLGHYGDINLL
SEG      .....
ImeyF    .....

SEQ      DPDTSQRQVDSTLAAYSKMMSPLKNSSDGLTSLNQSNSTLVALPEGRQELSDGQVKTGIS
SEG      .....
ImeyF    .....

SEQ      MSLLTVIEKLRERTDQNASDDDLKELQDNAQCQPNSDTSLSGNNVVEYIPNAERPYRCR
SEG      .....
ImeyF    .....TTTEETT

SEQ      LCHYTSGNKGYIKQHLRVHRQRQPYQCPICEHIADNSKDLESHMIHHCKTRIYQCKQCEE
SEG      .....
ImeyF    TTTCEETTHHHHHHHHHHHHTTCCCEETTTTEEECHHHHHHHHHHHHCCCCCEETTTTE

SEQ      SFHYKSQLRNHEREQHSLPDTLSIATSNEPRISSDTADGKCVQEGNKSSVQKQYRCQVCD
SEG      .....
ImeyF    EECCHHHHHHHHHHHHC.....

SEQ      YTSTTYVGVNRHRIHNSDKPYRCSLCGYVCSHPPSLKSHMWKHASQNYNYEQVNKAIN
SEG      .....
ImeyF    .....

SEQ      DAISQSGRVLGKSPGKTQLKSSEESADPVTGSSSENAVSSSELMSQTPSEVLGTNENEKLS
SEG      .....
ImeyF    .....

SEQ      PTSNTSYSLEKISSLAPPSMEYCVLLFCCCICGFESTSKENLLDHMKHEGEIVNIILNK
SEG      .....
ImeyF    .....

SEQ      DHNTALNTN
SEG      .....
ImeyF    .....

```

Prosites for DKFZphtes3_2el2.1

PS00001	104->108	ASN_GLYCOSYLATION	PDOC00001
PS00001	445->449	ASN_GLYCOSYLATION	PDOC00001
PS00001	454->458	ASN_GLYCOSYLATION	PDOC00001
PS00001	457->461	ASN_GLYCOSYLATION	PDOC00001
PS00001	497->501	ASN_GLYCOSYLATION	PDOC00001
PS00001	646->650	ASN_GLYCOSYLATION	PDOC00001
PS00001	784->788	ASN_GLYCOSYLATION	PDOC00001
PS00004	98->102	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	378->382	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	59->62	PKC_PHOSPHO_SITE	PDOC00005
PS00005	101->104	PKC_PHOSPHO_SITE	PDOC00005
PS00005	306->309	PKC_PHOSPHO_SITE	PDOC00005
PS00005	357->360	PKC_PHOSPHO_SITE	PDOC00005
PS00005	385->388	PKC_PHOSPHO_SITE	PDOC00005
PS00005	425->428	PKC_PHOSPHO_SITE	PDOC00005
PS00005	678->681	PKC_PHOSPHO_SITE	PDOC00005
PS00005	696->699	PKC_PHOSPHO_SITE	PDOC00005
PS00005	726->729	PKC_PHOSPHO_SITE	PDOC00005
PS00005	817->820	PKC_PHOSPHO_SITE	PDOC00005
PS00006	62->66	CK2_PHOSPHO_SITE	PDOC00006
PS00006	106->110	CK2_PHOSPHO_SITE	PDOC00006
PS00006	126->130	CK2_PHOSPHO_SITE	PDOC00006
PS00006	232->236	CK2_PHOSPHO_SITE	PDOC00006
PS00006	262->266	CK2_PHOSPHO_SITE	PDOC00006
PS00006	300->304	CK2_PHOSPHO_SITE	PDOC00006
PS00006	314->318	CK2_PHOSPHO_SITE	PDOC00006
PS00006	323->327	CK2_PHOSPHO_SITE	PDOC00006
PS00006	355->359	CK2_PHOSPHO_SITE	PDOC00006
PS00006	381->385	CK2_PHOSPHO_SITE	PDOC00006
PS00006	485->489	CK2_PHOSPHO_SITE	PDOC00006
PS00006	499->503	CK2_PHOSPHO_SITE	PDOC00006
PS00006	617->621	CK2_PHOSPHO_SITE	PDOC00006
PS00006	626->630	CK2_PHOSPHO_SITE	PDOC00006
PS00006	741->745	CK2_PHOSPHO_SITE	PDOC00006
PS00006	758->762	CK2_PHOSPHO_SITE	PDOC00006
PS00006	766->770	CK2_PHOSPHO_SITE	PDOC00006
PS00006	817->821	CK2_PHOSPHO_SITE	PDOC00006

PS00007	331->339	TYR_PHOSPHO_SITE	PDOC00007
PS00007	703->711	TYR_PHOSPHO_SITE	PDOC00007
PS00007	596->605	TYR_PHOSPHO_SITE	PDOC00007
PS00008	142->148	MYRISTYL	PDOC00008
PS00008	185->191	MYRISTYL	PDOC00008
PS00008	196->202	MYRISTYL	PDOC00008
PS00008	241->247	MYRISTYL	PDOC00008
PS00008	349->355	MYRISTYL	PDOC00008
PS00008	473->479	MYRISTYL	PDOC00008
PS00008	478->484	MYRISTYL	PDOC00008
PS00008	645->651	MYRISTYL	PDOC00008
PS00008	751->757	MYRISTYL	PDOC00008
PS00008	772->778	MYRISTYL	PDOC00008
PS00009	130->134	AMIDATION	PDOC00009
PS00009	376->380	AMIDATION	PDOC00009
PS00028	146->167	ZINC_FINGER_C2H2	PDOC00028
PS00028	684->705	ZINC_FINGER_C2H2	PDOC00028
PS00028	595->617	ZINC_FINGER_C2H2	PDOC00028
PS00190	53->59	CYTCHROME_C	PDOC00169

Pfam for DKFZphtes3_2e12.1

HMM_NAME Zinc finger, C2H2 type

HMM *CpwPDCgKtFrrwsNLrRHMRT.H*
 C++ C+ T R++++L++H H
 Query 53 CSE--CHITSRSQEELEAHVNV-DH 74

23.25 (bits) f: 539 t: 559 Target: dkfzphes3_2e12.1 similarity to finger proteins
 Alignment to HMM consensus:

Query *CpwPDCgKtFrrwsNLrRHMRT.H*
 C C++T ++ ++H+R+H
 dkfzphes3 539 CRL--CHYTSNGNGYIKQHLRVH 559

Query f: 567 t: 587 Target: dkfzphes3_2e12.1 similarity to finger proteins
 Alignment to HMM consensus:

HMM *CpwPDCgKtFrrwsNLrRHMRT.H*
 CP+ C+ ++ +L+ HM+ H
 Query 567 CPI--CEHIADNSKDLSEHMIHH 587

33.47 (bits) f: 595 t: 616 Target: dkfzphes3_2e12.1 similarity to finger proteins
 Alignment to HMM consensus:

Query *CpwPDCgKtFrrwsNLrRHMRT.H*
 C+ C+++F ++S+LR+H R H
 dkfzphes3 595 CKQ--CEESFHYKSQLRNHERE-QH 616

Query f: 656 t: 676 Target: dkfzphes3_2e12.1 similarity to finger proteins
 Alignment to HMM consensus:

HMM *CpwPDCgKtFrrwsNLrRHMRT.H*
 C++ C++T ++ R+H+R+H
 Query 656 CDV--CDYTSTTYVGVNRHRIH 676

24.53 (bits) f: 684 t: 704 Target: dkfzphes3_2e12.1 similarity to finger proteins
 Alignment to HMM consensus:

Query *CpwPDCgKtFrrwsNLrRHMRT.H*
 C+ CG++ +++ +L+ HM H
 dkfzphes3 684 CSL--CGYVCSHPPSLKSHMWKH 704

Query f: 809 t: 829 Target: dkfzphes3_2e12.1 similarity to finger proteins
 Alignment to HMM consensus:

HMM *CpwPDCgKtFrrwsNLrRHMRT.H*
 C+ CG +++++NL HM+ H
 Query 809 CCI--CGFESTSKENLLDHMKEH 829

DKF2phtes3-2f14

group: testes derived

DKF2phtes3 2f14 encodes a novel 129 amino acid protein with very weak similarity to human omega protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

weak similarity to omega protein

complete cDNA, complete cds, 1 EST hit

Sequenced by EMBL

Locus: unknown

Insert length: 2353 bp

Poly A stretch at pos. 2341, no polyadenylation signal found

```
1 GCAGATTCTC CAGGCCAGC ATCTGCCTCA CCGTGGCCCC CCACAAGCCA
51 AGCGCCTGCC TTTCAGCAGC CTCTACACAC CCAGCTCCTG CCACCCAATG
101 GCTCTTTAGG CCAAGCTCAT ACCTCAGCAT GATTTTTCCTA GGCCCAACTT
151 TTGTCTCATG GCAACCTTCC CTGGCCAAGT TTCCACCTAT TTCCTGGCAG
201 CCTGGACAGG CCCAGGTCCT GCCACACACT GGCTCTCTA CGCCAGCTC
251 ATGCCTCACA GTGGCCTCTC CAGGCCAGC TCCTGTCCCG GGACATCATC
301 TCCAGGCCCA AAACCTCCTC AAGTCGGCCT CTCCAGGCC AGTTGCTGCC
351 TCCCGGCATT CTCTCCAGGC CTAGCTCTTC CTCTGGCTG TATCTACAAG
401 ACCAACTCCT GCCTCACAA ACCTTTTAT GGCTCAGCTC CTGCCCAACT
451 ACTGCCGGCC TTTGTAGGCC CAAAACCTCC TCAAGTCAAG CTCTTTAGGC
501 CCACCTTCCTG CCTTGCAGTG GCCTGTACAG ACCCAGCTCT GGCTTGAGAA
551 CAGCCTCTGC AGGCCCTGCT CTTGCCTCTT AGCTCCCTCT CCAGGCCCAT
601 CTCTTGCCCTC ACAGTGGCTT CCGTGGGCCA AGTTCCCGCC TGCCCTCCAG
651 CAGCCTCAAC AGGCCTAGCT CCTCCCTCAC AATGGCTTGT TTAGGTCCAG
701 TTGATGCCCTC TGGCAACCTG TCCAGGCCCA GCTCCTGCCT CACACTGGCC
751 TCTCTAGGCC GAGGTCTTTT CTCATACTGG CCGTGGGCCA AGTTCCCGCC TGCCCTCCAG
801 TCCTCTTGTC ATCTCTCCAG GCCCAGCTTT TGCTGTGTGT TGGCCTCTAC
851 CTCACAGTGC ACCTTCCAGT CCCACCTCTT GCCTCACCAT GGCCTCCTCT
901 GACCAGGTTT CTGCCTTTTG GCAGCCTCTA CAGGCCTAGC TGCTGCCTCC
951 CAATGGCCTT TGTAGGCCAC GCTCATGCCT CACTGTGGCC TTTCCAGGCC
1001 TAGCTTTTGC TTTTGGCCA CTCCAGGCC AGAACTTCCC CCAGTCAGCC
1051 TCTCCAGGCC CAGCTCTTCC TCCCAGCAAC CTCTGCAGGC CCAAATCATC
1101 CTCAAATTGG CCTCTTCTT CCCAGCTCCT GCCTCCTGGT GGCCTCTGAA
1151 GACCCAAATC GTCTCCAGT TGGTTTTTCC AGGCCAGCT CTGCCTTTT
1201 GGTGGCCTCT CCAGGTGCAA AACTTCCTCC CATCAGCCTG TCCAGGCCCA
1251 GCTCATGCCT CTGGGTGGCC TTCTCAGGCC CTGCTTTTGA CTTGGTGGCC
1301 TCTTCAGGCC CAGAAGTTGA ACTCAAGTCA GCCTCTCCAG GCCCAGCTCC
1351 TGCCTTCTTA AGGTCTGTAC AGGCCAGGCC TCTACCTCAC AGCGGACTCT
1401 CCACACCCAG CTCTTGCCCTC ACTGTAGCCT CCCCAGTCCA AAATCCTGCT
1451 CTTTTGGCAG CTTGACAAAG CCCAGCTCCT GCCTTTCAAT GACCTCTTTA
1501 GGCCCGGCTC ATTCTTTACA ACGGCCTTTC CAGGCCAGT TTTTCCCTTT
1551 TGGCGGCCCTC TCCAGGCCCA GAACTTCCTC AAGTCGGCCT CTTTAGGCC
1601 AGTTGCTGCC TCCTGGCATC CTCTGCAGGC CGAGCTCTTC CTCCCTGCTG
1651 TGTCTACAGG CCCAACTCCT GCCTCACAA ACCTCCTTG GACTCAGCTT
1701 CTGCCAGCTC CTGGGTGGCC TTTGTAGGCT CAAAATTTTC TCAAATCAAG
1751 CTCTCCAGGC CTACTGTCAG CCGTGGGCA GCCTAAACAG GCCCAGCTCC
1801 TGCCTGACAA TGGCCTCTCC AGGCTTTTCT CCGCCTCGC AGCAGGCTTT
1851 CCAGGCCAGC CTCTTGCCCTC ATGGTGGCCT TCCCGGCCA TGTCTCTATC
1901 CTAGTTCTGG CAGCCTCAAC CGGCCAGCT TCTGCCTCAC ACTGGCCTCT
1951 CTAGGCCAGC CTCTTTTTC ACAGTGGCCT CACTACGCCC ATCTCCTACC
2001 TCAGATCTGC CTCCCAAGAC CCAGCTCCTG TCTCATGGTG GTCTCTCTTA
2051 CACCAGCTCC TGCCTCACAA TGGCCTCGTC TGGCCCATCT TCTGCCTCAC
2101 AGTGGCCACT CAAGGCCCAT CTTTGGCTC ATGGTAGCCT CTTCTGGTTT
2151 TGCTCTTGCC TCACAGTTGC CTCTTCCAGA TCCAGCTTTA AGCCTTTGAT
2201 GGTCAACAGC ATCAAGGAGC CTAAGCTTC CCGGACTCT CATTGTGTTA
2251 CTTTACAGCA GAGTGCCTTA GCAAAAACCTG TCTCTTAACC TTGAGAGTGG
2301 ATTTCTGACA AATCGATAGT AAATTCTGCC TGTGTGGTTT CAAAAAATAA
2351 AAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 158 bp to 544 bp; peptide length: 129
Category: similarity to known protein

1 MATFPGQVST YFLAAWTGPG PATHWPLYAQ LMPHSGLSRP SSCPGTSSPG
51 PKLPQVGLSR PSCCLPAFSP GLALPPGCIY KTNLSCLTTTF YGSAPAQLLP
101 AFGVGPQLPQV KLFRTFCLA VACTDPALA

BLASTP hits

Entry I70697 from database PIR:
omega protein - human (fragment)
Score = 79, P = 2.8e-03, identities = 32/94, positives = 38/94

Alert BLASTP hits for DKFZphtes3_2f14, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3_2f14, frame 2

Report for DKFZphtes3_2f14.2

[LENGTH] 129
[MW] 13421.76
[pI] 9.14
[PROSITE] MYRISTYL 2
[KW] Irregular
[KW] LOW_COMPLEXITY 10.85 %

SEQ MATFPGQVSTYFLAAWTGPGPATHWPLYAQLMPHSGLSRPSSCPGTSSPGPKLPQVGLSR
SEGXXXXXXXXXXXXXXXXX.....
PRD cccccccceehhhhhccc

SEQ PSCCLPAFSPGLALPPGCIYKTNLSCLTTTFYGSAPAQLLPAGVGPQLPQVKLFRTFCLA
SEG
PRD cc

SEQ VACTDPALA
SEG
PRD ccccccccc

Prosite for DKFZphtes3_2f14.2

PS00008	6->12	MYRISTYL	PDOC00008
PS00008	92->98	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_2f14.2)

DKFZphtes3_2g7

group: testes derived

DKFZphtes3_2g7 encodes a novel 359 amino acid protein with similarity to neurofilament proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to neurofilament proteins

complete cDNA, complete cds, 6 EST hits (5 hits are out of a testis library)

Sequenced by EMBL

Locus: unknown

Insert length: 1613 bp

Poly A stretch at pos. 1595, polyadenylation signal at pos. 1557

```

1  GCCACACAGG CTCCTTGGAG TAAGAGTGTG AGAAACTGGA TGAAGACAGC
51  TGTATTCTTT TGGAAAGCGTT CGAGATTGGT CTGTCTCTAC CAACTAAAAA
101 CTTCTAGCCTT AAGTGCAGAG ATTTAAGGAG ATCAACAAAA ACTCAGTCTA
151 GACATATTAT GAGGCTGGGA GGGTATCAAC AGACTTGAGT TCTTGTGAGC
201 AAGATCACCT GCTTTTAATA TTGTCTCAG GGTCTGAGCA CATCTGGAAG
251 TGAGGTCAAT CAAGTTAGAC CCCAAAAACT TTTGTGACAA CAGTGAAGAG
301 GGGAAAATAA ACACACCACA AACATGAACC TCAACCCCCC GACATCTGCT
351 CTTCAGATCG AGGGCAAAGG CAGCCATATT ATGGCTAGAA ATGTAAGCTG
401 CTTTCTAGTC AGGCACACCC CTCATCCCAG AAGAGTCTGC CACATCAAAG
451 GCTTGAATAA CATTCCAATC TGTACTGTGA ATGATGATGA GAATGCATTT
501 GGAACATTGT GGGAAAGTTGG CCAGTCTAAC TACTTAGAGA AGAACAGGAT
551 ACCATTTGCC AATTGCAGTT ACCCCCCGAG CACTGCAGTC CAGAAGAGCC
601 CTGTAAGAGG AATGTCGCCA GCCCCAAACG GTGCCAAAGT GCCTCCACGG
651 CCTCATTCTG AGCCCAGTAG AAAAATTAAA GAGTGCTTCA AACTTCCAG
701 TGAGAATCCC TTAGTAATTA AAAAGGAAGA AATTAAGGCC AAAAGACCAC
751 CATCACCTCC AAAGGCATGC TCTACTCCTG GCTCCTGTTC TTCAGGGATG
801 ACAAGTACCA AGAATGATGT GAAAGCAAAC ACCATTGCA TACCAAATA
851 TCTGGATCAG GAAATAAAAA TCCTGGCAAA GCTCTGTAGC ATTTTGCATA
901 CTGATTCTCT GGCAGAAGTT TTACAGTGGC TGCTTCATGC AACTTCAAAA
951 GAAAAAGAGT GGGTCTCAGC TTTGATTCAT TCTGAGCTTG CCGAGATAAA
1001 CCTGTAACT CATCACAGAA GAAACACCTC AATGGAACCA GCAGCAGAGA
1051 CTGGGAAGCC ACCCAGATT AAATCACCAC CCACAGTTAA ATTGCCCCCA
1101 AATTTTACTG CAAAATCAAA AGTGCTGACC AGAGATACAG AAGGGGATCA
1151 ACCAACCAGA GTGTCAAGTC AAGGATCTGA AGAAAACAAG GAAGTACCAA
1201 AAGAGGCTGA GCACAAGCCT CCACTACTTA TAAGAAGAAA TAATATGAAA
1251 ATACCTGTTG CAGAATATTT CAGCAAACCA AATTCTCCTC CCAGGCCTAA
1301 CACTCAGGAG AGTGGATCAG CAAAACCACT GTCAGCAAGG AGTATACAAG
1351 AATACAACCT CTGTCCCAA AGAGCATGTT ATCCTTCAAC ACACCGGAGG
1401 TAGAAGTTCT AGACTGGGTG AATTCTTTCA TGAATATGAG CTTACATTT
1451 ACATCATCAA ATTATTTTTC AAATGAATAT TTTTGGTATT GAGGAATCAA
1501 GTGGTCCTCT TTATGGTGGC ACATGTAAAT CTAAAAATAC CTGTATGTAA
1551 TGCTACAAAT AAATATTACT GGAAATGATA TTTCCATTG TAGTTAAAAA
1601 AAAAAAAAAA AAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 324 bp to 1400 bp; peptide length: 359
Category: similarity to known protein


```
1 MNLNPPTSAL QIEGKGSHIM ARNVSCFLVR HTPHPRRVCH IKGLNNIPIC
51 TVNDDENAFG TLWEVGQSNY LEKNRIPFAN CSYPPSTAVQ KSPVRGMSPA
101 PNGAKVPPRP HSEPSRKIKE CFKTSSSENPL VIKKEEIKAK RPPSPPKACS
151 TPGSCSSGMT STKNDVKANT ICIPNYLDQE IKILAKLCSI LHTDSLAEVL
201 QWLLHATSKE KEWVSALIHS ELAEINLLTH HRRNTSMEPA AETGKPPTVK
251 SPPTVKLPPN FTAKSKVLTR DTEGDQPTRV SSQGSEENKE VPKEAEHKPP
301 LLIRRNMMKI PVAEYFSKPN SPPRPNTQES GSAKPVARS IQEYNLCQPR
351 ACYPSTHRR
```

BLASTP hits

Entry A43427 from database PIR:
neurofilament triplet H1 protein - rabbit (fragment)
Score = 118, P = 5.6e-04, identities = 79/290, positives = 110/290

Entry RNNFH_1 from database TREMBL:
Rat high molecular weight neurofilament (NF-H) protein mRNA, 3' end.
Score = 115, P = 9.5e-04, identities = 69/281, positives = 100/281

Entry B43427 from database PIR:
neurofilament protein H form H2 (repetitive region) - rabbit (fragment)
Score = 111, P = 1.3e-03, identities = 64/269, positives = 102/269

Alert BLASTP hits for DKFZphtes3_2g7, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_2g7, frame 3

Report for DKFZphtes3_2g7.3

```
[LENGTH]      359
[MW]           39725.53
[pI]           9.45
[PROSITE]      MYRISTYL      3
[PROSITE]      CAMP_PHOSPHO_SITE      1
[PROSITE]      CK2_PHOSPHO_SITE      9
[PROSITE]      PKC_PHOSPHO_SITE     10
[PROSITE]      ASN_GLYCOSYLATION      4
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY      4.18 %
```

```
SEQ      MNLNPPTSALQIEGKGSHIMARNVSCFLVRHTPHPRRVCHIKGLNNIPICTVNDDENAFG
SEG      .....
PRD      ccccccccccecccccccccecccccccccccccccccccccccccccccccccccccc

SEQ      TLWEVGQSNYLEKNRIPFANCSYPPSTAVQKSPVRGMSPAPNGAKVPPRPHSEPSRKIKE
SEG      .....
PRD      cccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhh

SEQ      CFKTSSSENPLVIKKEEIKAKRPPSPPKACSTPGSCSSGMTSTKNDVKANTICIPNYLDQE
SEG      .....
PRD      hccccccccceehhhhhhccccccccccccccccccccccccccccccccccccceehhccccchhh

SEQ      IKILAKLCSILHTDSLAEVLQWLLHATSKEKEWVSALIHS ELAEINLLTHHRRNTSMEPA
SEG      .....
PRD      hhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccc

SEQ      AETGKPPTVKSPPTVKLPPNFTAKSKVLTRDTEGDQPTRVSSQGSEENKEVPKEAEHKPP
SEG      ....xxxxxxxxxxxxxxxxx.....
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ      LLIRRNMMKIPVAEYFSKPNSPPRPNTQESGSAKPVARS IQEYNLCQPRACYPSTHRR
SEG      .....
PRD      eeeeeccccccccccccccccccccccccccccccccchhhhhcccccccccccccccccc
```

Prosite for DKFZphtes3_2g7.3

```
PS00001      23->27      ASN_GLYCOSYLATION      PDOC00001
PS00001      80->84      ASN_GLYCOSYLATION      PDOC00001
PS00001      234->238     ASN_GLYCOSYLATION      PDOC00001
```

PS00001	260->264	ASN_GLYCOSYLATION	PDOC00001
PS00004	232->236	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	115->118	PKC_PHOSPHO_SITE	PDOC00005
PS00005	161->164	PKC_PHOSPHO_SITE	PDOC00005
PS00005	207->210	PKC_PHOSPHO_SITE	PDOC00005
PS00005	243->246	PKC_PHOSPHO_SITE	PDOC00005
PS00005	248->251	PKC_PHOSPHO_SITE	PDOC00005
PS00005	254->257	PKC_PHOSPHO_SITE	PDOC00005
PS00005	262->265	PKC_PHOSPHO_SITE	PDOC00005
PS00005	332->335	PKC_PHOSPHO_SITE	PDOC00005
PS00005	337->340	PKC_PHOSPHO_SITE	PDOC00005
PS00005	356->359	PKC_PHOSPHO_SITE	PDOC00005
PS00006	51->55	CK2_PHOSPHO_SITE	PDOC00006
PS00006	61->65	CK2_PHOSPHO_SITE	PDOC00006
PS00006	124->128	CK2_PHOSPHO_SITE	PDOC00006
PS00006	162->166	CK2_PHOSPHO_SITE	PDOC00006
PS00006	195->199	CK2_PHOSPHO_SITE	PDOC00006
PS00006	207->211	CK2_PHOSPHO_SITE	PDOC00006
PS00006	235->239	CK2_PHOSPHO_SITE	PDOC00006
PS00006	272->276	CK2_PHOSPHO_SITE	PDOC00006
PS00006	340->344	CK2_PHOSPHO_SITE	PDOC00006
PS00008	153->159	MYRISTYL	PDOC00008
PS00008	158->164	MYRISTYL	PDOC00008
PS00008	284->290	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_2g7.3)

DKFZphtes3_2h1

group: transmembrane protein

DKFZphtes3_2h1 encodes a novel 116 amino acid protein with weak similarity to C. elegans cosmid C13F10.

The novel protein contains 1 transmembrane region.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

similarity to C.elegans C13F10.5

TRANSMEMBRANE 1

Sequenced by EMBL

Locus: /map="2"

Insert length: 1156 bp

Poly A stretch at pos. 1143, polyadenylation signal at pos. 1121

```
1  GGCCATCAAA  ATAATAAAC  CATGTCATTT  GGAGCAACAA  AGCCACTGCG
51  GCCTCCATTT  GGGCCAAGCT  CTGACTGCAA  TGATGCCTCT  GCGCCGACCC
101  GGGCCTCGCT  GTGACTGACA  ATGCCGCTGC  ATCTTTTCAG  CAGTCATTGA
151  TGAGGAAGTA  TCTACATCCT  CCTTCCCACT  ACCAGATTTT  GCTTGGAGAA
201  AAGCAGTTTC  CTGAAATAAT  TCTGTGACGA  GCTTCTTCCA  CATTAGGACA
251  AAAATGCTGG  AAGCGGCTCA  GCGCCAGGGC  AGCACATCAG  AGACACCATG
301  GAACACAGCC  ATTCTCTGTC  CGTCGTGCTG  GGACCAAGTCT  TTCTTGACCA
351  ATATCACCTT  CTTGAAGGTT  CTTCTCTGGT  TGGTCCTGCT  GGGACTGTTT
401  GTGGAAGTGG  AATTTGGCCT  GGCATATTTT  GTCTGTCTCT  TGTCTATTG
451  GATGTACGTC  GGGACACGAG  GCCCTGAAGA  GAAGAAAGAG  GGAGAGAAGA
501  GCGCCTACTC  TGTGTTCAAT  CCAGGCTGTG  AAGCCATCCA  GGGCACCCTG
551  ACTGCAGAGC  AGTTGGAGCG  CGAGTTACAG  TTGAGACCCC  TGGCAGGGAG
601  ATAGGACCCA  GCTGTGCTGT  CATGCAGCTA  ACCTCTGATG  TGGTCTTCCT
651  CACCATTGGC  TATGGATTTG  ATTTGAGGTG  TATAGGACTA  AGGGCAGCTT
701  GCGGGTTAGC  TCTGTGACTG  CATAGTTTTT  CTACCTTCTT  TCCCTGATCT
751  TTTGCTGCCA  TTTGATCTTT  GATAGTTTGT  GTGAAACTCT  CTAATAATCA
801  TTCCTGTGGG  GTCCGACGCA  ATTTATAAAA  ATTATGTACT  CAAGAAGGGA
851  GACCTGTTTG  TTTCAATTTT  CATCTGTTTG  GGAGATGATT  TTAGAGCACT
901  AGAAAGGCAC  TGGGGAGATT  CTCAGCTTAA  AACATCCAGC  AGTTTGAAGT
951  ATGATTAGGT  ACATCAGGGC  TGCATTGTCA  ATGTTCTCTT  TAAGTCTTTT
1001  AACATTTATA  GCAATTTTTT  TTTTCCCGGA  GAGTTTAGGT  TGCAAGTTTT
1051  GGGTTTCTTG  TTTGTTTTTG  TTTTGCTTCC  TGCTTTAATT  CTTTAATTTT
1101  CAGTCATTAC  TGGTATTGAA  AAATAAAATA  TCTTTAAAC  ATCAAAAAAA
1151  AAAAAA
```

BLAST Results

Entry HS313307 from database EMBL:

human STS SHGC-16715.

Score = 1222, P = 1.4e-48, identities = 248/251

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 254 bp to 601 bp; peptide length: 116
Category: similarity to unknown protein

```
1  MLEAAQPQGS  TSETPWNTAI  PLPSCWDQSF  LTNITFLKVL  LWLVLLGLFV
51  ELEFGLAYFV  LSLFYWMYVG  TRGPPEEKKEG  EKSAYSVFNP  GCEAIQGTLT
101  AEQLERELQL  RPLAGR
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2h1, frame 2

TREMBL:CEUC13F10_2 gene: "C13F10.5"; Caenorhabditis elegans cosmid
C13F10., N = 1, Score = 141, P = 8.2e-10

>TREMBL:CEUC13F10_2 gene: "C13F10.5"; Caenorhabditis elegans cosmid
C13F10.

Length = 171

HSPs:

Score = 141 (21.2 bits), Expect = 8.2e-10, P = 8.2e-10
Identities = 32/82 (39%), Positives = 52/82 (63%)

Query: 27 DQSFLTNTFLKVLWLVLGLFVELEFGLAYFVLSLFYWMYVGTRGPPEEKKEGEKSAYS 86
+QS ++ T + V++++V L ++FG +F+LSL + Y T G ++ GE SAYS
Sbjct: 90 EQSVVS--TRIAVVVVVVGQALAAWVQFVAVFFILSLILFTYWNT-G--RRRRGEMSAYS 144

Query: 87 VFNPGCEAIQGTLTAEQLEREL 108
VFN CE + G++TAE ER++
Sbjct: 145 VFNDNCERLAGSMTAEHFERDM 166

Pedant information for DKFZphtes3_2h1, frame 2

Report for DKFZphtes3_2h1.2

[LENGTH] 116
[MW] 13092.19
[pI] 4.64
[PROSITE] MYRISTYL 1
[PROSITE] CK2_PHOSPHO_SITE 2
[PROSITE] TYR_PHOSPHO_SITE 2
[PROSITE] ASN_GLYCOSYLATION 1
[KW] TRANSMEMBRANE 1
[KW] LOW_COMPLEXITY 32.76 %

SEQ MLEAAQPQGSTSETPWNTAIPSPSCWDQSFLTNTFLKVLWLVLGLFVELEFGLAYFV
SEGXXXXXXXXXXXXXXXXXXXXX.....
PRD cccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEMMMMMMMMMMMMMMMMMMMMM.....

SEQ LSLFYWMYVGTRGPPEEKKEGEKSAYSVFNPGCEAIQGTLTAEQLERELQLRPLAGR
SEGXXXXXXXXXXXXXXXXXXXXX.....
PRD hhhhhhhhhccccchhhhhccccceeeccccccccccccchhhhhhhhhhhccccccccc
MEMcc

Prosite for DKFZphtes3_2h1.2

PS00001	33->37	ASN_GLYCOSYLATION	PDOC00001
PS00006	10->14	CK2_PHOSPHO_SITE	PDOC00006
PS00006	24->28	CK2_PHOSPHO_SITE	PDOC00006
PS00007	78->86	TYR_PHOSPHO_SITE	PDOC00007
PS00007	77->86	TYR_PHOSPHO_SITE	PDOC00007
PS00008	97->103	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_2h1.2)

DKFZphtes3_2h15

group: testes derived

DKFZphtes3_2h15 encodes a novel 855 amino acid protein with very weak similarity to *S. pombe* cdc23.

No informative BLAST results; no predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to cdc23

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 4619 bp

Poly A stretch at pos. 4598, polyadenylation signal at pos. 4589

```
1 GAAGGCGTCC CGGCATCGGC CAAGATTCTA CATTGCTCAT CTGGGCATCT
51 GAGCCTCCTT CGAAGTTTCC TGTCACAACT GTCCTCTTGA CAGCATGGAT
101 GAGGAGGAAG ACAATCTGTC TCTGCTGACC GCACTGCTGG AAGAAAATGA
151 GTCAGCCTTG GATTGTAATT CAGAAGAAAA TAACTTCTTG ACGCGGGAAA
201 ATGGCGAGCC CGACGCATTT GATGAGCTCT TTGATGCCGA CGGCGACGGT
251 GAATCTTATA CAGAAGAGGC TGATGATGGA GAAACAGGAG AGACAAGAGA
301 CGAAAAGGAA AATCTGGCCA CTCTCTTTGG AGATATGGAG GACTTAACAG
351 ATGAAGAAGA AGTTCCCGCA TCACAGTCAA CTGAAAATAG GGTCTCCCT
401 GCTCCTGCCC CCAGGCGAGA GAAAACGAAT GAAGAGTTGC AAGAGGAATT
451 AAGGAATTTG CAAGAGCAAA TGAAGGCCCTT ACAAGAGCAG CTAAGAAGTAA
501 CAACAATTAA ACAGACAGCA AGCCCAGCCC GTCTGCAAAA ATCCCTTGAG
551 AAGTCTCCCC GGCCACCTCT TAAGGAGAGG AGAGTTCAGA GAATTCAGGA
601 GTCAACATGC TTTTCTGCGG AGCTTGATGT CCCTGCGCTA CCAAGAACCA
651 AGAGGGTGGC TCGAACACCA AAGCCTTCAC CTCCAGATCC CAAAAGCTCA
701 TCTTCAAGGA TGACAAGTGC ACCCTCCCAA CCCCTACAGA CGATTTCTCG
751 GAACAAACCT AGTGGGATAA CTAGAGGTCA AATTGTGGGG ACCCCAGGAA
801 GTTCTGGGGA AGCAACTCAA CCCATCTGTG TGGGAAGCCTT CTCTGGTCTG
851 CGGCTCAGGC GGCCTCGAGT ATCCTCCACA GAAATGAACA AGAAAATGAC
901 CGGCCGAAAA CTGATCAGAC TGTCTCAGAT CAAGGAAAAG ATGGCCAGAG
951 AGAAGCTGGA AGAAATAGAT TGGGTGACAT TTGGGGTTAT ATTGAAGAAG
1001 GTTACGCCAC AGAGTGTGAA TAGTGGAAAA ACCTTCAGCA TATGGAAACT
1051 GAATGATCTT CGTGACCTGA CACAATGTGT GTCCTTGTTC TTATTTGGAG
1101 AAGTTCACAA AGCGCTCTGG AAGACGGAGC AGGGGACTGT CGTAGGGATC
1151 CTCAATGCCA ACCCATGAA GCCCAAGGAT GGTTCAGAGG AGGTGTGTTT
1201 ATCTATCGAT CATCCTCAGA AGGTCTTAAT TATGGGTGAA GCTCTTGACC
1251 TGGGAACCTG TAAAGCCAAG AAGAAGAATG GAGAGCCGTG CACGCAGACT
1301 GTGAATTTGC GTGACTGTGA GTACTGTGAG TACCATGTCC AGGCTCAGTA
1351 CAAGAAGCTC AGTGCAAAAGC GTGCGGATCT GCAGTCCACC TTCTCTGGAG
1401 GACGAATTCC AAAGAAGTTT CCCCAGCAGG GCACCAGCCT CAAAGAACGG
1451 CTGTGCCAAG ATGGCTTTTA CTACGGAGGG GTTCTTCTG CCTCGTATGC
1501 AGCTTCAATT GCAGCAGCTG TGGCTCCTAA GAAGAAGATT CAAACCACTC
1551 TGATTCTCTT GTTGTGTAAG GGCACAACT TGATCATCCA GGAACACGG
1601 CAAAAACTCG GAATACCCCA GAAGAGCCTG TCTTGCTCTG AGGAGTTCAA
1651 GGAAGTATG GACCTGCCGA CGTGTGGAGC CAGGAACCTA AAACAACATT
1701 TAGCCAAAGC CTCAGCTTCA GGGATTATGG GGAGCCCAAA ACCAGCCATC
1751 AAGTCCATCT CGGCCTCAGC ACTCTTGAAG CAACAGAAAGC AGCGGATGTT
1801 GGAGATGAGG AGAAGGAAAT CAGAAGAAAT ACAGAAGCGA TTCTGCAGA
1851 GCTCAAGTGA AGTTGAGAGC CCAGCTGTGC CATCTTCATC AAGACAGCCC
1901 CCTGCTCAGC CTCCACGGAC AGGATCCGAG TTCCCCAGGC TGGAGGGAGC
1951 CCCGGCCACA ATGACGCCCCA AGCTGGGGCG AGGTGTCTTG GAAGGAGATG
2001 ATGTTCTCTT TTATGATGAG TCACCACCAC CAAGACCAAA ACTGAGTGCT
2051 TTAGCAGAAG CCAAAAAGTT AGCTGCTATC ACCAAATTAA GGGCAAAAGG
2101 CCAGGTTCTT ACAAACACAA ACCCAACAG CATTAGAAG AAACAAAAGG
2151 ACCCTCAGGA CCACTGGAG GTGAAGGAAC GTGTAGAAAA AAACACCATG
2201 TTTTCTTCTC AAGCTGAGGA TGAATTGGAG CCTGCCAGGA AAAAAAGGAG
2251 AGAACAACCT GCCTATCTGG AATCTGAGGA ATTCAGAAA ATCCTAAAAG
2301 CAAATCAAAA ACACACAGGC ATCCTGAAAG AGGCCGAGGC TGAGATGCAG
2351 GAGCGCTACT TTGAGCCACT GGTGAAAAAA GAACAAATGG AAGAAAAGAT
2401 GAGAAACATC AGAGAAGTGA AGTGCCGTGT CGTGACATGC AAGACGTGCG
2451 CCTATACCCA CTTCAAGCTG CTGGAGACCT GCCTCAGTGA GCAGCATGAA
2501 TACCACTGGC ATGATGGTGT GAAGAGGTTT TTCAAATGTC CCTGTGAAA
2551 CAGAAGCATC TCCTTGGAAC GACTCCCGAA CAAGCACTGC AGTAACTGTG
2601 GCCTCTACAA ATGGGAACGG GACGGAATGC TAAAGGTATG CCATTTGCGT
2651 ACTAATTTTT GACTCCTTTT AGTGACCCAT GCTAATAATG TGAACCATC
```

```

2701 TGGTATTAAAT ATATTTTCAT TTTTCTAGGA AAAGACTGGT CCAAAGATAG
2751 GAGGAGAAAC TCTGTTACCA AGAGGAGAAG AACATGCTAA ATTTCTGAAC
2801 AGCCTTAAAT AACCCGAAC TCAGACATTT TCCCACAGAC TTCCTGGCCT
2851 CCTGTGACTC TGGAAAGCAA AGGATTGGCT GTGTATTGTC CATTGATTCC
2901 TGATTGACGC CGTCAAAAAC AAATGCTTGT TAAGCCCATTA AGCTTTGCCT
2951 GCTTACTTTT TGCCATTGGG TTGGTTTGAT ACCACATTTA ACATTGACAT
3001 TTAAGTGGAA AACCAAGTTA TCATTGTCTT TTCTAAGCTC AGTGTGGATG
3051 ATTGCATTAC TTCATTCACT GAAGTTTTTG CCAAAAATT GGAAGGTAAA
3101 CAGAGAGCTA TGTTCCTGTA TCTTTTGGTT ATAGAGTGTT CACTTCTTTA
3151 TCATAACAAA ATTCTAGTGT TTATACGAAC ACCCAGAGGC AAAAGAATTT
3201 GGCTTAATTC TCACTCCAGG TAAGTAGCTT AACTTCTGGG CTTCAGTTTT
3251 CTCATCTGTA AAATCAGGAA GATTGGACTA AGTGATCTG AAATGTATTT
3301 TTTAGCACTG GATTTCCTACA AATAATAAAA CTTTCCCATC TAGATAATGA
3351 TGATCACATA GTCTTGATGT ACGGACATTA AAAGCCAGAT TTCTTCAATC
3401 AATTCTGTTT TCTCTGTTTT ACTCTTGAA ATTGATCAAG CCACTGAATC
3451 ACTTTGCATT TCAGTTTATA TATAGAGAGA GAAAGAAGGC TGTCTGCTCT
3501 TACATTATTG TGGAGCCCTG TGATAGAAAT ATGTAAATC TCATATTATT
3551 TTTTTTTTAA TTTTTTTATT TTTTATGACA GGGTCTCACT ATGTCACCCT
3601 GGCTGGAGTG CAGTAGTGCG ATCGCGGCAC ACTGCAGCCT TGGCTTCCTT
3651 GGCTCAAGC AGTCTCCCA CCTCAGTCTC CCAAATAGCT AGGACTACAG
3701 GCGTGCGTGA CCAAGCCAG CTAATTTTTG CATTTTTTGT AGAGATGGGG
3751 TTTTGCCATG TTGCTCAGGC TGGTCTCAAA CTCCTGAGCA CTAGCAATCC
3801 ACCCACCTCT GTTTCAAAAA AAAAAAAAAA AATGAAAGGT CAACCCCTAT
3851 GCAAATTACC ACAGCAAAGG TTTCACTCAG GAGATTCTTC CATCTGGGCA
3901 ACCTGGTTTT CCAAATATCA TTTGACCTAA GTGAATGTTG ATACTAGCTA
3951 AAGATTGGGT AAATTGGTTG AATTATTGTA TTGAAGCTTG AGCTGTAGCT
4001 AAAAGTAATT TAGGTTTCCC CTAAGATGTT ATTATGTTAG GGACATAACA
4051 CTTTTGGGAG GTTGTGTGGG GAGATGGTTG ATTTAGGTTT TCAAAAGCTA
4101 GAAATAAAAT TTACATGCCT TAGATTTCAT AAAATTCTGC TCTAATTGGG
4151 TGAAGGTGCT TGTATCTAAC TTGTGTTCTT CTAAGGTTA TGTCTAATA
4201 ACTATTCTTT TAGGAGTATA CTTCTACTTT ATAGAAGGTT GCTTTTCTTT
4251 TTAATTTTTT CTAACAAAGA AAAGAATAAA GTATTTATTA ATAAGAACCA
4301 GAAAGCACTT GAAACTGATG TTTTAAATGG CTCATTAGG GTAGATTAT
4351 TTATCTCATT AACTTAAAC AGCTATGTGT ATGAAATAGG TCACAACAGA
4401 ACTTGAACAC CAGGTGGTG TCTGAGCAAT CCCTTTCTTA TGGGAAAAAC
4451 AATGTTCTTG TTTGAACAGA GGGTATCATT GCAGTCAGTA TTCACGTGTA
4501 TATTGTTATA TAAGTTGTAT AATATGCTTG TAAAGGCTGA GGGTGAGCTG
4551 TATCTGGATG CCTTTTACA ATTTGATTTT AACTTTTAA ATAAATTTAA
4601 AACATAAAAA AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 95 bp to 2659 bp; peptide length: 855
 Category: similarity to known protein
 Classification: Cell division

```

1 MOEEDNLSL LTALLEENES ALDCNSEENN FLTRENGEPD AFDELFDAAG
51 DGESEYTEEAD DGETGETRDE KENLATLFGD MEDLTDEEEV PASQSTENRV
101 LPAPAPRREK TNEELQEELR NLQEQMKALQ EQLKVTTIKQ TASPRLQKS
151 PEKSPRPPLK ERRVQRIQES TCFSALDVP ALPRTKRVAR TPKSPDPK
201 SSSSRMTSAP SQPLQTSIRN KPSGITRQGI VGTGSSSET TQPICVEAFS
251 GLRLRRPRVS TSMNKKMTG RKLIRLSQIK EKMAREKLEE IDWVTFGVIL
301 KKVTPQSVNS GKTFSIWKLN DLRDLTQCVS LFLFGEVHKA LWKTEQGTVV
351 GILNANPMKP KDGSEEVCLS IDHPQKVLIM GEALDLGTCK AKKKNGEPT
401 QTVNLRDCEY CQYHVQAQYK KLSAKRADLQ STFSGGRIPK KFARRGTSLK
451 ERLCQDGFY GGVSSASYAA SIAAAVAPKK KIQTTLNLV VKGTNLIIQE
501 TRQLGIPQK LKSCSEEFKE LMDLPTCGAR NLKQHLAKAS ASGIMGSPKP
551 AIKSIASAL SLQKQKQRMLE MRRRKSEEIQ KRFLQSSSEV ESPAVPSSSR
601 QPPAQPRTG SEFPRLGAP ATMTPKLGRG VLEGDDVLFY DESPPRPKL
651 SALAEAKKLA AITKLRAKGQ VLTKTNPSI KKKQKDPQDI LEVKERVEKN
701 TMFSSQAEDE LEPARKRRE QLAYLESEEF QKILKAKSKH TGILKEAEAE
751 MQERYFEPLV KKEQMEEMR NIREVKCRVV TCKTCAYTHF KLETCVSEQ
801 HEYHWDGK RFFKPCGNR SISLDRLPNK HCSNCGLYKW ERDGMKLVCH
851 LRTNF

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2h15, frame 2

TREMBLNEW:SPBC1347_10 gene: "cdc23"; "SPBC1347.10"; product: "cell division cycle protein 23"; S.pombe chromosome II cosmid c1347., N = 2, Score = 284, P = 7e-21

PIR:S48384 DNA43 protein - yeast (Saccharomyces cerevisiae), N = 2, Score = 203, P = 7e-12

TREMBL:SCDNA52A_1 gene: "DNA52"; Saccharomyces cerevisiae DNA52 gene, complete cds., N = 2, Score = 201, P = 7.9e-12

TREMBLNEW:AC006234_6 gene: "F5H14.6"; Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence., N = 2, Score = 211, P = 1.7e-15

PIR:S48384 DNA43 protein - yeast (Saccharomyces cerevisiae), N = 2, Score = 203, P = 7.2e-12

>TREMBLNEW:SPBC1347_10 gene: "cdc23"; "SPBC1347.10"; product: "cell division cycle protein 23"; S.pombe chromosome II cosmid c1347.
Length = 593

HSPs:

Score = 284 (42.6 bits), Expect = 7.0e-21, Sum P(2) = 7.0e-21
Identities = 97/383 (25%), Positives = 186/383 (48%)

Query: 109 EKTNEELQEELRNLOEQMKALQEQLKVTTIKQTASPARLOKSPEKSPRPPLKERRVQRIQ 168
E+ + +L+E + LQ Q+ +QE+ ++ + ++ AS + + PR P ++ RV +
Sbjct: 8 EENDLDLEE--KRLQROLNEIQEKKRLRSAQKEASSENAEVI--QVPRSPPQQVRVLTVS 63

Query: 169 ESTCFSAE----LDVPALPRTKRVARTPKPSPDPKSSSSRMTSAPSQP-----LQTIS 218
+ + + L + K V+ P P PK R+ A +Q L+T+
Sbjct: 64 SPSKLSKPKRLILGIDKGKTGKDVSLGKGPRGPLPKPFHERLAEARNQERKRSCLKTKMTK 123

Query: 219 RNKPSGITRGQIVGTPGSSGETTQPI-C--VEAFSGLRLRRPRVSSTEMNKKMTGRKLIR 275
+N+ R + + G S E P+ C ++ +S + +S + + G ++
Sbjct: 124 KNRKQSFQRKRNILEDGKSEEEKFPMKCDEIDPYSRQAIVIRYISDEVAKENIGGNQVYL 183

Query: 276 LSQIKEKMAREKLE--EID-WVTFGVILKKV-TPQSVNSGKTFSIWKLNDLRDLTQCIVSL 331
+ Q+ + + K E E+D +V G++ T ++VN K + + L DL+ +C
Sbjct: 184 IHQLKLVRAPKFEAPEVDNYYVMGIVASNSGTRTVNGNK-YCMLTLTDLKWQLEC--- 239

Query: 332 FLFGEVHKA LWKTEQGT VVGILNANPMKPKDGS-EEVCLSIDHPQKVLI-MGEALDLGTC 389
FLFG+ + WK + GTV+ +LN +KPK+ L +D VL+ +G + LG C
Sbjct: 240 FLFGKAFERYWKIQSGTVIALNPEVLKPKNPDIGRFSCLKDSEYDVLLEIGRSKHLGYC 299

Query: 390 KAKKNGEPCQTQTVNLRDCEYCYHVQAQYKKLSAKRADLQSTFSGGRIPKKFARRGTS 449
+++K+GE C ++ R + C+YHV ++ + R + S+ + P+ ARR
Sbjct: 300 SSRKSGELCKHWLDKRGADVCEYHVDLAVQRSMSTRTEFASMATMHEPR--ARR--- 353

Query: 450 KERLCQDGF--YYGGVSSASIAAIAAVAPKKKIQT 484
++R GF Y+ G ++ ++A + +QT
Sbjct: 354 EKRRFGQGFQGYFAGEKYSAIPNAVAGLYDAEDAVQT 390

Score = 41 (6.2 bits), Expect = 7.0e-21, Sum P(2) = 7.0e-21
Identities = 12/43 (27%), Positives = 17/43 (39%)

Query: 453 LCQDGFYYGGVSSASIAAIAAVAPKKKIQTTLNLVVKGTN 495
L +D -- S AS A++ K + SN -+GTN-
Sbjct: 465 LSKDSEIDSSTKKPSVLASFNASIMNPKSSLPSFSNSAILGTN 507

Score = 40 (6.0 bits), Expect = 8.9e-21, Sum P(2) = 8.9e-21
Identities = 13/26 (50%), Positives = 18/26 (69%)

Query: 536 LAKASGIMGSPKPAIKSISASALL 561
LA +AS IM +PK ++ S S SA+L
Sbjct: 481 LASFNAS-IM-NPKSSLPSFSNSAIL 504

Pedant information for DKFZphtes3_2h15, frame 2

Report for DKFZphtes3_2h15.2

```
[LENGTH]      855
[MW]           96135.01
[pI]           8.96
[HOMOL]        TREMBLNEW:SPBC1347_10 gene: "cdc23"; "SPBC1347.10"; product: "cell division
cycle protein 23"; S.pombe chromosome II cosmid c1347. 5e-16
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YIL150c] 1e-11
[FUNCAT]       03.16 dna synthesis and replication [S. cerevisiae, YIL150c] 1e-11
[FUNCAT]       30.10 nuclear organization [S. cerevisiae, YIL150c] 1e-11
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY      12.05 %
[KW]           COILED COIL        4.21 %
```

```

SEQ      MDEEEDNLSLLTALLEENESALDCNSEENNFLTRENGEPDAFDELFDADGDGESYTEEAD
SEG      .....xxxxx
PRD      cccchhhhhhhhhhhhhhhhhhhhhccccccccceeeccccccccceeeccccccccceeeec
COILS

```

```

SEQ      DGETGETRDEKENLATLFGDMEDLTDEEEVPASQSTENRVLPAPAPRREKTNEELQEELR
SEG      xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD      cccccccccccchhhhhhhccccccccceecccccccccccccccccccccchhhhhhhhhhh
COILS    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

```
SEQ      NLQEQMKALQEQLKVTTIKQTASPARLQKSPEKSPRPPLKERRVQRIQESTCFS AELDVP
SEG      xxxxx.....
PRD      hhhhhh hhhhhh hhhhhh hhhhhh hhhhhhccccccccccccccccccceeecccccccccccccc
COILS    CCCCCCCCCCCCCCCCCCCC
```

SEQ ALPRTKRVARTPKPSPDPKSSSRMTSAPSQPLQTI SRNKPSGITRGQIVGTPGSSGET
 SEGXXXXXXXXXXXXX.....
 PRD cccccceeeccccccccccccchhhhhhhccccchhhhhccccccccceeecccccccc
 COILS

```
SEQ      TQPICVEAFSGLRLRRPRVSSTEMNKKMTGRKLIRLSQIKEKMAREKLEEIDWVTFGVIL
SEG      .....
PRD      ccccccccchhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccceeeeeee
COILS
```

SEQ KKVTPQSVNSGKTFISIWLNDLRDLTQCVSLFLFGEVHKALWKTEQGTVVGILNANPMKP
SEG
PRD cccccccccccceeeeeecchhhhhhheeeecchhhhhhcccccccccccccc
COILS

SEQ KDGSEEVCLSIDHPQKVLIMGEALDLGTCKAKKKNGEPTQTVNLRDCEYCYHVQAQYK
SEG
PRD cccccceeeccccceeeccccccccccccccccccccccccccccccccchhhhhhhhh
COILS

```

SEQ      KLSAKRADLQSTFSGGRIPKKFARRGTS LKERLCQDGFYFGVSSASAYAASIAAAVAPKK
SEG      .....XXXXXXXXXXXXXXXXXXXXX...
PRD      hhhhhhhhhhhhhccccccccccccccchhhhhhhccccccccccchhhhhhhhhhhhhcch
COILS

```

SEQ KIQTTLNVLVVGKTNLIIQETRQKLGIPQKSLSCSEEFKELMDLPTCGARNLKQHLAKAS
 SEG
 PRD hhhhhhhheeeccccceeehhhhhhccccccchhhhhhhhhccccccchhhhhhhhhh
 COILS

```
SEQ      ASGIMGSPKPAIKSISASALLKQKQRMLEMRRRKSEETQKRFLQSSESVEVSPAVPSSSR  
SEG      .....XXXXXXXXXXXXXX  
PRD      hhccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccc  
COILS
```

SEQ QPPAQPPRTGSEFPRLEGPATMTPKLGRGVLEGDDVLFYDESPPPRPKLSALAEAKKLA
SEG xxxxxxxxx.....xxxxxxxxxxx
PRD ccccccccccccccceeeeeccccchhhhhhhh
COILS

SEQ AITKLRAKGQVLTKTNPNISIKKKQKDPQDILEVKERVEKNTMFSSQAEELEPARKKRRE
SEG xxxxx.....
PRD hhhhhhhhhheeeeeccccccccccccchhhhhhhhhhhccchhhhhhhhhhhhhhhhh
COLS

SEQ QLAYLESEEFQKILKAKSKHTGILKEAEAEMQERYFEPLVKKEQMEEKMRNIREVCKRVV
SEG
PRD hhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhheee
COLS

SEQ TCKTCAYTHEKLLCTCVSEOHEYHWHDGVKRFEFKPCGNBSISLDRI.PNKHC SNCGLYKW


```

SEQ      ERDGMLKVCHLRTNF
SEG      .....
PRD      CCCCCCCCCCCCCC
COILS    .....

```

(No Pfam data available for DKFZphtes3_2h15.2)

_DKFZphtes3_2i5.

group: testes derived

DKFZphtes3_2i5 encodes a novel 151 amino acid protein with weak similarity to. C.elegans
cosmid F20D12.3

No informative BLAST results: No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific
genes.

similarity to C.elegans F20D12.3

many ATGs in front of the start of the ORF,
unspliced intron in 5' region?

Sequenced by EMBL

Locus: unknown

Insert length: 2142 bp

Poly A stretch at pos. 2121, polyadenylation signal at pos. 2102

```
1 GCAGTAAATA TGATATGAAA GAATTCTCTA ACTTGGGGGT GGCTTGTAAC
51 CTGTAATAAA AATATTGCTA AAATACCTTC TCTCACTTTG AAAAAGCATC
101 TGAGCAATCC TCAGTTATTG GTGAATTCTT ACCAGTGTTC AATTCCTCTC
151 TTTCCGTTAT GGTCTTAGTG TGGTTGTCTT GGTGTAGTAT TTCAAGAGGA
201 ACCTGCAGCA AGATGAAAAG AGAGTGGGAC TTGGAGCTAA GAACGTTTTT
251 GGCTTTAAGT GCTACGTTAA CTCATTAAAT TCTTAGTGAT CTTGGGGAAG
301 TCCCCTCACC AGTGTGAGCC TCAGTTTTCT TATCTAATAA GTAAGGATAA
351 TCTTACCCAC CTTATTGCGG GGGCCCGAGG ATTACATGAT TGGTGTAACA
401 GTAGCACCTT GTACATTTGA AAGGACTAAT ACCAGTGGAC TTTAACCTTG
451 GCTGGGGCTT GGAATTCTTG GTGGGACTTT TTAATCATGT AGATTCTCAG
501 GCCCCTGCCT GGCCTGTGGA ACCACAGACT CTATAGGTGG GCCCTTCCAG
551 AAGGCCTCAT GGGTGGTTCT CATGTGGAAC CTGTGTTGCA AGCCACTGCA
601 TGGTGTTACT GCTATTAAACA TTAATACTTA TATTTTCCTT ATTGTGTGGA
651 TATATCTGTG GTGTTTGCCC ATGTATACTT CATTTTACAT TTCTTAAAGA
701 ATAGAATGGA ATGGTTTTTA GCACGCTACA TTGTCCAGGT TATACCCACA
751 GAAGAGCTGT TGTGTAACAG AATCAGCATC ATACCTGAAT CATTGTGACA
801 TTGCATATAA GACTATGTCT AAGTAGAAGA TGCTATGAAA TCATGTCTGC
851 TGTGGGGCCA GGCATAATTA TGAATGTTAC TTAAGAGCAT AGGTGAGGTG
901 AGAAAAGGGA ATGTGACTAG TGTTTTAGTA TTTTCTTGGT GTGGGATGAA
951 GTATAATTCT TTTTTTTTTT TCTCAACAAA GCAGTAAAC TAGAAAGAAG
1001 GAGAACTCTT CCCTCAAGAA TGGCTGTACC TTCATATCTA GAGGCACATT
1051 AAAAAAAGA ACGTCTGTAC CTAAAAATG GAGGTCATTT CATTGTGTTT
1101 ATTTTCAAGG TTGTTGTATG GCTCGGTCAG AACTTTCTGT TACCAGAAGA
1151 CACTCACATT CAGAATGCTC CATTTCAAGT GTGTTTACA TCTTTACGGA
1201 ATGGCGGCCA CCTGCATATA AAAATAAAAC TTAGTGGAGA GATCACTATA
1251 AATACTGATG ATATTGATTT GGCTGGTGAT ATCATCCAGT CAATGGCATC
1301 ATTTTGTGCT ATTGAAGACC TTCAAGTAGA AGCGGATTTT CCTGTCTATT
1351 TTGAGGAATT ACGAAAGGTG CTAGTTAAGG TGGATGAATA TCATTCACTG
1401 CATCAGAAGC TCAGTGCTGA TATGGCTGAT CATTTCTAAT TGATCCGAAG
1451 TTTGTGCTG GAGCTGAGG ATGCTCGTCT GATGAGGGAC ATGAAAACAA
1501 TGAAGAGTCG TTATATGGAA CTCTATGACC TTAATAGAGA CTTGCTAAAT
1551 GGATATAAAA TTCGCTGTAA CAATCACACA GAGCTGTTGG GAAACCTCAA
1601 AGCAGTAAAT CAAGCAATTC AAAGAGCAGG TCGTCTGCGG GTTGGAAAAA
1651 CAAAGAACCA GGTGATCACT GCTTGTGCGG ATGCAATTCG AAGCAATAAC
1701 ATCAACACAC TGTTCAAAAT CATGCGAGTG GGGACAGCTT CTTCTAGGT
1751 GAGGAAAATA CAGGTCATGA AGTTCCTGGC AAAGATTTTC TGTTAAAAAC
1801 CTATGCTGGT TTGCTTTGGA TCACACCCTG GTGAACCCCG GGTGCTAAGA
1851 ATGAAAAATA CCTTGGTGAG TTGTACAAAT TAAAGACAAA GAACTACATG
1901 TGAAGATAGA CTTGCTTTCT ATTTTAAAT CAGTAGTAGT ACTGTTGCTG
1951 AATAATACTA GGTTTTTATG GAATAGGATG AATGCTTTTG AAGTATTAGG
2001 GCTTCAGAGT CCAATTTTGC TTATTTATGG TATATAAATA CATATTTTTT
2051 TCTTGAAATT GCAATTGAGT TTGTACTTTT CAAATAGATT ATCTACTTTT
2101 TCATTAAAT GTAAAGATGT TAAAAAATA AAAAAAATA AA
```

BLAST Results

No BLAST result

Medline entries

Peptide information for frame 3

```

1 MASFFAIEDL QVEADFPVYF EELRKVLVKV DEYHSVHQKL SADMADHSNL
51 IRSLLVGAED ARLMRDMKTM KSRYMELYDL NRDLNGYKI RCNNHTELLG
101 NLKAVNQAIQ RAGRLRVGKP KNQVITACRD AIRSNNINTL FKIMRVGTAS
151 S

```

Alert BLASTP hits for DKFZphtes3 2i5, frame 3

```
>TREMBL:CEF20D12_1 gene: "F20D12.3"; Caenorhabditis elegans cosmid F20D12.  
Length = 699
```

Score = 173 (26.0 bits), Expect = 4.5e-12, P = 4.5e-12
Identities = 33/130 (25%), Positives = 72/130 (55%)

```

Query:      20 FEELRKVLVKVDEYHSVHQKLSADMADHSNLRSLLVGAEDARLMRDMKTKMSRYMELYD 79
             F+E ++L ++D   V  +L+A++ +   ++ +++ AED+  + ++   + Y+ L
Sbjct:     569 FKEADEILEEIDPMTVEVRDLTAELQERQAAVKEIIIRAEDSIAIDNIPDARKFFYIRLKA 628

Query:      80 LNRDLLNGYKIRCNNHTELLGNLKAVNQAIQIRAGRLRVGPKPNQOVITACRDAIRSNNT 139
             +   ++R NN   + +L+ +N+ I+   RLRVG+P  Q++ +CR AI  +N
Sbjct:     629 NDAARQAQQLRWNNQERCVKSLRRLNKIIENC SRLRVGEPGRQIVVSCRSAIADDNKQI 688

Query:     140 LFKIMRVGTA 149
             + KI++ G +
Sbjct:     689 ITKILQYGAS 698

```

Pedant information for DKFZphtes3 2i5, frame 3

Report for DKFZphtes3_2i5.3

```
[LENGTH]      151
[MW]           17304.07
[pI]           9.33
[HOMOL]        TREMBL:CEF20D12_1 gene: "F20D12.3"; Caenorhabditis elegans cosmid F20D12. 2e-12
[KW]           Alpha Beta
```

```
SEQ      MASFFAIEDLQVEADFPVYFEELRKVLVKVDYEHSVHQKLSADMADHSNLIIRSLLVGAED  
PRD      cceeeehhhhhhccccchhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhhhhhhhhh
```



```
SEQ      ARLMRDMKTMSRYMELYDLNRDLLNGYIKRCNNHTELLGNLKAVNQAIQRAGRRLVGKP  
PRD      hhhhcccchhhhhhheecchhhhhhheeeeccchhhhhhhhhhhhhhhhhhhc
```



```
SEQ      KNQVITACRDAIRSNNINTLFKIMRVGTASS  
PRD      cceeeehhhhhhcccccccccccccccc
```

(No Prosite data available for DKFZphtes3_2i5.3)

(No Pfam data available for DKFZphtes3_2i5.3)

DKFZphtes3_2119

group: testes derived

DKFZphtes3_2119 encodes a novel 166 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, no EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 1079 bp

Poly A stretch at pos. 1053, polyadenylation signal at pos. 1038

```
1 CCACAGGACA CACTGTTCCC AGGGCACAGA CACCCTGGGC TTTGGTTGGG
51 TCTTGGCCTC CAGGTAGGGC CCTGTTGGGC AGCGGGCAGC AACTCCTGAG
101 ACACTACTGT GATTCTTGGT GGTGGCTGTG GTAAAAAACC TGCAGGGGTA
151 GAGTTTGGGG TGAGATTGAG CAGTAACTGT GGCCTCTCCT AGTGACAGTA
201 TGTCACCTCC ACTCCAGCA CGCATGCCCA CAGGCCACGG CCTCCACATC
251 ACAAACCCCC CACCAAGTTG CCCATCTATG GAGCAGCTCC CATACGGCAG
301 GGTCAGGCTC TTACCTCCAC CTCCAGGGCA CAGACAGGGG GAGCTCTGTC
351 TCACTGTAAG GCAATGAGGA GAGTTGAGGG CCCAGACCAG GCTAGGGGCC
401 ATCCCCTTTC CCGAGCAGGC CTCAGGGAAG GACCAGCCCC ATTCCCCTCT
451 GACCTAGGTC TTAGCCCAGG AGCCTGCATA GGGGAAGAAAG GACAGACAGG
501 GCCTCCTTAC TGGCTGACAC TCAGGAGGGG CTGGGGCAAG AGAGCAGAGG
551 GAGCGCAGGG CCAGGCAGGG GCTGCTGAGG ATCCATGGGA GCTCAGGGTG
601 CACAAGGGGG CTGCCCTTCC TGGGCTGCAG GCAGCATCCC TATGGGAGCT
651 GAGAAAGTCC AATCCTGAGA TGGGACAGTG CTGCCAGGG GTGTGTGGCT
701 GGGCCCTGAC AACAGTCTCC CAAAAGTGA CCACATCACC AGGCTCAGTT
751 CCAGGAAGGC TGAGAAAGTG CCAGTACACT GAGGATGCAC CTCAGTTACA
801 TAAAATAAAT GAAACTGGAG TACTAACGTA CAGTTAAAG GTTATAGTTA
851 CTATTTTAT ATGATATACT AGTAATTTT GAATAGGGTA AACTTTAGGT
901 GTTTTGACAC CAAAAGAAAA CTACATGACT TCATGCATGT GTTAAATTGC
951 TTTACTGTAG TAATCATTTA CATGTATATG TATATATGAA TATAATTATG
1001 GGCTCATTAA ATTTAAATAT TATAAATAGG TGACAAAGAA TAAAGTTAAC
1051 TGGAAAAAAA AAAAAAATAA AAAAAAATAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 364 bp to 861 bp; peptide length: 166

Category: putative protein

Classification: no clue

```
1 MRRVEGPDQA RGHPLSRAGL REGPAPFSPD LGLSPGACIG KKGQTGPPYW
51 LTLRRGWGKR AEGAQQQAGA AEDPWELRVH KGAALPGLQA ASLWELRKN
101 PEMGQCCPGV CGWALTTVSP KVTTSPPGSPV GRLRSAQYTE DAPQLHKINE
151 TGVLTYSCLKV IVTIFI
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2119, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_2119, frame 1

Report for DKFZphtes3_2119.1

[LENGTH] 166
[MW] 17691.35
[pI] 9.54
[KW] All_Beta
[KW] LOW_COMPLEXITY 7.23 %

SEQ MRRVEGPDQARGHPLSRAGLREGPAPFPSDLGLSPGACIGKKGQTGPPYWLTLRRGWGKR
SEG
PRD ccc

SEQ AEGAQQAGAAEDPWELRVHKGAALPGLQAASLWELRKSNPEMQCCPGVCGWALTTVSP
SEG xxx
PRD ccc

SEQ KVTTSPPSVPGRLRSAQYTEDAPQLHKINETGVLTYSLKVIIVTIFI
SEG
PRD ccc

(No Prosite data available for DKFZphtes3_2119.1)

(No Pfam data available for DKFZphtes3_2119.1)

DKFZphtes3_2ml8

group: nucleic acid management

DKFZphtes3_2ml8 encodes a novel amino acid protein, with similarity to mouse Dhml.

The protein seems to play a role in nucleotide metabolism, RNA metabolism, but also in DNA repair and cell cycle. The yeast homologue is a DNA strand exchange protein required for sporulation and homologous recombination.

The novel protein can find application as multifunctional nuclease / exoribonuclease.

nearly identical to mouse Dhml

complete cDNA, complete cds, start at Bp 42, EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 3022 bp

Poly A stretch at pos. 3004, polyadenylation signal at pos. 2981

```

1  CTCGTCAGCC GGTGGGCCGC CGCCTCCAGC CGTGTGCCGC TATGGGAGTC
51  CCGGCGTTCT TCCGCTGGCT CAGCCGCAAG TACCCGTCCA TCATAGTCAA
101 CTGCGTGGAA GAGAAGCCAA AAGAATGCAA TGGTGTAAG ATTCCAGTTG
151 ATGCCAGTAA ACCTAATCCA AATGATGTGG AGTTTGATAA TCTGTATTTG
201 GATATGAATG GAATCATCCA TCCCTGTACT CATCCTGAAG ACAAAACCAGC
251 ACCAAAAAAT GAAGATGAAA TGATGGTTGC AATTTTGTAG TACATGACA
301 GACTTTTTCAG TATTGTAAGA CCAAGAAGAC TTCTCTACAT GGCAATAGAT
351 GGAGTGGCAC CACGTGCTAA AATGAACCAG CAGCGTTCAA GGAGGTTTCAG
401 GGCATCAAAA GAAGGAATGG AAGCAGCAGT CGAGAAGCAG CGAGTCAGGG
451 AAGAAATATT GGCAAAAGGT GGCTTCTTTC CTCCAGAAGA AATAAAAGAA
501 AGATTTTGACA GCAACTGTAT TACACCAGGA ACTGAATTCA TGGACAATCT
551 TGCTAAATGC CTTGCTATT ACATAGCTGA TCGTTAAAT AATGACCCTG
601 GGTGGAAAAA TTTGACAGTT ATTTTATCTG ATGCTAGTGC TCCTGCTGAA
651 GGAGAACATA AAATCATGGA TTACATTAGA AGGCAAAGAG CCCAGCCTAA
701 CCATGACCCA AATACTCATC ATTGTTTATG TGGAGCAGAT GCTGATCTCA
751 TTATGCTTGG CCTTGCCACA CATGAACCGA ACTTTACCAT TATTAGAGAA
801 GAATTCAAAC CAAACAAGCC CAAACCATGT GGTCTTTGTA ATCAGTTTGG
851 ACATGAGGTG AAGGATTGTG AAGGTTGCC AAGAGAAAAG AAGGGAAAGC
901 ATGATGAACT TGCCGATAGT CTTCTTTGTG CAGAAGGAGA GTTTATCTTC
951 CTTGGGCTTA ATGTTCTTCG TGAGTATTTG GAAAGAGAAC TCACAATGGC
1001 CAGCCTACCA TTCACATTTG ATGTTGAGAG GAGCATTGAT GACTGGGTTT
1051 TCATGTGCTT CTTTGTGGGA AATGACTTCC TCCCTCATTT GCCATCGTTA
1101 GAGATTAGGG AAAATGCAAT TGACCGTTTG GTTAACATAT ACAAAAATGT
1151 GGTACACAAA ACTGGGGGTT ACCTTACAGA AAGTGTTTAT GCTCAATCTGC
1201 AAAGAGTACA GATGATCATG TTAGCAGTTG GTGAAGTTGA GGATAGCATT
1251 TTTAAAAAGA GAAGGATGTA TGAGGACAGT TTTAGAAGAC GACAGAAAAG
1301 AAAAAGAAAG AGAATGAAGA GAGATCAACC AGCTTTCAC CTAGTGGA
1351 TATTAACCTC TCATGCCTTG GGTTCAGAA ATTACACAGG TTCTCAAGTA
1401 GCCAGTAATC CGAGACAAGC AGCCTATGAA ATGAGGATGC AGAATAACCTC
1451 TAGTCCTTTC ATATCTCCTA ATACGAGTTT CACATCTGAT GGCTCCCCGT
1501 CTCCATTAGG AGGAATTAAG CGAAAAGCAG AAGACAGTGA CAGTGAACCT
1551 GAGCCAGAGG ATAATGTCAG GTTATGGGAA GCTGGCTGGA AGCAGCGGTA
1601 CTACAAGAAC AAATTTGATG TGGATGCAGC TGATGAGAAA TTCCGTCGGA
1651 AAGTTGTGCA GTCGTACGTT GAAGGACTTT GCTGGGTTCT TAGATATTAT
1701 TACCAGGGCT GTGCTTCCTG GAAGTGGTAT TATCCATTTC ATTATGCACC
1751 ATTTGCTTCA GACTTTGAAG GCATTGCAGA CATGCCATCT GATTTTGAGA
1801 AGGGTACGAA ACCGTTTAAA CCACTAGAAC AACTTATGGG GGTATTTCCTA
1851 GCTGCAAGTG GTAATTTTCT ACCTCCATCA TGGCGGAAGC TCATGAGTGA
1901 TCCTGATTCT AGTATAATTG ACTTCTATCC TGAAGATTTT GCTATTGATT
1951 TGAATGGGAA GAAATATGCA TGGCAAGGTG TTGCTCTCTT GCCATTCGTG
2001 GATGAGCGAA GGTACGAGC TGCCCTAGAA GAGGTATACC CAGACCTCAC
2051 TCCAGAAGAG ACCAGAAGAA ACAGCCTTGG AGGTGATGTC TTATTGTGG
2101 GGAACATCA CCCACTCCAT GACTTCATTT TAGAGCTGTA CCAGACAGGT
2151 TCCACAGAGC CAGTGGAGGT ACCCCCTGAA CTATGTCATG GGATTCAAGG
2201 AAAGTTTCTT TTGGATGAAG AAGCATTCT TCCAGATCAA ATAGTATGTT
2251 CTCCTGTTCC TATGTTAAGG GATCTGACAC AGAACACTGT AGTCAGTATT
2301 AATTTTAAAG ACCACAGATT TGCTGAAGAT TACATTTTAA AAGCTGTAAT
2351 GCTTCCAGGA GCAAGAAAGC CAGCAGCAGT ACTGAAACCT AGTGACTGGG
2401 AAAAATCCAG CAATGGACGG CAGTGAAGC CTCAGCTTGG CTTTAACCGT
2451 GACCGGAGGC CTGTGACCTT GGATCAGGCA GCCTTCAGGA CTTTGGGCCA
2501 TGTGATGCCA AGAGGCTCAG GAACTGGCAT TTACAGCAAT GCTGCACCAC
2551 CACCTGTGAC TTACCAGGGA AACTTATACA GGCCGCTTTT GAGAGGACAA
2601 GCCCAGATTC CAAAACCTAT GTCAATATAG AGGCCCCAGG ATTCCTGGCG
2651 AGGTCTCTCT CCCCTTTTCC AGCAGCAAAG GTTTGACAGA GGCGTTGGGG

```

```

2701 CTGAACCTCT GCTCCCATGG AACCGGATGC TGCAAACCCA GAATGCAGCC
2751 TTCCAGCCAA ACCAGTACCA GATGCTAGCT GGGCCTGGTG GGTATCCACC
2801 CAGACGAGAT GATCGTGGAG GGAGACAGGG ATATCCCAGA GAAGGAAGGA
2851 AATACCCTTT GCCACCACCC TCAGGAAGAT ACAATTGGAA TTAAGCTTTT
2901 GTAAAGCTTT CCCAAATCCT TTCATCATTC TACAGTTTTA TGCTATTTGT
2951 GGAAAGATTT CCTTCTCAAG TAGTAGTTT TAATAAACT ACAGTACTTT
3001 GTGTAAGAAA AAAAAAAA AA

```

BLAST Results

No BLAST result

Medline entries

95192042:
Characterization of cDNA encoding mouse homolog of fission yeast dhpl+
gene: structural
and functional conservation.

97361754:
Cloning and characterization of mouse Dhml cDNA, a functional homolog
of budding yeast
SEP1.

Peptide information for frame 3

ORF from 42 bp to 2891 bp; peptide length: 950
Category: strong similarity to known protein

```

1  MGVPAFFRWL SRKYPSSIIVN CVEEKPKECN GVKIPVDASK PNPNDVEFDN
51  LYLDMNGIIH PCTHPEDKPA PKNEDEMMVA IFEYIDRLFS IVRPRRLLYM
101 AIDGVAPRAK MNQQRSRFR ASKEGMEAAV EKQVRREEIL AKGGFLPPEE
151 IKERFDSNCI TPGTEFMDNL AKCLRYIIAD RLNDPQWKN LTVILSDASA
201 PGEGEHKIMD YIRRQRAQPN HDPNTHHCLC GADADLIMLG LATHEPNFTI
251 IREEFKPNKP KPCGLCNQFG HEVKDCEGLP REKKGKHDEL ADSLPCAEGE
301 FIFLRLNVLR EYLERELTMA SLPFTFDVER SIDDWVFMCF FVGNDFLPHL
351 PSLEIRENAI DRLVNIYKNV VHKTGGYLTE SGYVNLQRVQ MIMLAVGEVE
401 DSIFKKRKDD EDSFRRRQKE KRKRMRKRDQ AFTPSGILTP HALGSRNSPG
451 SQVASNPRQA AYEMRMQNNS SPSISPNTSF TSDGSPSPLG GIKRKAEDSD
501 SEPEPEDNVR LWEAGWKQRY YKNKFDVDA DEKFRKRVVQ SYVEGLCWVL
551 RYYYQGCASW KWYYPFHYAP FASDFEGIAD MPSDFEKGTK PFKPLEQLMG
601 VFPAASGNFL PPSWRKLMSD PDSSIIDFYP EDFAIDLNGK KYAWQGVALL
651 PFVDERRLRA ALEEVYPDLT PEETRRNSLG GDVLFVGGKH PLHDFILELY
701 QTGSTPEVEV PPELCHGIQG KFSLDDEEAIL PDQIVCSPVP MLRDLTQNTV
751 VSINFKDPQF AEDYIFKAVM LPGARKPAAV LKPSDWEKSS NGRQWKPOLG
801 FNRDRRPVHL DQAAFRTLGH VMPRGSGTGI YSNAAPPPVT YQGNLYRPLL
851 RGQAQIPKLM SNMRPQDSWR GPPPLFQQQR FDRGVGAEP LPPNRMLQTO
901 NAAFQPNQYQ MLAGPGGYPP RRDDRGGRQG YPREGRKYPL PPSGRYNWN

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_2m18, frame 3

PIR:I49635 mouse Dhml protein - mouse, N = 1, Score = 4765, P = 0

PIR:S43891 dhpl protein - fission yeast (Schizosaccharomyces pombe), N = 3, Score = 1172, P = 2e-197

PIR:S20126 exoribonuclease RAT1 (EC 3.1.11.-) - yeast (Saccharomyces cerevisiae), N = 2, Score = 1146, P = 3.8e-175

PIR:S72531 exonuclease II - fission yeast (Schizosaccharomyces pombe), N = 4, Score = 622, P = 4.2e-125

>PIR:I49635 mouse Dhml protein - mouse
Length = 947

HSPs:

Score = 4765 (714.9 bits), Expect = 0.0e+00, P = 0.0e+00
Identities = 884/930 (95%), Positives = 895/930 (96%)

```

Query:      1  MGVPAFFRWLSRKYPSSIIVNCVEEKPKCEKNGVKIPVDASKPNPNDFEFDNLYLDMNGIIH 60
             MGVPAFFRWLSRKYPSSIIVNCVEEKPKCEKNGVKIPVDASKPNPNDFEFDNLYLDMNGIIH
Sbjct:      1  MGVPAFFRWLSRKYPSSIIVNCVEEKPKCEKNGVKIPVDASKPNPNDFEFDNLYLDMNGIIH 60

Query:     61  PCTHPEDKPAPKNEDEMMVAIFEYIDRLFSIVRPRRLLYMAIDGVAPRAKMNQQRSSRRFR 120
             PCTHPEDKPAPKNEDEMMVAIFEYIDRLF+IVRPRRLLYMAIDGVAPRAKMNQQRSSRRFR
Sbjct:     61  PCTHPEDKPAPKNEDEMMVAIFEYIDRLFNIVRPRRLLYMAIDGVAPRAKMNQQRSSRRFR 120

Query:    121  ASKEGMEAAVEKQVRREEILAKGGFLPPEEIKERFDSNCITPGTEFMDNLAKCLRYIIAD 180
             A K GMEAAVEKQVRREEILAKGGFLPPEEIKERFDSNCITPGTEFMDNLAKCLRYIIAD
Sbjct:    121  AIKGGMEAAVEKQVRREEILAKGGFLPPEEIKERFDSNCITPGTEFMDNLAKCLRYIIAD 180

Query:    181  RLNNDPGWKNLTVILSDASAPGEGEHKIMDYIRRQRAQPNHDPNTHHCLCGADADLIMLG 240
             RLNNDPGWKNLTVILSDASAPGEGEHKIMDYIRRQRAQPN DPNTHHCLCGADADLIMLG
Sbjct:    181  RLNNDPGWKNLTVILSDASAPGEGEHKIMDYIRRQRAQPNQDPNTHHCLCGADADLIMLG 240

Query:    241  LATHEPNFTIIREEFKPNKPKPCGLCNQFGHEVKDCEGLPREKKKGKDELADSLPCAEGE 300
             LATHEPNFTIIREEFKPNKPKPC LCNQFGHEVKDCEGLPREKKKGKDELADSLPCAEGE
Sbjct:    241  LATHEPNFTIIREEFKPNKPKPCALCNQFGHEVKDCEGLPREKKKGKDELADSLPCAEGE 300

Query:    301  FIFLRLNVLREYLERELTMASLPFTFDVERSIDDWVFMCFVGNDFLPHLPSLEIRENAI 360
             FIFLRLNVLREYLERELTMASLPF FDVERS DDW FMCFFVGNDFLPHLPSLEIRE AI
Sbjct:    301  FIFLRLNVLREYLERELTMASLPFPFDVERSNDWVEFMCFVGNDFLPHLPSLEIREGAI 360

Query:    361  DRLVNIYKNVVKHTGGYLTESGYVNLQRVQMIMLAVGEVEDSIFKKRKDDDEDSFRRRQKE 420
             DRLVNIYKNVVKHTGGYLTESGYVNLQRVQMIMLAVGEVEDSIFKKRKDDDEDSFRRRQKE
Sbjct:    361  DRLVNIYKNVVKHTGGYLTESGYVNLQRVQMIMLAVGEVEDSIFKKRKDDDEDSFRRRQKE 420

Query:    421  KRKRMRDQPAFTPSGILTPhALGSRNSPGSQVASNPRQAAYEMRMQNNSSPSISPNTSF 480
             KRKRMRDQPAFTPSGILTPhALGSRNSPG QVASNPRQAAYEMRMQ NSSPSISPNTSF
Sbjct:    421  KRKRMRDQPAFTPSGILTPhALGSRNSPGCQVASNPRQAAYEMRMQNNSSPSISPNTSF 480

Query:    481  TSDGSPSPPLGGIKRKAEDSDSEPEPEDNVRLWEAGWKQRYKKNKFDVDAADEKFRRKVVQ 540
             SDGSPSPPLGGI+RKAEDSDSEPEPEDNVRLWEAGWKQRYKKNKFDVDAADEKFRRKVVQ
Sbjct:    481  ASDGSPSPPLGGIRRKAEDSDSEPEPEDNVRLWEAGWKQRYKKNKFDVDAADEKFRRKVVQ 540

Query:    541  SYVEGLCWVLRYYYQGCASWKWYYPFHAYAFASDFEGADIADMPDFEKGTKPFKPLEQLMG 600
             SYVEGLCWVLRYYYQGCASWKW YPFHAYAFASDFEGADIAD S+FEKGTKPFKPLEQLMG
Sbjct:    541  SYVEGLCWVLRYYYQGCASWKWLYPFHAYAFASDFEGADIADMSSEFEKGTKPFKPLEQLMG 600

Query:    601  VFPAASGNFLPPSWRKLMSDPDSSIIDFYPEDFAIDLNGKKYAWQGVALLPFVDERRLRA 660
             VFPAASGNFLPP+WRKLMSDPDSSIIDFYPEDFAIDLNGKKYAWQGVALLPFVDERRLRA
Sbjct:    601  VFPAASGNFLPPTWRKLMSDPDSSIIDFYPEDFAIDLNGKKYAWQGVALLPFVDERRLRA 660

Query:    661  ALEEVPDLTPEETRNSLGGDVLFGVKKHPLHDFILELYQTGSTPEVPELCHGIQG 720
             ALEEVPDLTPEE RRNSLGGDVLFGVK HPL DFILELYQTGSTPEV+VPELCHGIQG
Sbjct:    661  ALEEVPDLTPEENRRNSLGGDVLFGVKKHPLRDFILELYQTGSTPEVDVPELCHGIQG 720

Query:    721  KFSLDEEAILPDQIVCSPVPMRLDLTQNTVVSINFKDPQFAEDYIFKAVMLPGARKPAV 780
             FSLDEEAILPDQ VCSVPVPMRLDLTQNT VSINFKDPQFAEDY+FKA MLPGARKPA V
Sbjct:    721  TFSLDEEAILPDQTVCSVPVPMRLDLTQNTAVSINFKDPQFAEDYVFKAMLPGARKPATV 780

Query:    781  LKPSDWEKSSNGRQWKPOLGFNRDRRPVHLDQAAFRTLGHVMPRGSGTGIYSNAAPPVPT 840
             LKP DWEKSSNGRQWKPOLGFNRDRRPVHLDQAAFRTLGHV PRGSGT +Y+N A P
Sbjct:    781  LKPGDWEKSSNGRQWKPOLGFNRDRRPVHLDQAAFRTLGHVTPRGSGTSVYTNTALLPAN 840

Query:    841  YQGNLYRPLLRGQAQIPKLMSNMRPQDSWRGPPPLFQQQRFDRGVGAEPPLPWNRMLQTQ 900
             YQGN YRPLLRGQAQIPKLMSNMRP+DSWRGPPPLFQQ RF+R VGAEPPLPWNRM+Q Q
Sbjct:    841  YQGNLYRPLLRGQAQIPKLMSNMRPKDSWRGPPPLFQQHFRFERSVGAEPPLPWNRMIQNQ 900

Query:    901  NAAFQPNQYQMLAGPGGYPPRRDD-RGGRQ 929
             NAAFQPNQYQML GPGGYPPRRDD RGGRQ
Sbjct:    901  NAAFQPNQYQMLGGPGGYPPRRDDHRRGGRQ 930

```

Pedant information for DKFZphtes3_2m18, frame 3

Report for DKFZphtes3_2m18.3

```

[LENGTH]      950
[MW]           108582.68
[pI]           7.26
[HOMOL]        PIR:I49635 mouse Dhml protein - mouse 0.0
[FUNCAT]       08.01 nuclear transport [S. cerevisiae, YOR048c] 1e-123
[FUNCAT]       04.01.04 rna processing [S. cerevisiae, YOR048c] 1e-123

```


SEQ K F S L D E E A I L P D Q I V C S P V P M L R D L T Q N T V V S I N F K D P Q F A E D Y I F K A V M L P G A R K P A A V
 SEG

```
PRD      ccccccccccceeeccccccccccccccccccccccccchhhhhhheeecccccccccccee
MEM      .....

SEQ      LKPSDWEKSSNGRQWKPLGFNRDRRPVHLDQAAFRTLGHVMPRGSGTGIYSNAAPPVT
SEG      .....
PRD      eccccccccccccccccccccccccccccccccccccchhhhhhhhhhhcccccccccccccccccc
MEM      .....

SEQ      YQGNYLRPLLGRGAQIPKLMSNM RPQDSWRGPPPLFQQQRFD RGVGAEP LLPWNRM LQTQ
SEG      .....
PRD      cccccchhhhhccccchhhhhccccccccccccccccccccchhhhhccccccccccccchhhhhh
MEM      .....

SEQ      NAAFQPNQYQLAGPGGYPPRRDDRGGRQGYPREGRKYPLPPSPGRYNWN
SEG      .....xxxxxxxxxxxxxxxxxxxxxx
PRD      hccccccccceeecccccccccccccccccccccccccccccccccccccc
MEM
```

Prosites for DKFZphtes3 2ml8.3

PS000001	190->194	ASN_GLYCOSYLATION	PDOC000001
PS000001	247->251	ASN_GLYCOSYLATION	PDOC000001
PS000001	468->472	ASN_GLYCOSYLATION	PDOC000001
PS000001	477->481	ASN_GLYCOSYLATION	PDOC000001
PS000002	826->830	GLYCOSAMINOGLYCAN	PDOC000002
PS000004	675->679	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	11->14	PKC_PHOSPHO_SITE	PDOC000005
PS000005	116->119	PKC_PHOSPHO_SITE	PDOC000005
PS000005	413->416	PKC_PHOSPHO_SITE	PDOC000005
PS000005	559->562	PKC_PHOSPHO_SITE	PDOC000005
PS000005	613->616	PKC_PHOSPHO_SITE	PDOC000005
PS000005	674->677	PKC_PHOSPHO_SITE	PDOC000005
PS000005	868->871	PKC_PHOSPHO_SITE	PDOC000005
PS000005	944->947	PKC_PHOSPHO_SITE	PDOC000005
PS000006	63->67	CK2_PHOSPHO_SITE	PDOC000006
PS000006	331->335	CK2_PHOSPHO_SITE	PDOC000006
PS000006	499->503	CK2_PHOSPHO_SITE	PDOC000006
PS000006	501->505	CK2_PHOSPHO_SITE	PDOC000006
PS000006	541->545	CK2_PHOSPHO_SITE	PDOC000006
PS000006	573->577	CK2_PHOSPHO_SITE	PDOC000006
PS000006	583->587	CK2_PHOSPHO_SITE	PDOC000006
PS000006	619->623	CK2_PHOSPHO_SITE	PDOC000006
PS000006	624->628	CK2_PHOSPHO_SITE	PDOC000006
PS000006	670->674	CK2_PHOSPHO_SITE	PDOC000006
PS000006	723->727	CK2_PHOSPHO_SITE	PDOC000006
PS000006	784->788	CK2_PHOSPHO_SITE	PDOC000006
PS000007	659->667	TYR_PHOSPHO_SITE	PDOC000007
PS000008	125->131	MYRISTYL	PDOC000008
PS000008	375->381	MYRISTYL	PDOC000008
PS000008	450->456	MYRISTYL	PDOC000008
PS000008	600->606	MYRISTYL	PDOC000008
PS000008	825->831	MYRISTYL	PDOC000008
PS000008	829->835	MYRISTYL	PDOC000008
PS000008	926->932	MYRISTYL	PDOC000008
PS000009	638->642	AMIDATION	PDOC000009
PS000009	934->938	AMIDATION	PDOC000009

(No Pfam data available for DKFZphtes3_2ml8.3)

DKFZphtes3_2m20

group: testes derived

DKFZphtes3_2m20 encodes a novel 183 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

group: unknown

DKFZphtes3_2m20 encodes a novel

amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

EST hits are only from testis or uterus librarys
remaining intron in 3' UTR see EST-BLAST

Sequenced by EMBL

Locus: unknown

Insert length: 1341 bp

Poly A stretch at pos. 1320, polyadenylation signal at pos. 1300

```
1  GCAATCCAGG AGCTGAATGG TAACTCTTCC ACAAGCGAAA ACTGTTCGTG
51 AATACAAAGCA AAAGGCCCCC CAAGAGGACC CCTGATATGA TCCAGCAGCC
101 TCGGGGCCCCG CTGGTGTTGG AGAAGGCTTC TGGTGAAGGA TTTGGCAAAA
151 CCGCCGCTAT TATACAGCTC GCTCCTAAAG CTCCTGTGA CCTGTGTGAG
201 ACAGAGAAAC TGAGGGCAGC CTTCTTTGCA GTCCCGTTGG AAATGAGAGG
251 GTCCTTCTTG GTGCTGCTCC TGAGGGAATG CTTCCGAGAC CTGAGCTGGC
301 TGGCACTCAT CCATAGCGTC CGTGGGGAGG CGGGGCTGCT GGTGACGAGT
351 ATCGTCCCGA AGACCCCGTT TTTCTGGGCC ATGCACATCA CTGAGGCTCT
401 GCACCAGAAC ATGCAGGCTC TGTTTAGCAC CCTGGCTCAG GCGGAGGAGC
451 AGCAGCCCTA CCTGGAGGCT CCACCGTTAT GCGCGGGACT CGCTGTCTGG
501 CAGAGTACCA CCTGGGGGAT TATGGACACG CCTGGAACAG GTGTTGGGTG
551 CTGGACAGGG TGGACACCTG GGCTGTGGTC ATGTTTCATTG ATTTTGGACA
601 GTTGGCCACC ATCCCTGTGC AGTCTCTGCG CCAGCTAGAC AGCGACGACT
651 TCTGGACCAT CCCACCCCTG ACTCAGCCAT TCATGCTGGA GAAAGACATT
701 TTGAGTTCGT ATGAGGTTGT CCATCGAATC CTCAAAGGGA AAATCACTGG
751 TGCTTTGAAC TCGGCGGTAA CTGCTCCTGC ATCTAACTTG GCTGTGTCTC
801 CTCCTCTCCT GCCCTTGGGG TGCTCTGCAGC AGGCTGCTGC CTAGGCTTGG
851 ACACATTGCA CATCCTAAAG TTTGAAGAGT CTAAATAACG GGGCTTCCCT
901 CAGCATGTTT CCTCTCCTGT TTGCCACGGA TCCAGAGCCA CCTGCCCTGT
951 CTTCTCGTAC CCCTTCACT CTTGAGGCCT GGGAGGTGAA AAAGGCCAGA
1001 CTGTGCCCAG GATTGATTCA ATTTTGCTTT TACTCCCAGC TTCCCTCTCA
1051 AAAGAGAGTG AAGTCTCATT TGTCATGTGT CTTCACTTCC CCAACTTGGC
1101 ATGAACATTT GAACCAAACA TAGGAAACTA CCATTAGGTT GAAAGCCTGA
1151 GGCAGCTGGG ATGGTCTTTC TTGTGTCTCT TCTTTGCACC CCAGAGCATG
1201 ATATAAGTGG TCCTAACAGA TTCTGGATAA TGGAGAAGCC CTCTGCTGGT
1251 TTTCTGGCA TTCCATGTAG AATAGGTAGA GAATATTTAA CCAATGAGCA
1301 AATAAATGTT GGCATGTTTC ATGAAAAAAA AAAAAAAAAA A
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 479 bp to 841 bp; peptide length: 121
 Category: questionable ORF
 Classification: no clue

1 MRGTRCLA EYHLGDYGHAWN RCWVLD RVD TWAVVMFIDFG QLATIPVQSL
 51 RQLDSDDFWT IPPLTQPFML EKDILSSYEV VHRILKGKIT GALNSAVTAP
 101 ASNLAVVPPL LPLGCLQQA A

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2m20, frame 2

No Alert BLASTP hits found

Peptide information for frame 3

ORF from 87 bp to 635 bp; peptide length: 183
 Category: putative protein
 Classification: no clue

1 MIQQPRAPLV LEKASGEGFG KTA AIIQLAP KAPVDLCETE KLRAAFFAVP
 51 LEMRGSFLVL LRECFRDL S WLALHSVRG EAGLLVTSIV PKTPFFWAMH
 101 ITEALHQNMQ ALFSTLAQAE EQQPYLEAPP LCAGLAVWQS TTWGIMDTPG
 151 TGVGCWTGWT PGLWSCSLIL DSWPPSLCSL CAS

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2m20, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_2m20, frame 2

Report for DKFZphtes3_2m20.2

[LENGTH] 121
 [MW] 13436.69
 [pI] 5.81
 [KW] Alpha_Beta

SEQ MRGTRCLA EYHLGDYGHAWNRCWVLD RVD TWAVVMFIDFGQLATIPVQSLRQLDSDDFWT
 PRD cccchhhhhcc

SEQ IPPLTQPFMLEKDILSSYEVVHRILKGKITGALNSAVTAPASNLAVVPPLPLGCLQQA
 PRD cccccchhhhhhccchhhhhhhhhccccchhhhhhcccccccccccccccccccccccc

SEQ A
 PRD C

(No Prosite data available for DKFZphtes3_2m20.2)

(No Pfam data available for DKFZphtes3_2m20.2)

Pedant information for DKFZphtes3_2m20, frame 3

Report for DKFZphtes3_2m20.3

[LENGTH] 183
 [MW] 19971.49
 [pI] 5.31
 [KW] Alpha_Beta

```
SEQ      MIIQPPRAPLVLEKASGEGFGKTAIIQLAPKAPVDLCETEKLRAAFFAVPLEMRGSFLVL
PRD      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
SEQ      LLRECFRDLSWLALIHSVRGEAGLLVTSIVPKTPFFWAMHITEALHQNMQALFSTLAQAE
PRD      hhhhhhhcchhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccc
SEQ      EQQPYLEAPPLCAGLAVWQSTTWGIMDTPGTGVGCWTGWTGWLWSCSLILDSWPPSLCSL
PRD      hhccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
SEQ      CAS
PRD      ccc
```

(No Prosite data available for DKFZphtes3_2m20.3)

(No Pfam data available for DKFZphtes3_2m20.3)

DKFZphtes3_2n9

group: testes derived

DKFZphtes3_2n9 encodes a novel 184 amino acid protein with very weak similarity to Homo sapiens PAC clone DJ0771P04 from 7q11.21-q11.23.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

on genomic level encoded by HS1186N24, no splice pattern but EST matches

Sequenced by EMBL

Locus: unknown

Insert length: 1000 bp

Poly A stretch at pos. 988, polyadenylation signal at pos. 970

```

1  CAACTTTTTA AAGATGTGAA TTGGACAGCC AGACTTGCTT ATTTGTCTGA
51  TATCTTCAGT ATTTTAAAT GATCTTAATG CTTCTATGCA AGGGAAGAAT
101 GCAACTTATT TTTCAATGGC AGATAAAGTT GAAGGACAAA AACAGAAGTT
151 AGAAGCTTGG AAAAACAGAA TTTCTACAGA TTGTTATGAC ATGTTTCATA
201 ATTTAACAAC AATTATCAAT GAAGTAGGTA ATGATCTTGA TATTGCACAT
251 CTGCGAAAAG TTATCAGTGA ACATCTTACA AATTGTGTTAG AATGTTTTGA
301 ATTTTATTTT CCATCAAAAAG AAGATCCACG CATAGGAAAT TTGTGGATCC
351 AAAATCCATT TCTTTCATCA AAAGATAACT TAAATTTAAC TGTAACCTTA
401 CAGGATAAGT TGTGAAGCT GGCTACCGAC GAAGGATTGA AAATCAGTTT
451 TGAAAATACA GCATCACTTC CTTCATTTTG GATAAAAGCT AAAAATGACT
501 ATCCTGAGCT TGCTGAGATT GCTTTAAAT TGCTGCTTCT TTTCCCTCA
551 ACATACCTCT GTGAGACCGG ATTCTCTACT TTAAGTGTTA TTAAACAAA
601 ACATAGAAAC AGTTTAAATA TACATTATCC CCTGAGGTAG CATTGTCATC
651 AATCCAACCT AGATTAGACA AATTAACAAG CAAGAAGCAA GCTCACTTAT
701 CACATTAAAA GCTTTAAATA TTGATATGTA AGGTATTGGT TCAAAGTATG
751 CATATAAGCA TTGAGTGTGA GGAATTTGCT ATTTCACTTT AAACTTTCTG
801 TCTAGTTACA GTTATGGAAG TATGAGAAGT TATGAGTGAA ACAGCAATTT
851 TCTATATAAA TTGCCTATAT GTATATTTTC AATTAAGAAT GTGTACAGTT
901 TTTATAATTC TATTTTTCCT CATATTTGTC GTATTTATTA AAATATAATT
951 TTAAATCTGT TGATTCTAAT ATTAAACAT TTGATCTTAA AAAAAAAAAA

```

BLAST Results

Entry HS1186N24 from database EMBLNEW:
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1186N24
 Score = 4921, P = 5.8e-215, identities = 989/992

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 86 bp to 637 bp; peptide length: 184
 Category: similarity to unknown protein
 Classification: no clue

```

1  MQGKNATYFS MADKVEGQKQ KLEAWKNRIS TDCYDMFHNH TTIINEVGND
51  LDIAHLRKVI SEHLTNLLEC FEFYFPSKED PRIGNLWIQN PFLSSKDNLN
101 LVTTLQDKLL KLATDEGLKI SFENTASLPS FWIKAKNDYP ELAEIALKLL
151 LLFPSTYLCE TGFSTLSVIK TKHRNSLNIH YPLR

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_2n9, frame 2

TREMBLNEW:AC004883_3 gene: "WUGSC:H_DJ0771P04.2"; Homo sapiens PAC clone DJ0771P04 from 7q11.21-q11.23, complete sequence., N = 1, Score = 94, P = 0.042

>TREMBLNEW:AC004883_3 gene: "WUGSC:H_DJ0771P04.2"; Homo sapiens PAC clone DJ0771P04 from 7q11.21-q11.23, complete sequence.
Length = 533

HSPs:

Score = 94 (14.1 bits), Expect = 4.3e-02, P = 4.2e-02
Identities = 39/177 (22%), Positives = 75/177 (42%)

```
Query:      1 MQGKNATYFSMADKVEGQKQKLEAWKNRISTDCYDMFHNLTIIINEVGNDLD-IAHLRKV 59
             +QG +      M D +      KL W+ ++ +      F L      + L+ I + ++
Sbjct:     354 LQGHQSIVTQMYDLIRAFKAKLCLWETHLTRNNLAHFPTLKLASRNESDGLNYIPKIAEL 413

Query:      60 ISEHLTNLLECFEFYFPSKEDPRIGNLWIONPFLSSKDNLNLTVTLQDKLLKLATDEGLK 119
             +E      L + F+ Y      + + +      +PF + D+++      LQ +++ L + LK
Sbjct:     414 KTEFQKRLSD-FKLY---ESELTL----FSSPFSTKIDSVH--EELQMEVIDLQCNTVLK 463

Query:      120 ISFENTASLPFSWIKAKNDYPXXXXXXXFPSTYLCETGFSTLSVIKTKHRNSL 177
             ++      +P F+      YP      F STY+CE FS + + KTK+ + L
Sbjct:     464 TKYDKVG-IPEFYKYLWGSYPKYKHKCAKILSMFGSTYICEQLFSIMKLSKTKYCSQL 520
```

Pedant information for DKFZphtes3_2n9, frame 2

Report for DKFZphtes3_2n9.2

```
[LENGTH]      184
[MW]           21203.53
[pI]           6.52
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY      6.52 %
```

```
SEQ  MQGKNATYFSMADKVEGQKQKLEAWKNRISTDCYDMFHNLTIIINEVGNDLDIAHLRKVI
SEG  .....
PRD  cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhcchhhhhccceeeccccccchhhhhhhhh

SEQ  SEHLTNLLECFEFYFPSKEDPRIGNLWIONPFLSSKDNLNLTVTLQDKLLKLATDEGLKI
SEG  .....
PRD  hhhhhhhhhhhhhccccccccccccceeeccccccccccccceeehhhhhhhhhhhhccce

SEQ  SFENTASLPFSWIKAKNDYPELAELKLLLPSTYLCETGFSTLSVIKTKHRNSLNIH
SEG  .....xxxxxxxxxxxxxxxx.....
PRD  eccccccccceeeccchhhhhhhhhhhhhccccccccccccceeeccccccccceec

SEQ  YPLR
SEG  ....
PRD  cccc
```

(No Prosite data available for DKFZphtes3_2n9.2)

(No Pfam data available for DKFZphtes3_2n9.2)

DKF2phtes3_30f4

group: testes derived

DKF2phtes3_30f4 encodes a novel 192 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

Sequenced by LMU

Locus: /map="717.2-8 cR from top of Chr8 linkage group"

Insert length: 1388 bp

Poly A stretch at pos. 1330, polyadenylation signal at pos. 1310

```
1  CACTGAGCCC TCCTCAGATG GTTAGTGGCT TCCAACAGCC ATCAGGAGTG
51 TTTCTTGAAT GCCCCAGGTG TGGAGGACTT GGTCTGTGAC CACCTAGAAC
101 CCCAGAGCTG AACAGGAAGC CGTCCCTGCA GCAACAAGAG GGCTGGAAGG
151 GGGAGCTGCA GGCCACCCTC GGCTCTCCCA CTGCTGGGGC GGTGATGTTT
201 GGGTGACATG TTTGAAAAAT ACTCTTAAAG ATACCAACTG TTCCCTTATA
251 TGGCTAATGG TTTGTGCAGC CACCAGCGAT GCGGGCCCCT ATTAGAGACC
301 AGGTTTGTTA AAACACCAAA TATTGCTGTC CACACTAGAC ATTAACCGGC
351 TTCAGAAAAG ATGGACACCT TTTCCACACG TGTTCGCTT CTTAACTTTG
401 GTCCAGCTTT AGCCACCACA CAGCGTGTGA GGGACTGCTG CTGCGGAGTC
451 AGCCTCGTTT GTCCCTCCGC CTCCCACCAG CATGCGCCGC TTCTGAGAGA
501 CACCAGCTCC CTGCCTCCAA GCCTGGTGCC ACAGGCCTGT CGTGAGGGAC
551 CCCTGCTTCC GAGAGCTCCT GGGGGGGTTC TGCCCTTCAC CACCTGGGAG
601 AGGTGTCACT TCAGTTCCGA GTTGAACAAG GCCCGTGCAC ACAGCATGTT
651 GGGGGGCCAG CCCAAAGTTC TTGTCACTC CTCATGCAAA GCCAGCCATC
701 ACCCTCCGGC CAGAGCTCAA GGTGGCCCTT TGGCCAGCCC TCCTTGGGT
751 CCTCCAGGAG GACTGAGCAC CCCTCCTAGC GGCATCCCTT GCCCTCCACA
801 GTGCTGCCAG GGGCACGTCG CTCTGTGCCG TGGACTGAGA CCATCCCCTG
851 GTGACAGAAT GACCCGTTTG TTGGAATATG CTCGTTGCCA GAGAACTCC
901 CCAGGCATCT CGGAACGAAA CTATTTAGTT CCATTGTGAA CTGGCCACGG
951 GACAGCTTTT TATCAACTTA TTAAGTTGGA GCACTGTAAT CGCGCTTGCT
1001 GAGTTAGCAG TGGTGGTAAG CGTGTGTTAA ACACATAATG TTACGTTTTA
1051 GGAGAGAGAG GTCGTAAGGA AGTGTGCTGT CGCTCATGAC TCTCTTCTAT
1101 TAGTTGGGTA ACAGTGGCCT CATGTTTGTG TCTGTGTGTA CACAGAGCCC
1151 TTAGGTTCTG CTCTGTTTCT TTGCCAGGTG AATGTTTGTG GCATGCGCTG
1201 CTGTCCGCGC CCCTCTGTCC TGCGCAGGGT TCAGCTGTGC GCGGCCCTGA
1251 TTTCTCCCAT GCACACAGAA CCTCCTTGTG TCTGTTTCTC TGTTCCTCTG
1301 TGGCTGACTC AATAAACTTT TCCCTCTGAC ATGAAAAAAA AAAAAAAA
1351 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAG
```

BLAST Results

Entry HS548358 from database EMBL:

human STS EST67250.

Score = 2126, P = 1.5e-89, identities = 444/472

Entry HS670351 from database EMBL:

human STS WI-18501.

Score = 2089, P = 7.1e-88, identities = 445/476

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 361 bp to 936 bp; peptide length: 192

Category: putative protein

Classification: no clue


```
1 MDTFSHAVSL LNFGPALATT QRVRDCCCGV SLVCPASASHQ HAPLLRDTSS
51 LPPSLVPQAC REGPLLPRAP GGVLPTTWE RCQFSSELNK ARAHSMGLAQ
101 PKVLVTSSCK ASHHPPARAQ GGPLASPSLG PPGGLSTPPS GIPCPQCCQ
151 GHVALCRGLR PSPGDRMTRL LEMPRCQRNS PGISERNYLV PL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_30f4, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_30f4, frame 1

Report for DKFZphtes3_30f4.1

```
[LENGTH]      192
[MW]           20281.56
[pI]           9.21
[BLOCKS]      BL01013C Oxysterol-binding protein family proteins
[KW]           Ali_Alpha
[KW]           LOW_COMPLEXITY    10.94 %

SEQ    MDTFSHAVSLLNFGPALATTQRVRDCCCGVSLVCPASASHQHAPLLRDTSSLPPSLVPQAC
SEG    .....
PRD    ccchhhhheeeccccchhhhhhhccccceeeccccccccccccccccccccccccccccc

SEQ    REGPLLPRAPGGVLPFTTWERCQFSSELNKARAHSMGLAQPKVLVTSSCKASHHPPARAQ
SEG    .....
PRD    cccccccccccccccccccchhhhhhhhhhhhhccccceeecccccccccccccccccc

SEQ    GGPLASPSLGPPGGLSTPPSGIPCPQCCQGHVALCRGLRPSPGDRMTRLLEMPCQRNS
SEG    xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD    cccccccccccccccccccccccccccccccccchhhhhhhhhccccccchhhhhcccccccccc

SEQ    PGISERNYLVPL
SEG    .....
PRD    cccccccccccc
```

(No Prosite data available for DKFZphtes3_30f4.1)

(No Pfam data available for DKFZphtes3_30f4.1)

DKFZphtes3_35b4

group: cell cycle

DKFZphtes3_35b4 encodes a novel 1780 amino acid protein which is C-terminal identical to human M-phase phosphoprotein-1 (MPP1).

The novel protein contains a N-terminal Pfam kinesin motor domain and a ATP/GTP-binding site motif A (P-loop). MPP1 is expressed and phosphorylated in the metaphase. Therefore the novel protein seems to be involved in the mitotic spindle during cell division.

The new protein can find application in modulation of the mitotic spindle.

"M-phase phosphoprotein-1" extension

motor protein

Sequenced by DKFZ

Locus: /map="750_H_1; 758_H_7; 759_C_9; 847_D_4; 906_D_1; 931_D_3; 944_C_1; 750_G_12; 800_A_11; 512.1 cR from top of Chr10 linkage group"

Insert length: 6284 bp

No poly A stretch found, no polyadenylation signal found

```
1 ATCGCAGTGC TGCTCGCGGG TCTGGCTAGT CAGGCGAAGT TTGCAGAATG
51 GAATCTAATT TTAATCAAGA GGGAGTACCT CGACCATCTT ATGTTTTTAG
101 TGCTGACCCA ATTGCAAGGC CTTCAGAAAT AAATTTTCGAT GGCATTAAGC
151 TTGATCTGTC TCATGAATTT TCCTTAGTTG CTCCAATAC TGAGGCAAAAC
201 AGTTTTCGAAT CTAAAGATTA TCTCCAGGTT TGTCTTCGAA TAAGACCATT
251 TACACAGTCA GAAAAAGAAC TTGAGTCTGA GGGCTGTGTG CATATTCTGG
301 ATTCACAGAC TGTTGTGCTG AAAGAGCCTC AATGCATCCT TGGTCGGTTA
351 AGTGAAAAAA GCTCAGGGCA GATGGCACAG AAATTCAGTT TTTCCAAGGT
401 TTTTGGCCCA GCAACTACAC AGAAGGAATT CTTTCAGGGT TGCATTATGC
451 AACCACTAAA AGACCTCTTG AAAGGACAGA GTCGTCTGAT TTTTACTTAC
501 GGGCTAACCA ATTCAGGAAA AACATATACA TTTCAAGGGA CAGAAGAAAA
551 TATTGGCATT CTGCCTCGAA CTTTGAATGT ATTATTTGAT AGTCTTCAAG
601 AAAGACTGTA TACAAAGATG AACCTTAAAC CACATAGATC CAGAGAATAC
651 TTAAGGTTAT CATCAGAACA AGAGAAAGAA GAAATTGCTA GCAAAAGTGC
701 ATTGCTTCGG CAAATTAAG AGGTTACTGT GCATAATGAT AGTGATGATA
751 CTCTTTATGG AAGTTTAACT AACTCTTTGA ATATCTCAGA GTTTGAAGAA
801 TCCATAAAAG ATTATGAACA AGCCAACTTG AATATGGCTA ATAGTATAAA
851 ATTTTCTGTG TGGGTTTCTT TCTTTGAAAT TTACAATGAA TATATTTATG
901 ACTTATTGTG TCCTGTATCA TCTAAATTCC AAAAGAGAAA GATGCTGCCG
951 CTTTCCCAAG ACGTAAAGGG CTATTCTTTT ATAAAAGATC TACAATGGAT
1001 TCAAGTATCT GATTCCAAAG AAGCCTATAG ACTTTTAAAA CTAGGAATAA
1051 AGCACCAGAG TGTTCCTTC ACAAAATTGA ATAATGCTTC CAGTAGAAGT
1101 CACAGCATAT TCACTGTTAA AATATTACAG ATTGAAGATT CTGAAATGTC
1151 TCGTGTAAAT CGAGTCAGTG AATTATCTTT ATGTGATCTT GCTGGTTCAG
1201 AACGAACATAT GAAGACACAG AATGAAGGTG AAAGGTTAAG AGAGACTGGG
1251 AATATCAACA CTCTTTTATT GACTCTGGGA AAGTGATTA ACGTCTTGAA
1301 GAATAGTGAA AAGTCAAAGT TTCAACAGCA TGTGCCTTTC CGGGAAAGTA
1351 AACTGACTCA CTATTTTCAA AGTTTTTTTA ATGGTAAAGG GAAAATTTGT
1401 ATGATTGTCA ATATCAGCCA ATGTTATTTA GCCTATGATG AAACACTCAA
1451 TGTATTGAAG TTCTCCGCCA TTGCACAAAA AGTTTGTGTC CCAGACACTT
1501 TAAATTCTCT TCAAGATAAA TTATTTGGAC CTGTCAAATC TTCTCAAGAT
1551 GTATCACTAG ACAGTAATTC AAACAGTAAA ATATTAATG TAAAAAGAGC
1601 CACCATTTCA TGGGAAAAATA GTCTAGAAGA TTTGATGGAA GACGAGGATT
1651 TGGTTGAGGA GCTAGAAAAC GCTGAAGAAA CTCAAATGT GGAAACTAAA
1701 CTCTTTGATG AAGATCTAGA TAAAACATTA GAGGAAAAATA AGGCTTTCAT
1751 TAGCCACGAG GAGAAAAAGAA AACTGTTGGA CTTAATAGAA GACTTGAAAA
1801 AAAAACTGAT AAATGAAAAA AAGGAAAAAT TAACCTTGGA ATTTAAATTT
1851 CGAGAAGAAG TTACACAGCA GTTACTCAG TATTGGGCTC AACGGGAAGC
1901 TGACTTTAAG GAGACTCTGC TTCAAGAACG AGAGATATTA GAAGAAAAATG
1951 CTGAACGTCG TTTGGCTATC TTCAAGGATT TGGTTGGTAA ATGTGACACT
2001 CGAGAAGAAG CAGCGAAAGA CATTGTGCC ACAAAGTTG AAACGTGAAGA
2051 AGCTACTGCT TGTTTAGAAC TAAAGTTTAA TCAAATTAAG GCTGAATTAG
2101 CTAAAACCAA AGGAGAATTA ATCAAAACCA AAGAAGAGTT AAAAAAGAGA
2151 GAAAATGAAT CAGATTCATT GATTCAAGAG CTTGAGACAT CTAATAAGAA
2201 AATAATTACA CAGAATCAAA GAATTAAAGA ATTGATAAAT ATAATTGATC
2251 AAAAAAGAGA TACTATCAAC GAATTCAGA ACCTAAAGTC TCATATGGAA
2301 AACACATTTA AATGCAATGA CAAGGCTGAT ACATCTTCTT TAATAATAAA
2351 CAATAAATTG ATTTGTAATG AAACAGTTGA AGTACCTAAG GACAGCAAAAT
2401 CTAAAACTGT TTCAGAAAGA AAAAGAGTAA ATGAAAATGA ACTTCAGCAA
2451 GATGAACCAC CAGCAAAGAA AGGCTCTATC CATGTTAGTT CAGCTATCAC
2501 TGAAGACCAA AAGAAAAGTG AAGAAGTGC ACCGAACATT GCAGAAATTG
2551 AAGACATCAG AGTTTTACAA GAAAATAATG AAGGACTGAG AGCATTTTTA
```

2601 CTCACTATTG AGAATGAAC TAAAAATGAA AAGGAAGAAA AAGCAGAATT
2651 AAATAAACAG ATTGTTTCATT TTCAGCAGGA ACTTCTCTTT TCTGAAAAAA
2701 AGAATTTAAC TTTAAGTAAA GAGGTCCAAC AAATTCAGTC AAATATATGAT
2751 ATTGCAATTG CTGAATTACA TGTGCAGAAA AGTAAAAATC AAGAACAGGA
2801 GGAAAAAGATC ATGAAATTGT CAAATGAGAT AGAACTGCT ACAAGAAGCA
2851 TTACAAATTA TGTTCACAA ATAAATTTAA TGCACACGAA AATAGACGAA
2901 CTACGTACTC TTGATTCAGT TTCTCAGATT TCAAACATAG ATTTGCTCAA
2951 TCTCAGGGAT CTGTCAAATG GTTCTGAGGA GGATAATTTG CCAAATACAC
3001 AGTTAGACCT TTTAGGTAAT GATTATTTGG TAAGTAAGCA AGTTAAAGAA
3051 TATCGAATTC AAGAACCCAA TAGGGAAAAAT TCTTTCCACT CTAGTATTGA
3101 AGCTATTGGG GAAGAATGTA AAGAGATTGT GAAGGCCTCT TCCAAAAAAA
3151 GTCATCAGAT TGAGGAACCTG GAACAACAAA TTGAAAAATT GCAGGCAGAA
3201 GTAAAAGGCT ATAAGGATGA AAACAATAGA CTAAAGGAGA AGGAGCATAA
3251 AAACCAAGAT GAGCTACTAA AAGAAAAAGA AACTCTTATA CAGCAGCTGA
3301 AAGAAGAAAT GCAGAAAAA AATGTTACTC TTGATGTTCA AATACAGCAT
3351 GTAGTTGAAG GAAAGAGAGC GCTTTCAGAA CTTACACAAG GTGTTACTTG
3401 TCAGAAAGCA AAAATAAAGG AACTTGAAAC AATTTTAGAG ACTCAAAAG
3451 TTGAACGTAG TCATTCAGCC AAGTTAGAAC AAGACATTTT GGAAAGGAA
3501 TCTATCATCT TAAAGCTAGA AAGAAATTTG AAGGAATTTT AAGAATCTCT
3551 TCAGGATTGT GTCAAAAAACA CCAAGATTT AAATGTAAAG CCACTCAAGC
3601 TGAAAGAAGA AATCACACAG TTAACAAATA ATTTGCAAGA TATGAAACAT
3651 TTAATTCAT TAAAGAAGA AGAAGAAGAA ACCAACAGGC AAGAAACAGA
3701 AAAATTGAAA GAGCAACTCT CTGCAAGCTC TGCTCGTACC CAGAATCTGA
3751 AAGCAGATCT TCAGAGGAAG GAAGAAGATT ATGCTGACCT GAAAGAGAAA
3801 CTGACTGATG CCAAAAAAGCA GATTAAGCAA GTACAGAAAG AGGTATCTGT
3851 AATGCGTGAT GAGGATAAAT TACTGAGGAT TAAAATTAAT CAACTGGAGA
3901 AAAAGAAAAA CAGTGTCTCT CAGGAATTAG ATATGAAGCA GCGAACCATT
3951 CAGCAACTCA AGGAGCAGTT AAATAATCAG AAAGTGAAG AAGCTATACA
4001 ACAGTATGAG AGAGCATGCA AAGATCTAAA TGTTAAAGAG AAAATAATTG
4051 AAGACATGCG AATGACACTA GAAGAACAGG AACAACTCA GGTAGAACAG
4101 GATCAAGTGC TTGAGGCTAA ATTAGAGGAA GTTGAAAGGC TGGCCACAGA
4151 AATGGAAAAA TGGAAAGGAA AATGCAATGA TTTGGAAACC AAAAAATC
4201 AAAGGTCAAA TAAAGAACAT GAGAACAACA CAGATGTGCT TGGAAAGCTC
4251 ACTAATCTTC AAGATGAGTT ACAGGAGTCT GAACAGAAAT ATAATGCTGA
4301 TAGAAAGAAA TGGTTAGAA AAAAAATGAT GCTTATCACT CAAGCGAAAG
4351 AAGCAGAGAA TATACGAAAT AAAGAGATGA AAAAATATGC TGAGGACAGG
4401 GAGCGTTTTT TTAAGCAACA GAATGAAATG GAAATACTGA CAGCCCAGCT
4451 GACAGAGAAA GATAGTGACC TTCAAAAAGT GCGAGAAAGAA CGAGATCAAC
4501 TGGTTGCAGC TTTAGAAATA CAGCTAAAAG CACTGATATC CAGTAATGTA
4551 CAGAAAGATA ATGAAATTGA ACACTAAAA AGGATCATAT CAGAGACTTC
4601 TAAAAATGAA ACACAAATCA TGGATATCAA GCCCAAACGT ATTAGTTTCA
4651 CAGATCCTGA CAACTTTCAA ACTGAACCTC TATCGACAAG TTTTGAAATT
4701 TCCAGAAATA AAATAGAGGA TGGATCTGTA GTCCTTGACT CTTGTGAAGT
4751 GTCAACAGAA AATGATCAAA GCACTCGATT TCCAAAACCT GAGTTAGAGA
4801 TTCAATTTAC ACCTTTTACAG CCAACAAAAA TGGCAGTGAA ACACCTTGGT
4851 TGTACCACAC CAGTGACAGT TGAGATTCCC AAGGCTCGGA AGAGGAAGAG
4901 TAATGAAATG GAGGAGGACT TGGTGAAATG TGAAAATAAG AAGAATGCTA
4951 CACCCAGAAC TAATTTGAAA TTTCCCTATT CAGATGATAG AAATCTTCTT
5001 GTCAAAAAGG AACAAAAAGG TGCCATACGT CCATCATCTA AGAAAAATA
5051 TTCTTTACGG AGTCAGGCAT CCATAATTGG TGTAAACCTG GCCACTAAGA
5101 AAAAAGAAAG AACACTACAG AAATTTGGAG ACTTCTTACA ACATTCTCCC
5151 TCAATTTCTC AATCAAAAAGC AAAGAAGATA ATTGAAACAA TGAGCTCTTC
5201 AAAGCTCTCA AATGTAGAAG CAAGTAAAGA AAATGTGTCT CAACCAAAAC
5251 GAGCCAAACG GAAATTATAC ACAAGTGAAA TTTTCATCTC TATTGATATA
5301 TCAGGCCAAG TGATTTTAAAT GGACCAGAAA ATGAAGGAGA GTGATCACCA
5351 GATTATCAAA CGACGACTTC GAACAAAAAC AGCCAAATAA ATCACTTATG
5401 GAAATGTTTA ATATAAATTT TATAGTCATA GTCATTGGAA CTTGCATCCT
5451 GTATTGTAAA TATAAATGTA TATATTATGC ATTAATACAC TCTGCATATA
5501 GATTGCTGTT TTATACATAG TATAATTTTA ATTCAATAAA TGAGTCAAAA
5551 TTTGTATATT TTTATAAGGC TTTTATATAA TAGCTTCTTT CAAACTGTAT
5601 TTCCCTATTA TCTCAGACAT TGGATCAGTG AAGATCCTAG GAAAGAGGCT
5651 GTTATTCTCA TTTATTTTGC TATACAGGAT GTAATAGGTC AGGTATTTGG
5701 TTTACTTATA TTTAACAATG TCTTATGAAT TTTTCTTACT TTATCTGTTA
5751 TACAACGTAT TTTACATATC TGTTTGGATT ATAGCTAGGA TTTGGAGAA
5801 AAGTGTGTAC AGATCACAAA ACATGTATAT ACATTATTTA GAAAAGATCT
5851 CAAGTCTTTA ATTAGAATGT CTCACCTTAT TTGTAAACAT TTTGTGGGTA
5901 CATAGTACAT GTATATATTT ACGGGGTATG TGAGATGTTT TGACACAGGC
5951 ATGCAATGTG AAATACGTGT ATCATGGAGA ATGAGGTATC CATCCCCTCA
6001 AGCATTTTTC CTTTGAATTA CAGATAATCC AATTACATTC TTTAGATCAT
6051 TAAAAAATAT ACAAGTAAGT TATTATTGAT TATAGTCACT CATTTGTGCT
6101 ATCAGATAGT AGATCATTTCT TTTTATCTTA TTTGTTTTTG TACCCATTAA
6151 CCATCCCCAC CTCCCCCTGC AACCGTCAGT ACCCTTACCA GCCACTGGTA
6201 ACCATTCTTC TACTCTGTAT GCCCATGAGG TCAATTGATT TTATTTTATG
6251 ATCCCATAAA TAAATGAGAA CATGCAAAAA AAAA

BLAST Results

Entry HS898149 from database EMBL:
human STS WI-9217.

Score = 4247, P = 1.5e-187, identities = 855/862

Medline entries

94119956:

Cloning of cDNAs for M-phase phosphoproteins recognized by the MPM2 monoclonal antibody and determination of the phosphorylated epitope.

98101856:

Interaction of a Golgi-associated kinesin-like protein with Rab6.

95122643:

Identification and partial characterization of mitotic centromere-associated kinesin, a kinesin-related protein that associates with centromeres during mitosis.

Peptide information for frame 3

ORF from 48 bp to 5387 bp; peptide length: 1780

Category: known protein

Classification: Cell structure/motility

Prosite motifs: ATP_GTP_A (152-160)

```

1 MESNFNQEGV PRPSYVFSAD PIARPSEINF DGIKLDLSHE FSLVAPNTEA
51 NSFESKDYLO VCLRIRPFTQ SEKELESEGC VHILDSQTVV LKEPQCILGR
101 LSEKSSGQMA QKFSFSKVFG PATTOKEFFQ GCIMQPVKDL LKGQSRILFT
151 YGLTNSGKTY TFQGTENIG ILPRTLNVLF DSLQERLYTK MNLKPHRSRE
201 YLRSLSEQEK EEIASKSALL RQIKEVTVHN DSDDTLYGSL TNSLNISEFE
251 ESIKDYEQAN LNMANSIKFS VWVSFFEIYN EYIYDLFVPV SSKFQKRKML
301 RLSQDVKGYS FIKDLQWIVQ SDSKEAYRLL KLGKHKQSVF FTKLNNASSR
351 SHSIFTVKIL QIEDSEMSRV IRVSELSLCD LAGSERTMKT QNEGERLRRET
401 GNINTSLTLT GKCNVVKNS ESKKFQOHVP FRESKLTHYF QSFNGKGGKI
451 CMIVNISQCY LAYDETLNVL KFSIAQKVC VPDTLNSSQD KLFQPVKSSQ
501 DVSLDSNSNS KILNVKRATI SWENSLEDLM EDEDLVEELE NAEETQNVET
551 KLLDEDLDKT LEENKAFISH EEKRLLDLI EDLKKKLINE KKEKLTLEFK
601 IREEVTOEFT QYWAQREADF KETLLQEREI LEENAERRLA IFKDLVGKCD
651 TREEAAKDIC ATKVETEEAT ACLELKFNQI KAEKAKTKGE LIKTKEELKK
701 RENESDSLIQ ELETSNKKII TQNRKIKELI NIIDQKEDTI NEFQNLKSHM
751 ENTFCNDKA DTSSLIINNK LICNETVEVP KDSKSKICSE RKRNVNENELQ
801 QDEPPAKKGS IHVSSAIED QKKSEEVPRN IAEIEDIRVL QENNEGLRAF
851 LLTIENELKN EKEEKAELNK QIVHFQOELS LSEKKNLTLS KEVQIQSNY
901 DIAIAELHVQ KSKNQEQEEK IMKLSNEIET ATRSTITNVV QIKLMHTKID
951 ELRTLDVSQV ISNIDLLNLR DLSNGSEEDN LPNTQLDLLG NDYLVSKQVK
1001 EYRIQEPNRE NSFHSSIEAI WEECKEIVKA SSKKSHQIEE LEQQIEKLQA
1051 EVKGYKDENN RLKEKEHKNQ DDLKEKETL IQQLKEELOE KNVTLQVQIQ
1101 HVVEGKRALS ELTQGVTCYK AKIKELETIL ETQKVERSIS AKLEQDILEK
1151 ESIIILKLERN LKEFQEHQD SVKNTKDLNV KELKLKEEIT QLTNNLQDMK
1201 HLLQLKEEEE ETNRQETEKL KEELSASSAR TQNLKADLQR KEEDYADLKE
1251 KLTDAAKQIK QVQKEVSVMR DEDKLLRIKI NELEKKKNQC SQELDMKQRT
1301 IQQLKEQLNN QKVEEAIQY ERACKDLNVK EKIIEDMRMT LEEQEQTQVE
1351 QDQVLEAKLE EVERLATELE KWKEKCNLE TKNNQRSNKE HENNTDVLGK
1401 LTNLQDELQE SEQKYNADRK KWLEEKMLLI TQAKEAENIR NKEMKKYAE
1451 RERFFKQONE MEILTAQLTE KDSDLQKWRE ERDQLVAALE IQLKALISSN
1501 VQKDNEIEQL KRIISETSKI ETQIMDIKPK RISSADPDKL QTEPLSTSF
1551 ISRNKIEDGS VVLDSCVEST ENDQSTRFPK PELEIQFTPL QPNKMAVKHP
1601 GCTTPVTVEI PKARKRKSNE MEEDLVKCN KKNATPRTNL KFPISDDRNS
1651 SVKKEQKVAI RPSKKKTYSL RSQASIIQVN LATKKKEGTL QKFGDFLQHS
1701 PSILQSKAKK IETMSSSKL SNVEASKENV SQPKRAKRKL YTSEISSPID
1751 ISGQVILMDQ KMKESDHQII KRLRRTKTAK

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_35b4, frame 3

TREMBL:U93121_1 product: "M-phase phosphoprotein-1"; Human M-phase phosphoprotein-1 mRNA, partial cds., N = 1, Score = 3743, P = 0

PIR:A36881 MPM2-reactive phosphoprotein 1 - human (fragment), N = 2,
Score = 2808, P = 2.5e-294

TREMBL:AF070672_1 product: "rabkinesin6"; Homo sapiens rabkinesin6
mRNA, complete cds., N = 2, Score = 680, P = 2.6e-99

>TREMBL:U93121_1 product: "M-phase phosphoprotein-1"; Human M-phase
phosphoprotein-1 mRNA, partial cds.
Length = 753

HSPs:

Score = 3743 (561.6 bits), Expect = 0.0e+00, P = 0.0e+00
Identities = 752/753 (99%), Positives = 753/753 (100%)

Query: 1028 VKASSKKSHQIEELEQQIEKLQAEVKGKYNENRLKEKEHKNQDDLLKEKETLIQQLKEE 1087
Sbjct: 1 VKASSKKSHQIEELEQQIEKLQAEVKGKYNENRLKEKEHKNQDDLLKEKETLIQQLKEE 60

Query: 1088 LQEKNVTLDVQIQHVVEGKRALSELTOGVTCTYKAKIKELETILETQKVERSHSAKLEQDI 1147
Sbjct: 61 LQEKNVTLDVQIQHVVEGKRALSELTOGVTCTYKAKIKELETILETQKVERSHSAKLEQDI 120

Query: 1148 LEKESIIKLERNLKEFQEHLDQSVKNTKDLNVKELKLKEEITQLTNNLQDMKHLQLKE 1207
Sbjct: 121 LEKESIIKLERNLKEFQEHLDQSVKNTKDLNVKELKLKEEITQLTNNLQDMKHLQLKE 180

Query: 1208 EEEETNRQETEKLEELSASSARTQNLKADLQKKEEDYADLKEKLTDAKKQIKQVQKEVS 1267
Sbjct: 181 EEEETNRQETEKLEELSASSARTQNLKADLQKKEEDYADLKEKLTDAKKQIKQVQKEVS 240

Query: 1268 VMRDEDKLLRIKINELEKKKNQCSQELDMKQRTIQQLKEQLNNQKVVEAIQQYERACKDL 1327
Sbjct: 241 VMRDEDKLLRIKINELEKKKNQCSQELDMKQRTIQQLKEQLNNQKVVEAIQQYERACKDL 300

Query: 1328 NVKEKIIEDMRMTLEEQQEQTQVEQDQVLEAKLEEVERLATELEKWKEKCNLDLETNNQRS 1387
Sbjct: 301 NVKEKIIEDMRMTLEEQQEQTQVEQDQVLEAKLEEVERLATELEKWKEKCNLDLETNNQRS 360

Query: 1388 NKEHENNTDVLGKLTNLQDELQSEQKYNADRKKWLEEKMLITQAKEAENIRNKEMKKY 1447
Sbjct: 361 NKEHENNTDVLGKLTNLQDELQSEQKYNADRKKWLEEKMLITQAKEAENIRNKEMKKY 420

Query: 1448 AEDRERFFKQONEMEILTAQLTEKSDQKWRERDQVAALEIQKALISSNVQKDNEI 1507
Sbjct: 421 AEDRERFFKQONEMEILTAQLTEKSDQKWRERDQVAALEIQKALISSNVQKDNEI 480

Query: 1508 EQLKRIISETSKIETQIMDIKPKRISSADPKLQTEPLSTSFEISRNKIEDGSVVLDSCE 1567
Sbjct: 481 EQLKRIISETSKIETQIMDIKPKRISSADPKLQTEPLSTSFEISRNKIEDGSVVLDSCE 540

Query: 1568 VSTENDQSTRFPKPELEIQFTPLQPNKMAVKHFGCTTPVTVIIPKARKRKSNEEEDLVK 1627
Sbjct: 541 VSTENDQSTRFPKPELEIQFTPLQPNKMAVKHFGCTTPVTVIIPKARKRKSNEEEDLVK 600

Query: 1628 CENKKNATPRTNLKFPISSDRNSSVKKEQKVAIRPSSKKTYSLSQASIIGVNLATKKKE 1687
Sbjct: 601 CENKKNATPRTNLKFPISSDRNSSVKKEQKVAIRPSSKKTYSLSQASIIGVNLATKKKE 660

Query: 1688 GTLQKFGDFLQHSPSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSEISS 1747
Sbjct: 661 GTLQKFGDFLQHSPSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSEISS 720

Query: 1748 PIDISGQVILMDQMKESDHQIKRRLRTKTAK 1780
Sbjct: 721 PIDISGQVILMDQMKESDHQIKRRLRTKTAK 753

Score = 197 (29.6 bits), Expect = 2.1e-11, P = 2.1e-11
Identities = 114/542 (21%), Positives = 253/542 (46%)

Query: 692 IKTKELKKRENESDSLIQELTSNKKIITQNRKELINIIDQKEDTINEFQNLKSHM- 750
+K + + E + I++L+ K +N R+KE + ++D + E + L +
Sbjct: 1 VKASSKKSHQIEELEQQIEKLQAEVKGKYNENRLKEKEH--KNQDDLLKEKETLIQQLK 58

Query: 751 ENTFCNDKADTS-SLIINNKLICNETVEVPKDSKSKICSERKRVNENELQQDEPPAK-- 807
E + N D ++ K +E + K+KI E + + E + + AK
Sbjct: 59 EELQEKNVTLDVQIQHVVEGKRALSELTOGVTCTYKAKI-KELETILETQKVERSHSAKLE 117

Query: 808 KGSIHVSSAITEDQKKSEEVPRNIAE-IEDIRVLQENNEGLRAFLTIENELKNEK---- 862

+ + S I + ++ +E + ++ + +++ + L L+ + + N L++ K
 Sbjct: 118 QDILEKESIILKLERNLKEFQEHLDQSVKNTKDLNVKELKLKEEITQLTNNLQDMKHLLO 177
 Query: 863 --EKAELNKQIVH-FQQLSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQSKNQEQEE 919
 EE+ E N+Q ++ELS S + L ++Q+ + +Y A+L K K + ++
 Sbjct: 178 LKEEEEETNRQETEKLEELSASSARTQNLKADLQKKEEDY----ADL---KEKLTDK 230
 Query: 920 KIMKLSNEIETATRSITNNVSOIKLMHTKIDEL-RTLDVSQISNIDLLNLRDLSNGSEE 978
 +I ++ E+ S+ + + KL+ KI+EL + + SQ +D+ R + E+
 Sbjct: 231 QIKQVQKEV-----SVMRD--EDKLLRIKINELEKKNQCSQ--ELDMKQ-RTIQQLKEQ 280
 Query: 979 DNLPTQLDQLGNDYLVSKQVKEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHQI 1038
 N N +++ Y + K+ ++E E+ ++E + E + K ++
 Sbjct: 281 LN--NQKVEEAIQY--ERACKDLNVKEKIIED-MRMTLEEQTQVEQDQVLEAKLEEV 335
 Query: 1039 EELEQQIEKLQAEVKGKYNENRLKEKEHKNQDDLLKEKETLIQQLKEELQEKNT---- 1094
 E L ++EK + + + +NN+ KEH+N D+L + L +L+E Q+ N
 Sbjct: 336 ERLATELEKWKECNDLETNNQSRNKEHENNTDVLGKLTNLQDELQSEQKYNADRKKW 395
 Query: 1095 LDVQIQHVVEGKRA-----LSELTQGVTCYKAKIKELETILETQKVERSHSAKLEQDI 1147
 L+ ++ + + K A + + + + + E+E IL Q E+ + ++
 Sbjct: 396 LEEKMLITQAKEAENIRNKEMKKYAE DRERFFKQQNEME-ILTAQLTEKDSDLQKWE- 453
 Query: 1148 LEKESIILKLERNLKEFQEHLDQSVKNTKDLNVKELK-LKEEITQLTNNLQDMKHLLO 1206
 E++ ++ LE LK + +V+ KD +++LK + E +++ + D+K +
 Sbjct: 454 -ERDQLVAALEIQKAL---ISSNVQ--KDNEIEQLKRIISETSKIETQIMDIK---PKR 504
 Query: 1207 EEEEEETNRQETEKLEELSASSARTQ 1233
 + ++ +TE L S + ++
 Sbjct: 505 ISSADPDKLQTEPLSTSFEISRKNKIED 531
 Score = 186 (27.9 bits), Expect = 3.2e-10, P = 3.2e-10
 Identities = 131/674 (19%), Positives = 294/674 (43%)
 Query: 673 LELKFNQIKAEAKTGELIKT-KEELKKRENESDSLIQELETNKKIITQNRIKELIN 731
 L+ K ++ + +L K K LI+ KEEL+++ D IQ + + + Q +
 Sbjct: 35 LKEKEHKNQDDLLKEKETLIQQLKEELQEKNTLDVQIQHVVEGKRALSELTQGVTCYKA 94
 Query: 732 IIDQKEDTINEFQNL-KSHMENTFKCNKADTSSLIINNKLICNETVEVPKDSKSKICSE 790
 I + E TI E Q + +SH + D + S+I+ + E E +DS
 Sbjct: 95 KIKELE-TILETQKVERSHSAKLEQ--DILEKESIILKLERNLKEFQEHLDQSVKNTKDLNVKELKLKEEITQLTNNLQDMKHLLO 147
 Query: 791 RKRVENENELQ-QDEPPAKKGSIHVSSAITEDQKKSEEV-RPNIAEI-EDIRVLQENNEGL 847
 K +N EL+ ++E ++ + + +++ EE R ++ E++ + L
 Sbjct: 148 TKDLNVKELKLKEEITQLTNNLQDMKHLLOLQKEEEEETNRQETEKLEELSASSARTQNL 207
 Query: 848 RAFLITIENELKNEKEEKAELNKQIVHFQQLSLSEKKNLTLSKEVQQI-----QSNYDI 902
 +A L E + + KE+ + KQI Q+E+S+ ++ L ++ ++ Q + ++
 Sbjct: 208 KADLQKKEEDYADLKEKLTDKQKQVQKEVSVMRDEDKLLRIKINELEKKNQCSQEL 267
 Query: 903 AIAELHVQSKNQEQEEKIMKLSNEIETATRSITNNVSOIKLMHTKIDEL-RTLDVSQI 961
 + + +Q+ K Q +K+ + + E A + + I+ M ++E +T Q+
 Sbjct: 268 DMKQRTIQQLKEQLNNQKVEEAIQYERACKDLNVKEKIIEDMRMTLEEQTQVEQDQV 327
 Query: 962 SNIDLLNLRDLSNGSEEDNLPNTQLDQLGNDYLVSKQVKEYRI--QEPNRENSFHSSIEA 1019
 L + L+ E+ L+ N + + + N ++ S +
 Sbjct: 328 LEAKLEEVEERLATELEKWKECNDLETNNQSRNKEHENNTDVLGKLTNLQDELQSEQK 387
 Query: 1020 IWEECKEIVKASSKKSHQIEELEQQIEKLQAEVKGKYNENRLKEKEHKNQ--DDLLKEK 1077
 + K+ ++ Q +E E K E+K Y ++ R +++++ + L EK
 Sbjct: 388 YNADRKKWLEEKMLITQAKEAENIRNK--EMKKYAE DRERFFKQQNEMEILTAQLTEK 444
 Query: 1078 ETLIQQLKEELQEKNTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILETQKVER 1137
 ++ +Q+ +EE + L++Q++ ++ + + ++ +ET + K +R
 Sbjct: 445 DSDLQKWEERDQLVAALEIQKALISSNVQKDNEIEQLKRIISETSKIETQIMDIKPKR 504
 Query: 1138 SHSAKLEQDILEKESIILKLERNLKEFQEHLDQSVKNTKDLNVKELKLKEEITQLT 1193
 SA ++ E S ++ RN E + DS +N + + +L+ + T L
 Sbjct: 505 ISSADPDKLQTEPLSTSFEISRKNKIEDGSSVLDSCVSTENDQSTRFPKPELEIQFTPLQ 564
 Query: 1194 NNLQDMKH---LLQLKEEEEETNRQETEKLEEL-SASSARTQNLKADLQKKEEDYADLK 1249
 N +KH + + + +++++ ++E+L + + + +L+ D +
 Sbjct: 565 PNKMAVKHPGCTTPVTVKIPKARKKSNEMEEDLVKCNKKNATPRTNLKFPISDRNSS 624
 Query: 1250 EKLTDKQKQVQKEVSVMRDEDKLLRIKINELEKKNQCSQEL-DMKQRTIQQLKEQL 1308
 K + K I+ K+ +R + + I +N KKK Q+ D Q + L+ +
 Sbjct: 625 VK-KEQKVAIRPSSKKTYSLSQASI--IGVNLATKKKEGTQLQKFGDFLQHSPSILQSKA 681
 Query: 1309 NNQKVEEAIQYERACKDLNVKEKIIEDMR 1338
 +K+ E + + + + + KE + + R
 Sbjct: 682 --KKIETMSSSKLSNVEAS-KENVSQPKR 708

Score = 165 (24.8 bits), Expect = 5.8e-08, P = 5.8e-08
Identities = 140/626 (22%), Positives = 271/626 (43%)

Query: 536 VEELENAEETQNVETKLLDEDLTKLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEK- 594
+EELE E E K +D+ L+E+ H+ + LL E L ++L E +EK
Sbjct: 11 IEELEQQIEKLQAEVKGK-KDENNRLEKE-----HKNQDDLLKEKETLIQQLKEELQEK 65

Query: 595 LTLEFKIREEVT-----QEFTQYWAQREADFKE--TLLQEREILEENAERRLAIFKDLVG 647
+TL+ +I+ V E TQ +A KE T+L+ +++ E + +L +D++
Sbjct: 66 VTLDVQIQHVVEGKRALSELTOGVTCYKAKIKELETILETQKV-ERSHSAKLE--QDILE 122

Query: 648 KCDT---REEAAKDICATKVETEEATACLELKFNQIKAEAKTKGELIKTKEELKKRENE 704
K E K+ ++ + T L +K ++K E+ + L K L+ +E E
Sbjct: 123 KESIILKLERNLKEFQEHLDQSVKNTKDLNVKELKLKEEITQLTNLQDMKHLQLKEEE 182

Query: 705 SDSLIQELETSSNKKIITQNRIKELINIIDQKEDTINEFQNLKSHMENTFKCNDKADTSS 764
++ QE-E +++ + R + L + +KE+ + + + + K K + S
Sbjct: 183 EETNRQETEKLEELSASSARTQNLKADLQRKEEDYADLKEKLTDAKKQIKQVQK-EVSV 241

Query: 765 LIINNKLICNETVEVPKDSKSKICSERKRVNENELQODEPPAKKGSIHVSSAITEDQKKS 824
+ +KL+ + E+ K K CS+ + + +QQ+ + V AI + ++
Sbjct: 242 MRDEDKLLRIKINELEK--KKNQCSQELDMKORTIQQQLKEQLNNQK--VEEAIQYERAC 297

Query: 825 EEVRPNIAEIEDIRVLQENNEGLRAFLLLTIENELKNEKEEKAELNKQIVHFQOELSLSEK 884
+++ IED+R+ E E + + + L+ + EE L ++ +++ + E
Sbjct: 298 KDLNVKEKIIEDMRMTLEEQEQTQ--VEQDQVLEAKLEEVERLATELEKWKKECNDLET 354

Query: 885 KNLTLSEKVEQQIQSNYDIAIAELHVQSKNQEQEEKIMKLSNE-IETATRSITN-----N 938
KN S + + ++N D+ + +L + + QE E+K + +E IT N
Sbjct: 355 KNNQRSNK--EHENNTDV-LGKLTNLQDELQSEQKYNADRRKKWLEEKMLITQAKEAEN 411

Query: 939 VSQIKLMHTKIDELRTLDSVSQISNIDL-LNLRD--LSNGSEEDNLPNTQLDLLGNDYLV 995
+ ++ D R +++ + L +D L EE + L++ +
Sbjct: 412 IRNKEMKKYAEADRERFFKQNEIMEILTAQLTEKSDQLQKWEERDQLVAALEIQLKALIS 471

Query: 996 SKQVKEYRIQEPNRENSFHSSIEA-IWE-ECKEIVKASSKSHQIEELEQQIEKLQAEVK 1053
S K+ I++ R S S IE I + + K I A K Q E L E + +++
Sbjct: 472 SNVQKDNEIEQLKRIISETSKIETQIMDIKPKRISSADPKL-QTEPLSTSFEISRKIE 530

Query: 1054 GYKDENNRLKEKEHKNQDDLLKEK-----TLIQQLEELQEKNVTLQVQIQHVVEGKRA 1108
+ + +Q + E T+Q K ++ T V ++ KR
Sbjct: 531 DGSVVLDSCEVSTENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPKARKRK 590

Query: 1109 LSELTQG-VTCYKAKIKELETILETQ-KVERSHSAKLEQDILEKES 1152
+E+ + V C K T L+ +R+ S K EQ + + S
Sbjct: 591 SMEEDLVKCNKKNATPRTNLKFPISDDRNSSVKKEQKVAIRPS 636

Score = 143 (21.5 bits), Expect = 1.3e-05, P = 1.3e-05
Identities = 164/684 (23%), Positives = 304/684 (44%)

Query: 295 QKRKMLR-LSQDVKGYSFIKDLQWIOVSDSKEAYRLLKLGIKHQSVAFTKLNNASS---- 349
+K +++ L +++ + D+Q V + K A L G+ +L
Sbjct: 49 EKETLIQQLKEELQEKNVTLQVQIQHVVEGKRALSELTOGVTCYKAKIKELETILETQKV 108

Query: 350 -RSHSI-FTVKILQIEDSEMSRVIRVSELSLCLAGSERTMKTQNEGE-RLRETGNINTS 406
RSHS IL+ E + + E L S + K N E +L+E T+
Sbjct: 109 ERSHSAKLEQDILEKESIILKLERNLKEFQE-HLQDSVKNTKDLNVKELKLKEEITQLTN 167

Query: 407 LLTLGKICINVLNKSSEKSKFQHVFPRESKLTHTYFQSFFNGKGIKIMIVNISQCYLAYDET 466
L K + LK E+ +Q + +L+ N K + + Y E
Sbjct: 168 LQDMKHLQLKEEEETNRQETEKLEELSASSARTQNLKADL---QRKEEDYADLKEK 224

Query: 467 LNVLFKFSIAIAQKVCVPDTLNSSQDKLFGPVKSSQDVSLDSNSNKKILNVKRATISWENSL 526
L K I Q V ++ +DKL +K ++ + N S+ L++K+ TI
Sbjct: 225 LTDAK-KQIKQ-VQKEVSVMRDEDKLLR-IKINE-LEKKKNQCSQELDMKORTIQQLEKQ 280

Query: 527 EDLMEDEDLVEELENAEETQNVETKLLDEDLTKLEENKAFISHEEKRKLLDL-IEDLKK 585
+ + E+ +++ E A + NV+ K++ ED+ TLEE + + E+ ++L+ +E++++
Sbjct: 281 LNNQVVEEAIQYERACKDLNVKEKII-EDMRMTLEEQEQTQ--TQVEQDQVLEAKLEEVER 337

Query: 586 KLIN-EK-KEKLT-LEFKIREEVTQEFTQYWAQREADFKE--TLLQEREILEE-----NAERR 638
EK KEK LE K + +E + K T LQ+ E+ E NA+R+
Sbjct: 338 LATELEKWKKECNDLETKNNQRSNKEHEN--NTDVLGKLTNLQD-ELQSEQKYNADRK 393

Query: 639 LAIFKDLVGKCDTREAAKDICATKVETEEATACLELKFNQIKAEAKTKGELIKTKEEL 698
+ + ++ T+ + A++I K E ++ E F Q + E+ +L + +L
Sbjct: 394 KWLEEKMM--LITQAKEAENI-RNK-EMKKYAEADRERFFKQ-QNEMEILTAQLTEKSDL 448

Query: 699 KKRENESDSLIQELETSSNKKIITQN-QR---IKELINIIDQKEDTINEFQNLKSHMENTF 754
+K E D L+ LE K +I+ N Q+ I++L II + + ++K ++

Sbjct: 449 QKWREERDQLVAALIEIQLKALISSNVQKDNEIEQLKRIISETSKIETQIMDIKPKRISSA 508

Query: 755 KCNDKADTSSLIINNKLICN--ETVEVPKDSKSKICSERK---RVNENELQ-QDEF--PA 806
DK T L + ++ N E V DS ++ +E R + EL+ Q P P

Sbjct: 509 D-PDKLQTEPLSTSFEISRNKIEDGSVVLDS-CEVSTENDQSTRFPKPELEIQFTPLQPN 566

Query: 807 KKGSIH--VSSAITEDQKKSEEVPRNIAEIEDIRVLQENNEGLRA---FLLTIENELKNE 861
K H ++ +T K+ + + N E + ++ + N R F ++ + +

Sbjct: 567 KMAVKHPGCTTPVTVKIPKARKRKSNEEEDLVKCNKKNATPRTNLKFPISDDRNSSVK 626

Query: 862 KEEKAEL---NKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQKSKNQEQE 918
KE+K + +K+ + + S+ NL K+ +Q D + +SK ++

Sbjct: 627 KEQKVAIRPSSKKTYSLSQASIIGV-NLATKKKEGTLQKFGDFLQHSFSLQSKAKKII 685

Query: 919 EKIM--KLSNEIETATRSITNNVSQIKLMHTKI--DELRT-LDSVSQISNID 965
E + KLSN +E + NVSQ K K+ E+ + +D Q+ +D

Sbjct: 686 ETMSSSKLSN-VEASKE----NVSQPKRAKRKLYTSEISSPIDISGVILMD 732

Score = 133 (20.0 bits), Expect = 1.6e-04, P = 1.6e-04
Identities = 94/426 (22%), Positives = 188/426 (44%)

Query: 527 EDLM-EDEDLVEELENAEETQNVETKLLDEDLDKTLLENKAFISHEEKRLKLLDL-IEDLK 584
+DL+ E E L+++L+ + +NV LD + +E +A + I++L+

Sbjct: 44 DDLKKEKETLIQQLKEELQEKNV---LDVQIQHVVEGKRALSELQTQGVTCYKAKIKELE 100

Query: 585 KKLINKEKLEKTLFEKIREEVTVQ-EFTQYWAQREA-DFKETLLQEREILEENAERRLAIF 642
L +K E+ + K+ ++++ E +R +F+E L + ++ +L +

Sbjct: 101 TLETKQKVER-SHSAKLEQDILEKESIILKLERNLKEFQEHLDQSVKNTKDLNVKELKL- 158

Query: 643 KDLVGKCDTREEAAKDICKATKVETEEATACLELKFNIKAELAKTKGELIKTKEELKKRE 702
K+ + + + K + K E EE + ++K EL+ + K +L+++E

Sbjct: 159 KEEITQLTNNLQDMKHLQLKEEEETN---RQETEKLEELSASSARTQNLKADLQRKE 215

Query: 703 NESDSLQIELETSNKKIITQNRRIKELINIIDQK-EDTINEFQNLKSHMENTFKCNDKA- 760
+ L ++L T KK I Q Q+ ++ D+ INE + K+ +

Sbjct: 216 EDYADLKEKL-TDAKKQIKQVQKEVSVMRDEKLLRIKINELEKKNQCSQELDMKQRTI 274

Query: 761 DTSSLIINNKLICNETVE----VPKDS--KSKICSE-RKRVNENE---LQDEPPAKKGS 810
+NN+ + E ++ KD K KI + R + E E ++QD+ K

Sbjct: 275 QQLKEQLNNQKV-EEAIQYERACKDLNVKEKIIEDMRMTLEEQEQTQVEQDQVLEAKLE 333

Query: 811 IHVSSAITEDQKKSEEVPR-NIAEIEDIRVLQENNEGLRAFLLLTIENELKNEKEEKAELN 869
V TE +K E+ + ENN + L +++EL+ E E+K +

Sbjct: 334 -EVERLATELEKWKECNDLETNNQRNSKEHENNTDVLGKLTNLQDELQ-ESEQYNAD 391

Query: 870 KQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQKSKNQEEKIMKLSNEIE 929
++ ++++ L +T +KE + I++ + K E E+ K NE+E

Sbjct: 392 RK-KWLEEKMMML-----ITQAKEAENIRNK-----EMKKYAEDRERFFKQQNEME 435

Query: 930 TATRSITNNVSQIKLMHTKIDEL 952
T +T S ++ + D+L

Sbjct: 436 ILTAQLTEKDSDLQKWREERDQL 458

Pedant information for DKFZphtes3_35b4, frame 3

Report for DKFZphtes3_35b4.3

[LENGTH] 1780
[MW] 206176.77
[pI] 5.60
[HOMOL] TREMBL:U93121_1 product: "M-phase phosphoprotein-1"; Human M-phase phosphoprotein-1 mRNA, partial cds. 0.0
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YEL061c] 2e-37
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YEL061c] 2e-37
[FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YEL061c] 2e-37
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YEL061c] 2e-37
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 7e-30
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 7e-30
[FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YPR141c] 3e-23
[FUNCAT] 11.01 stress response [S. cerevisiae, YPR141c] 3e-23
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YPR141c] 3e-23
[FUNCAT] 03.13 meiosis [S. cerevisiae, YPR141c] 3e-23
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR141c] 3e-23
[FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YPR141c] 3e-23
[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 1e-21

[FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR309c] 6e-20
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YHR023w
 MYO1 - myosin-1 isoform] 4e-19
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 4e-19
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 1e-15
 [FUNCAT] 1 genome replication, transcription, recombination and repair [M.
 jannaschii, MJ1322] 2e-14
 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 2e-09
 [FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae, YKL179c] 3e-09
 [FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YLR086w] 2e-07
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YNL079c] 2e-07
 [FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL079c]
 2e-07
 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YGL086w] 1e-06
 [FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YHR158c]
 3e-06
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YDR217c] 4e-06
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR134c] 2e-05
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae,
 YAL035w] 2e-04
 [FUNCAT] r general function prediction [M. jannaschii, MJ1254] 0.001
 [BLOCKS] BL00387A
 [BLOCKS] BL00411H
 [BLOCKS] BL00411G
 [BLOCKS] BL00411F
 [BLOCKS] BL00411E Kinesin motor domain proteins
 [BLOCKS] BL00411D Kinesin motor domain proteins
 [BLOCKS] BL00411C Kinesin motor domain proteins
 [BLOCKS] BL00411B Kinesin motor domain proteins
 [BLOCKS] BL00411A Kinesin motor domain proteins
 [SCOP] d2kin.1 3.29.1.5.3 Kinesin [Rat (Rattus norvegicus) 2e-68
 [SCOP] d2tmab_1.105.4.1.1 Tropomyosin [rabbit (Oryctolagus cuniculus) 4e-05
 [SCOP] d3kar_3.29.1.5.4 Kinesin [Baker's yeast (Saccharomyce 2e-09
 [EC] 3.6.1.32 Myosin ATPase 5e-25
 [PIRKW] nucleus 4e-27
 [PIRKW] phosphotransferase 3e-16
 [PIRKW] duplication 6e-20
 [PIRKW] citrulline 6e-18
 [PIRKW] tandem repeat 4e-24
 [PIRKW] heterodimer 3e-28
 [PIRKW] endocytosis 1e-23
 [PIRKW] heart 1e-17
 [PIRKW] transmembrane protein 2e-28
 [PIRKW] serine/threonine-specific protein kinase 3e-16
 [PIRKW] zinc finger 1e-23
 [PIRKW] surface antigen 2e-16
 [PIRKW] DNA binding 1e-25
 [PIRKW] metal binding 1e-23
 [PIRKW] muscle contraction 4e-24
 [PIRKW] heterotetramer 4e-24
 [PIRKW] acetylated amino end 2e-19
 [PIRKW] actin binding 5e-25
 [PIRKW] mitosis 3e-58
 [PIRKW] microtubule binding 3e-58
 [PIRKW] ATP 3e-58
 [PIRKW] thick filament 4e-24
 [PIRKW] phosphoprotein 9e-29
 [PIRKW] leucine zipper 1e-12
 [PIRKW] skeletal muscle 8e-24
 [PIRKW] disulfide bond 1e-12
 [PIRKW] heterotrimer 1e-29
 [PIRKW] calcium binding 6e-18
 [PIRKW] alternative splicing 4e-21
 [PIRKW] P-loop 2e-63
 [PIRKW] coiled coil 3e-58
 [PIRKW] heptad repeat 1e-25
 [PIRKW] methylated amino acid 4e-24
 [PIRKW] peripheral membrane protein 1e-23
 [PIRKW] dimer 1e-12
 [PIRKW] cardiac muscle 1e-17
 [PIRKW] hydrolase 5e-25
 [PIRKW] microtubule 6e-15
 [PIRKW] muscle 7e-23
 [PIRKW] membrane protein 6e-20
 [PIRKW] GTP binding 8e-22
 [PIRKW] EF hand 6e-18
 [PIRKW] cell division 1e-25
 [PIRKW] cytoskeleton 4e-24
 [PIRKW] hair 6e-18
 [PIRKW] Golgi apparatus 8e-24
 [PIRKW] calmodulin binding 1e-23

[SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 3e-16
 [SUPFAM] myosin motor domain homology 5e-25
 [SUPFAM] alpha-actinin actin-binding domain homology 1e-13
 [SUPFAM] kinesin-related protein KIP1 9e-27
 [SUPFAM] kinesin-related protein CIN8 4e-36
 [SUPFAM] kinesin heavy chain 4e-24
 [SUPFAM] plectin 1e-13
 [SUPFAM] trichohyalin 6e-18
 [SUPFAM] kinesin-related protein KIF3 1e-29
 [SUPFAM] kinesin-related protein KIF2 3e-20
 [SUPFAM] ribosomal protein S10 homology 1e-13
 [SUPFAM] giantin 8e-24
 [SUPFAM] protein kinase homology 3e-16
 [SUPFAM] protein kinase C zinc-binding repeat homology 2e-13
 [SUPFAM] kinesin-related protein unc-104 8e-26
 [SUPFAM] human early endosome antigen 1 1e-23
 [SUPFAM] unassigned kinesin-related proteins 1e-28
 [SUPFAM] Mycoplasma genitalium hypothetical protein MG218 4e-17
 [SUPFAM] myosin heavy chain 5e-25
 [SUPFAM] conserved hypothetical P115 protein 4e-20
 [SUPFAM] centromere protein E 5e-24
 [SUPFAM] calmodulin repeat homology 6e-18
 [SUPFAM] kinesin-related protein KLP61F 1e-25
 [SUPFAM] hypothetical protein MJ0914 3e-12
 [SUPFAM] kinesin-related protein MKLP-1 2e-63
 [SUPFAM] pleckstrin repeat homology 8e-26
 [SUPFAM] hypothetical protein MJ1322 4e-13
 [SUPFAM] kinesin-related protein KIF1B 3e-28
 [SUPFAM] kinesin motor domain homology 2e-63
 [SUPFAM] kinesin-related protein KLPA 7e-25
 [SUPFAM] kinesin-related protein nodA 1e-12
 [SUPFAM] kinesin-related protein Eg5 5e-30
 [PROSITE] ATP_GTP_A 1
 [PFAM] Kinesin motor domain
 [KW] Irregular
 [KW] 3D
 [KW] LOW_COMPLEXITY 7.53 %
 [KW] COILED_COIL 19.78 %

SEQ MESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLSHEFSLVAPNTEANSFESKDYLO
 SEG
 COILS
 3kar-
 SEQ VCLRIRPFTQSEKELESEGCVHILDSQTVVLKEPQCILGRLSEKSSGQMAQKFSFSKVFG
 SEG
 COILS
 3kar-
 SEQ PATTQKEFFQGCIMQPVKDLLKGQSRILIFTYGLTNSGKTYTFQGTEENIGILPRTLNVLF
 SEG
 COILS
 3kar-
 SEQ DSLQERLYTKMNLKPHRSREYLRLSSEQEKEEIASKSALLRQIKEVTVHNDSDDTLYGSL
 SEG
 COILS
 3kar-
 SEQ TNSLNISEFEESIKDYEQANLNMANSIKFSVWVSFFEYNEYIYDLFVPVSSKFQKRKML
 SEG
 COILS
 3kar-EEEEEEEEETTEEEETTTCC-----CCEE
 SEQ RLSQDVRGYSFIKDLQWVSDSKEAYRLKLGKHSVAFTKLNNASSRSHSIFTVKIL
 SEG
 COILS
 3kar- EEETTTTE-EEETTCCEEECCGGGHHHHHHHHHHHCCTTTTCHHHHHHCEEEEEEEEE
 SEQ QIEDSEMSRVIRVSELSLCDLAGSERTMKTQNEGERLRETGNINTSLTLGKCINVLKNS
 SEG
 COILS
 3kar- E--EETTTTCEEEEEEEEEEECCCCC---CCCHHHHHHHHHHHHHHHHHHHHHHTT
 SEQ EKSQFQQHVPFRESKLTHYFQSFFNGKGKICMIVNISQCYLAYDETLNVLKFSIAIAQKVC
 SEG
 COILS
 3kar- TTTT--TCCTTTTTHHHHHHGGGCTTTTEEEEEEECCCGGHHHHHHHHHHHH.....
 SEQ VPDTLNSSQDKLFGPVKSSQDVSLDSNSKILNVKRATISWENSLEDLMEDEDLVEELE

SEGXXXXXXXXXXXXXXXXXXXX
COILS
3kar-

SEQ NAEETQNVETKLLDEDLDTLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFK
SEGXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXXXXXXXXX
COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
3kar-

SEQ IREEVTQEFQYWAQREADFKETLLQEREILEENAERRLAIFKDLVGKCDTREEAAKDIC
SEG
COILS CCCCCC.....
3kar-

SEQ ATKVETEEATACLELKFNQIKAEAKTKGELIKTKEELKKRENESDSLIELETSNKKII
SEG
COILSCCCCCCCCCCCCCCCC
3kar-

SEQ TQNQRIKELINIIDQKEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEVP
SEG
COILS CCCCCCCCCCCCCC.....
3kar-

SEQ KDSKSKICSERKRVNENELQODEPPAKKGSIHVSSAITEDQKKSEEVPRNIAEIEDIRVL
SEG
COILSCCCC
3kar-

SEQ QENNEGLRAFLTIENELKNEKEEKAEELNKQIVHFQOELSLSEKKNLTLSKEVQQIQSNY
SEGXXXXXXXXXXXXXXXXXXXX.....
COILS CC.....
3kar-

SEQ DIAIAELHVQSKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTLDSVSQ
SEG
COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
3kar-

SEQ ISNIDLLNLRDLSNGSEEDNLPNTQLDLLGNDYLVSKQVKEYRIQEPNRENSFHSSIEAI
SEG
COILS
3kar-

SEQ WEECKEIVKASSKSHQIEELEQQIEKLQAEVKGKIDENNRLKEKEHKNQDDLLKEKETL
SEGXXXXXXXXXXXXXXXXXXXX.....
COILSCCC.....
3kar-

SEQ IQQLKEELQEKNVTLQVQIQHVVEGKRALSELTOGVTCYKAKIKELETILETQKVERSHS
SEG
COILSCCC.....
3kar-

SEQ AKLEQDILEKESIILKLERNLKEFQEHLDQSVKNTKDLNVKELKLEETQLTNNLQDMK
SEG
COILS CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
3kar-

SEQ HLLQLKEEEEETNRQETELKEELSASSARTQNLKADLQREEDYADLKEKLTDAKKQIK
SEGXXXXXXXXXXXXXXXXXXXX.....
COILS CCCCC.....CCC
3kar-

SEQ QVQKEVSMRDEDKLLRIKINELEKKKNQCSQELDMKQRTIQQLKEQLNNQKVEEAIQQY
SEG
COILS CCCCCCCCCC.....
3kar-

SEQ ERACKDLNVKEKIIEDMRMTLEEQEQTQVEQDQVLEAKLEEVERLATELEKWKKEKNDLE
SEGXXXXXXXXXXXXXXXXXXXX.....
COILSCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
3kar-

SEQ TKNNQRSNKEHENNTDVLGKLTNLQDELQEQKYNADRKKWLEEKMLITQAKEAENIR
SEG
COILS CC.....
3kar-

SEQ NKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWREERDQLVAALEIQLKALISSN
SEG

```

COILS .....
3kar- .....

SEQ      VQKDNEIEQLKRIISETSKIETQIMDIKPKRISSADPKLQTEPLSTSFEISRNKIEDGS
SEG      .....
COILS    .....
3kar-    .....

SEQ      VVLDSCEVSTENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVEIPKARKRKSNE
SEG      .....
COILS    .....
3kar-    .....

SEQ      MEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQKVAIRPSSKKTYSLSQASIIGVN
SEG      .....
COILS    .....
3kar-    .....

SEQ      LATKKKEGTLQKFGDFLQHSPLQSKAKKI IETMSSSKLSNVEASKENVSQPKRAKRL
SEG      .....
COILS    .....
3kar-    .....

SEQ      YTSEISSPIDISGQVILMDQKMKESDHQIIKRRRLRTKTAK
SEG      .....
COILS    .....
3kar-    .....

```

Prosites for DKFZphtes3_35b4.3

PS00017 152->160 ATP_GTP_A PDOC00017

Pfam for DKFZphtes3_35b4.3

```

HMM_NAME      Kinesin motor domain

HMM            *RCRPlNeReindgcscvVQWPpwtGykthvnhghegds.....phks
               R+RP+ + E++ + +V + +++ ++ +
Query          64  RIRPFTQSEKELESEGCvHILDSQTvVLKEPQCILGRLEKSSGQMAQK 112

HMM            FtFDHVFwWncTQedvYdtvAHPiVDDcFhGYNCTIFAYGOTGSGKTYTM
               F+F +VF++++TQ++ +++ + V+D+++G IF+YG T SGKTYT
Query          113 FSFSKVFGPATtQKEFFQGCIMQPVKDLLKGQSRlIFTYGLTNSGKTYTF 162

HMM            MGpggehPDHmGIIPRcCHDIFdrIdkfgekDhdFW.....
               G +++GI+PR+++ +FD++ + +++
Query          163 QG---TEENIGILPRTLNVLFDSLQERL-YTKMNLKPHRSREYLRLSSE 207

HMM            .....
Query          208 QEKEEIASKSALLRQIkeVTVHNDSDDTLYGSLTNSLNISEFEESIKDYE 257

HMM            .....hvKCSYMEIYNEeIYDLLCPnF...qhMkpLnIHEHPN
               +V +S++EIYNE+IYDL +P++ Q++K L++ + +
Query          258 QANLNMANSIKFSVWVSFFeIYNEIYDLFVPVSSKFQKRKMLRLSQDVK 307

HMM            MGpYVqGCTEfHVCsYeDachWIWqGnknRHVAaTnMNdHSSRShtIFTI
               ++++++ V +A +++ +G K+ VA T++N SSRSH+IFT+
Query          308 GYSFIKDLQWlQVSDSKEAYRLKLGIKHQSVAFTKLNNASSRShtIFTV 357

HMM            HVeQrHk.qcdehvcHskMNLVDLAGSERvnrTGAEGQRlKEGcNINqSL
               ++ Q + + +++S ++L DLAGSER+ +T+ EG RL+E +NIN SL
Query          358 KILQIEDSEMSRVIRVSELSLCLAGSERTMKTQNEGERLRETGNINTSL 407

HMM            ttLGnVInaLaDgqTKYmYgghgHIPYRDSKLTWlLQDSLGGNcKTCMIA
               +TLG++IN+L + + + +H+P+R+SKLT+ +Q + G +K CMI+
Query          408 LTLGKCINVLKNSE---KSKFQQHVFPRESKLTHTYFQSFFNGKGKICMIV 454

HMM            CIWPadWNYEETLSTLRYAdRAKnlKnkPQINEDPca*
               +I+ + Y+ETL++L++ + A+++ + ++N+++++
Query          455 NISQCYLAYDETLNVLKFSAlAQKVCVPDTLNSSQDK 491

```

DKFZphtes3_35b5

group: metabolism

DKFZphtes3_35b5 encodes a novel 466 amino acid protein, with similarity to bovine accessory subunit for vacuolar ATPase and rat C7-1 protein.

The vacuolar proton-ATPase (V-ATPase) translocates protons into intracellular organelles or across the plasma membrane of specialized cells. The catalytic domain consists of a hexamer of 3 A subunits and 3 B subunits, plus accessory subunits C, D, and E. The rat homolog C7-1 seems to be enriched in aged adult rats in the frontal cortex.

The novel protein can find application in modulating the v-ATPase activity in endocytic and secretory organelles.

strong similarity to bovine vacuolar ATPase (EC 3.6.1.-) chain A

complete cDNA, complete cds potential start at Bp 8, EST hits matches perfect to I54197 hypothetical protein, but possess 186 aa additional at N-terminus

Sequenced by DKFZ

Locus: unknown

Insert length: 2043 bp

Poly A stretch at pos. 2033, polyadenylation signal at pos. 2012

```
1  GCGCGCCATG GCGACGGCTC GAGTGC GGCGG GGGGCCGCGG TCGCGCCAGG
51 CGCTCTGGCG CATGCCGTGG CTGCCGGTGT TTTGTGCGTT GCGCGCGGCG
101 GCGCGCGCGG CAGCGGCGGA GCAGCAGGTC CCGCTGGTGC TGTGGTCGAG
151 TGACCGGGAC TTGTGGGCTC CTGCGGCCGA CACTCATGAA GGCCACATCA
201 CCAGCGACTT GCAGCTCTCT ACCTACTTAG ATCCCGCCCT GGAGCTGGGT
251 CCCAGGAATG TGCTGCTGTT CCTGCAGGAC AAGCTGAGCA TTGAGGATTT
301 CACAGCATAT GGCGGTGTGT TTGGAACAA GCAGGACAGC GCCTTTTCTA
351 ACCTAGAGAA TGCCCTGGAC CTGGCCCCCT CCTCACTGGT GCTTCCTGCC
401 CTCGACTGGT ATGCAGTCAG CACTCTGACC ACTTACCTGC AGGAGAAGCT
451 CGGGGCCAGC CCCTTGCATG TGGACCTGGC CACCCTGCGG GAGCTGAAGC
501 TCAATGCCAG CTTCCCTGCT CTGCTGTCTA TTCGCCTGCC CTACACAGCC
551 AGCTCTGGTG TGATGGCACC CAGGGAAGTC CTCACAGGCA ACGATGAGGT
601 CATCGGGCAG GTCCTGAGCA CACTCAAGTC CGAAGATGTC CCATACACAG
651 CGGCCCTCAC AGCGGTCCGC CCTTCCAGGG TGGCCCCGTA TGTAGCCGTG
701 GTGGCCCGAG GGCTAGGTCG CCAGCTGCTA CAAAAACAGC CAGTATCACC
751 TGTGATCCAT CCTCCTGTGA GTTACAATGA CACCGCTCCC CGGATCCTGT
801 TCTGGGCCCA AAACCTTCTT GTGGCGTACA AGGACCAGTG GGAGGACCTG
851 ACTCCCCTCA CCTTTGGGGT GCAGGAACTC AACCTGACTG GCTCCTTCTG
901 GAATGACTCC TTGCGCAGGC TCTCACTGAC CTATGAACGA CTCCTTGGTA
951 CCACAGTGAC ATTCAAGTTC ATTCTGGCCA ACCGCCTCTA CCCAGTGTCT
1001 GCGCGGCACT GGTTTACCAT GGAGCGCCTC GAAGTCCACA GCAATGGCTC
1051 CGTCGCCTAC TTCAATGCTT CCCAGGTAC AGGGCCAGC ATCTACTCCT
1101 TCCACTGCGA GTATGTCAGC AGCCTGAGCA AGAAGCGTAG TCTCCTCGTG
1151 GCGCGCACGC AGCCCTCTCC CTGGCAGATG ATGCTTCAGG ACTTCCAGAT
1201 CCAGGCTTTC AACGTAATGG GGGAGCAGTT CTCCTACGCC AGCGACTGTG
1251 CCAGCTTCTT CTCCCCCGGC ATCTGGATGG GGCTGCTCAC CTCCCTGTTC
1301 ATGCTCTTCA TCTTCACCTA TGGCCTGCAC ATGATCCTCA GCCTCAAGAC
1351 CATGGATCGC TTGATGACC ACAAGGGCCC CACTATTTCT TTGACCCAGA
1401 TTGTGTGACC CTGTGCCAGT GGGGGGGTTG AGGCTGGGAC GGTGTCCGTG
1451 TTGTTGCTTT CCCACCCTGC AGCGCACTGG ACTGAAGAGC TTCCCTCTTC
1501 CTA CTGTCAGC ATGAAGTGA AGCTCCCCTC AGCCCATCTT GCTCCCTCTT
1551 CAGCCCCCTG AGGAGCTTTC TTGGGCTGCC CCCATCTCTC CCAACAAGGT
1601 GTACATATTC TGCGTAGATG CTAGACCAAC CAGCTTCCCA GGGTTCGTCG
1651 CTGTGAGGCG TAAGGGACAT GAATTCTAGG GTCTCCTTTC TCCTTATTTA
1701 TTCTTGTGGC TACATCATCC CTGGCTGTGG ATAGTGCTTT TGTGTAGCAA
1751 ATGCTCCCTC CTTAAGGTTA TAGGGCTCCC TGAGTTTGGG AGTGTGGAAG
1801 TACTACTTAA CTGTCTGTCC TGCTTGGCTG CCGTTATCGT TTTCTGGTGA
1851 TGTTGTGCTA ACAATAAGAA GTACACGGGT TTATTCTGTG GGCCTGAGAA
1901 GGAAGGGACC TCCACGACAG GTGGGCTGGG TGCGATCGCC GGCCTGTTTG
1951 CATGTTCCCA CCGGAGTGC CCGGCAGGAG CATGGGCTGC TTGCTTCTTT
2001 CCTTCCTAAT AAAATAAAGC CGGGTCGCCA TGCAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

95014142:
A novel accessory subunit for vacuolar H(+)-ATPase from chromaffin granules.

97215246:
Identification of a rat brain gene associated with aging by PCR differential display method.

Peptide information for frame 2

ORF from 8 bp to 1405 bp; peptide length: 466
Category: strong similarity to known protein

```

1 MATARVRMGP RCAQALWRMP WLPVFLSLAA AAAAAAAEQQ VPLVLWSSDR
51 DLWAPAADTH EGHITSDLQL STYLDPALEL GPRNVLLFLQ DKLSIEDFTA
101 YGGVFGNKQD SAFSNLENAL DLAPSSLVLP AVDWYAVSTL TTYLQEKLGA
151 SPLHVDLATL RELKLNASLP ALLLIRLPYT ASSGLMAPRE VLTGNDEVIG
201 QVLSTLKSED VPYTAALTAV RPSRVARDVA VVAGGLGRQL LQKQPVSPVI
251 HPPVSYNDTA PRILFWAQN FSVAYKDQWED LTPLTFGVQE LNLTGSFWND
301 SFARLSLTYE RLFGTTVTFK FILANRLYPV SARHWFTMER LEVHSNGSVA
351 YFNASQVTGP SIYSFHCEYV SLSKKGSL L VARTQSPWQ MMLQDFQIQA
401 FNMVGEQFSY ASDCASFFSP GIWMGLLTSL FMLFIFTYGL HMILSLKTMD
451 RFDDHKGPTI SLTQIV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35b5, frame 2

TREMBL:AF035387_1 gene: "C7-1"; product: "C7-1 protein"; Rattus norvegicus C7-1 protein (C7-1) mRNA, complete cds., N = 1, Score = 2088, P = 3.8e-216

PIR:A55116 vacuolar ATPase (EC 3.6.1.-) chain Ac45 - bovine, N = 1, Score = 2011, P = 5.5e-208

PIR:I54197 hypothetical protein - human, N = 1, Score = 1464, P = 5.1e-150

>TREMBL:AF035387_1 gene: "C7-1"; product: "C7-1 protein"; Rattus norvegicus C7-1 protein (C7-1) mRNA, complete cds.
Length = 463

HSPs:

Score = 2088 (313.3 bits), Expect = 3.8e-216, P = 3.8e-216
Identities = 408/463 (88%), Positives = 426/463 (92%)

```

Query:      4 ARVRMGPRCAQALWRMPWLPVFLSLAAAAAAAEQQVPLVLWSSDRDLWAPAADTHEGH 63
             +R+R G R A  LW      + LSL A AAA AAEQQVPLVLWSSDRDLWAP ADTHEGH
Sbjct:      8 SRIRGTWRWAPVLW-----LLLSIVAVAAVAAAEQQVPLVLWSSDRDLWAPVADTHEGH 61

Query:     64 ITSDLQLSTYLDPALELGPRNVLLFLQDKLSIEDFTAYGGVFGNKQDSAFSNLENALDLA 123
             ITSD+QLSTYLDPALELGPRNVLLFLQDKLSIEDFTAYGGVFGNKQDSAFSNLENALDLA
Sbjct:     62 ITSDMQLSTYLDPALELGPRNVLLFLQDKLSIEDFTAYGGVFGNKQDSAFSNLENALDLA 121

Query:    124 PSSLVLPVADWYAVSTLT TTYLQEKLGASPLHVDLATLRELKLNASLPALLLIRLPYTASS 183
             PSSLVLPVADWYA+STLT TTYLQEKLGASPLHVDLATL+ELKLNASLPALLLIRLPYTASS
Sbjct:    122 PSSLVLPVADWYAISTLT TTYLQEKLGASPLHVDLATLKEKLNASLPALLLIRLPYTASS 181

Query:    184 GLMAPREVL TGNDEVIGQVLSTLKSEDV P YTAALTAVRPSRVARDVAVVAGGLGRQLLQK 243
             GLMAPREVL TGNDEVIGQVLSTL+SEDPYTAALTAVRPSRVARDVA+VAGGLGRQLLQ
Sbjct:    182 GLMAPREVL TGNDEVIGQVLSTLESEDPYTAALTAVRPSRVARDVAMVAGGLGRQLLQT 241

Query:    244 QPVSPVIHPPVSYNDTAPRILFWAQNFSVAYKDQWEDLTPLTFGVQELNLTGSFWNDSFA 303
             Q SP IHPVSYNDTAPRILFWAQNFSVAYKD+W+DLT LTFGV+ LNLTGSFWNDSFA
Sbjct:    242 QVASPAIHPPVSYNDTAPRILFWAQNFSVAYKDEWKDLSLTFTGVENLNLTGSFWNDSFA 301

Query:    304 RLSLTYERLFGTTVTTFKFILANRLYPVSARHWFTMERLEVHSNGSVAYFNASQVTGPSIY 363
             LSLTYE LFG TVTFKFILA+R YPVSAR+WFTMERLE+HSNGSVA+FN SQVTGPSIY

```

Pedant information for DKFZphtes3_35b5, frame 2

Report for DKFZphtes3 35b5.2

```
SEQ      GIWMGLLTSLFLMFIIFTYGLHMILSLKTMDFDDHKGPTISLQIV
SEG      .
PRD      cccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccceeeccc
MEM      mmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmm
```

Prosite for DKFZphtes3_35b5.2

832

PS00001	292->296	ASN_GLYCOSYLATION	PDOC00001
PS00001	299->303	ASN_GLYCOSYLATION	PDOC00001
PS00001	346->350	ASN_GLYCOSYLATION	PDOC00001
PS00001	353->357	ASN_GLYCOSYLATION	PDOC00001
PS00004	375->379	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	3->6	PKC_PHOSPHO_SITE	PDOC00005
PS00005	48->51	PKC_PHOSPHO_SITE	PDOC00005
PS00005	159->162	PKC_PHOSPHO_SITE	PDOC00005
PS00005	205->208	PKC_PHOSPHO_SITE	PDOC00005
PS00005	318->321	PKC_PHOSPHO_SITE	PDOC00005
PS00005	331->334	PKC_PHOSPHO_SITE	PDOC00005
PS00005	374->377	PKC_PHOSPHO_SITE	PDOC00005
PS00005	445->448	PKC_PHOSPHO_SITE	PDOC00005
PS00006	48->52	CK2_PHOSPHO_SITE	PDOC00006
PS00006	72->76	CK2_PHOSPHO_SITE	PDOC00006
PS00006	94->98	CK2_PHOSPHO_SITE	PDOC00006
PS00006	114->118	CK2_PHOSPHO_SITE	PDOC00006
PS00006	159->163	CK2_PHOSPHO_SITE	PDOC00006
PS00006	193->197	CK2_PHOSPHO_SITE	PDOC00006
PS00006	255->259	CK2_PHOSPHO_SITE	PDOC00006
PS00007	207->214	TYR_PHOSPHO_SITE	PDOC00007
PS00008	102->108	MYRISTYL	PDOC00008
PS00008	103->109	MYRISTYL	PDOC00008
PS00008	200->206	MYRISTYL	PDOC00008
PS00008	295->301	MYRISTYL	PDOC00008
PS00008	314->320	MYRISTYL	PDOC00008
PS00008	421->427	MYRISTYL	PDOC00008
PS00008	425->431	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_35b5.2)

DKFZphtes3_35e21

group: differentiation/development

DKFZphtes3_35e21.2 encodes a novel 104 amino acid putative interleukin precursor, related to interleukin-7.

Due to the close relationship to human interleukin-7, the novel interleukin is expected to act as a new growth factor for human B lineage cells. Additionally, the protein should induce the gene rearrangement of the T-cell receptor repertoire, leading to thymocyte commitment, and subsequently induce both cytotoxic T-cell- and lymphocyte-activated killer cells.

This new interleukin could find clinical application in a variety of conditions of hematolymphopietic failure and different tumours, because of its recruitment of B cell lineage cells, cytotoxic T-cell- and lymphocyte-activated killer cells.

similarity to interleukin-7 precursor

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 2095 bp

Poly A stretch at pos. 2085, polyadenylation signal at pos. 2067

```
1  GGATGAAAGT  GATTTAATTC  ATTTTATAGAA  TTTTCTTTT  GTTTTGTTT
51  AGCAACATGC  TGAACAACCTA  ATTTACTTTA  AAAATAAGCC  AGTTAAACA
101  AAGGACGCTA  AGCCCAAGTG  GGGGGCAATA  TTAGTCAGGA  TCTTTGGGGT
151  CTAATTCAG  ACCAAGCTTC  AGAAGCATT  CTTTGTCTCT  GTTCTCACCT
201  CTGCTGTCCC  TCTCTCCCT  CATCCCCTAA  GAGAGACAAA  GATAAAAGCC
251  CACCTGCATC  CCTAAGTCTT  ACTGAGATCA  GCCACCCAG  GGGAGAGAAA
301  CTGGATCTAC  TTACAGCCAC  CCCCTGTTTC  CATCCATATA  CTTACTTCCC
351  CCAATTTGCA  TGTGATTATG  GAAACAAGTC  ATGCTCATGA  AAGCAACTGT
401  AAAATAAAAG  GTTATGGAGT  AGTTCAGCAA  CTTCTTCACA  GCCAGCTTTG
451  TGGAGCTGGG  GAGGACTTAG  GGCCCATGG  AGTCTCTTAT  GTGTACAGCT
501  TCAGGGCTGT  CCCTTTCAGT  TTGATTTTAA  GCAATGCCTC  ACTTCATAGC
551  TTAGGGGGTA  AGGATTCCAT  TCAGGTAGGT  TGTCTAAAGG  AACTAATGGG
601  ACCTCTCAGT  GAATTAGCTG  ACCAGATTTT  AGGAAATCTT  TTTAATTTCT
651  ATGATTTTCC  TTCTCACATT  TTGAAATGGT  AAAATTGACT  GGAAATAATT
701  TTTCTTGGTG  CCTTATTGCT  TTTCTTGCA  AACCTTTCTC  ATATTTTCTC
751  ATGACCATTT  CCAGTGACCA  AGGCCCATGT  GTGTGTTGTG  TGTAAATTGTG
801  ATGACCATTT  CCAGTGACCA  AGGCCCATGT  GTGTGTTGTG  TGTAAATTGTG
851  ATTCATTAGG  CTGTTGCCTC  CTGGGCTGGA  GCTGCGCTAA  TCCTGACACC
901  GGCTGCCAGG  AGAAAACCTC  ATGGATCACA  CACCAAACCT  TAATAACAGC
951  ATCCGTGACC  TGCACCTCTC  AGTACAGAAT  GGGAAACCCCA  GAGCTAGGAA
1001  ATGTAGTTGT  ATATTTTAAT  GAACTGCTAC  CCCAGCCAAA  GAAGCTTCTT
1051  TCACCTTTGT  GCTCTACAGA  AAGCCCAAGG  GGGGTAGGAG  GGACAGAGCT
1101  TTGAATAACT  GCTTTCTAAC  ACTAAATGTG  GCCAACAGGA  CAGAGCACAT
1151  CACACGTATA  GGCAGGTGTG  AGGGACAGTG  GCTAAGAATT  GCCTGCTCCC
1201  TCTGCATGCT  CTTTCTTGT  TCCAAAGTCC  AATCAAGTGA  TCCTGGGAAA
1251  CAAATCTGTC  TGGATTGCGG  AGGGTGGTTC  TGAAAGAACT  GCCAAGACGT
1301  TAAAGAAGGG  TGAAGAGTAG  GCAGAATATA  AGTAGCTAAC  CTGAGTCAAG
1351  ACTCTCAAAA  GCTAGCAGCC  TGATGACAAT  AGGATTTATT  TCAGCCAGGA
1401  TAGTGTCTGT  CTGTGAGTGC  ATCATTTTAA  GACAGTATGA  CTTTATGTTG
1451  TTACAAACTA  TGTATAGTAT  GTATGTTTGT  TGGGTTGTAT  ATATACATAA
1501  TATATATTAT  ATATATATAT  GAGAGATTGT  GTGACTTTTG  ATACGGGTTT
1551  GGTGCAGGTG  AATTTATTAC  TGAGCCAAAT  GAGGCACATA  CCGAGTCAGT
1601  AGTTGAAGTC  CAGGGCATTC  GATACTGTTT  ATGATTTCCA  TATATGTATA
1651  GTGCCTATCC  CATGCTGTAG  TCACTGTTAT  GTTAAATCCA  GAAGTTACAC
1701  TAGAGCCAGC  GATACTTTAT  TTGTAGACAA  TCAATTTGAA  TCCATATGTT
1751  ATTACTGGCA  GATGATACAT  GATTACAGTT  CTGAATCTGT  AACACTTACA
1801  AAAGGAACCC  CAGAGCAGCT  TGATGAGTTT  TTGTTTCTGC  TTCGTTCTCG
1851  GGAGTCAGTA  GAAACAGCAG  TTGTATGTGG  TTATGTTAGT  CTCAAGATAC
1901  TTAATTTGTT  GACCTTACTT  CAGAAAAATT  TTGTATGTAT  TATATTTGTG
1951  GGAAGGTAAA  ATAATCATTT  GAGATTTTAA  TCAAATATGA  AGATTAGTTA
2001  TTTATGAAAA  ACAAAGAAAT  GTCTATTTTT  CTTTGTTCCT  AATTAATGTA
2051  GATAAATTTT  AAAATGCATT  AAAGTAATGG  TCCGGAAAAA  AAAAA
```

BLAST Results

No BLAST result

Medline entries

89098903:
Human interleukin 7: molecular cloning and growth factor
activity on human and murine B-lineage cells.

Peptide information for frame 2

ORF from 368 bp to 679 bp; peptide length: 104
Category: similarity to known protein

1 METSHAHESN CKIKGYGVVQ QLLHSQLCGA GEDLGPIGVS YVVSFRAVPF
51 SLILSNASLH SLGGKDSIQV GCLKELMGPL SELADQILGN LFNFDFFPSH
101 ILKW

BLASTP hits

Entry B32223 from database PIR:
interleukin-7 precursor (clone 1) - human
Score = 66, P = 7.0e-01, identities = 21/70, positives = 33/70

Alert BLASTP hits for DKFZphtes3_35e21, frame 2

PIR:B32223 interleukin-7 precursor (clone 1) - human, N = 1, Score =
66, P = 0.72

TREMBL:PADAL1_1 gene: "dall"; P.abies dall mRNA, N = 2, Score = 59, P
= 0.77

PIR:C32223 interleukin-7 precursor (clone 4) - human, N = 1, Score =
66, P = 0.79

TREMBL:PRU76726_1 gene: "PrMADS3"; product: "MADS-box protein"; Pinus
radiata MADS-box protein (PrMADS3) mRNA, complete cds., N = 2, Score =
59, P = 0.94

>PIR:B32223 interleukin-7 precursor (clone 1) - human
Length = 133

HSPs:

Score = 66 (9.9 bits), Expect = 1.3e+00, P = 7.2e-01
Identities = 21/68 (30%), Positives = 33/68 (48%)

Query: 39 VSYVVSFRAVPFSLIL-----SNASLHSLGGK--DSIQVGCLKELMGPLSELADQILGNL 91
VS+ Y F P L+L S+ + GK +S+ + +L+ + E+ L N
Sbjct: 4 VSFRIYFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMVSIQQLDSMKEIGSNCLNNE 63

Query: 92 FNFYDFPSHI 101
FNF F HI
Sbjct: 64 FNF--FKRHI 71

Pedant information for DKFZphtes3_35e21, frame 2

Report for DKFZphtes3_35e21.2

[LENGTH] 104
[MW] 11339.12
[pI] 5.87
[PROSITE] MYRISTYL 2
[PROSITE] PKC_PHOSPHO_SITE 1
[PROSITE] ASN_GLYCOSYLATION 1
[KW] Alpha_Beta

SEQ METSHAHESNCKIKGYGVVQQLLHSQLCGAGEDLGPIGVS YVVSFRAVPFSLILSNASLH
PRD ccchhhhhccccccccchhhhhhhhhhhccccccccceeeeeeeccccceeecccccc

SEQ SLGGKDSIQVGCLKELMGPLSELADQILGNLFNFYDFPSHILKW
PRD cccccceccccccccccccchhhhhhhcccccccccccccccc

Prosites for DKFZphtes3_35e21.2

PS00001	56->60	ASN_GLYCOSYLATION	PDOC00001
PS00005	44->47	PKC_PHOSPHO_SITE	PDOC00005
PS00008	63->69	MYRISTYL	PDOC00008
PS00008	89->95	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_35e21.2)

DKFZphtes3_35g6

group: testes derived

DKFZphtes3_35g6 encodes a novel 482 amino acid protein with high partial similarity to H. sapiens chromosome 19, cosmid R27216.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

strong similarity to R27216_1

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: /map="15"

Insert length: 3177 bp

Poly A stretch at pos. 3167, polyadenylation signal at pos. 3148

```

1  GGAGGCAGCG  CCGGCCTCCG  GAGGCGGCCCT  GGGCGATGGC  GGCGGAGTTT
51  TGTCCATAAC  CTGGGCAACC  GCGCAGCTGG  AGGATGGCCT  CACTCGGGCC
101  TGCCGCAGCT  GGGGAGCAGG  CGTCGGGGGC  TGAGGCGGAG  CCGGGCCCCG
151  CGGGGCCGCC  GCCCGGCCCC  TCACCGTCCT  CTCTGGGGCC  CCTGCTCCCC
201  CTGCAGCGGG  AACCTCTCTA  CAACTGGCAG  GCGACCAAGG  CGTCGCTGAA
251  GGAGCGCTTC  GCCTTCCTCT  TCAACTCGGA  GCTGCTGAGC  GATGTGCGCT
301  TCGTACTGGG  CAAGGGTCGC  GCGCCGCGCG  CCGCTGGGGG  CCCGCAGCGC
351  ATCCCGGCCC  ACCGCTTCGT  GCTGGCGGCC  GGCAGCGCCG  TCTTTGACGC
401  CATGTTCAAC  GCGCGCATGG  CCACCACGTC  GGCCGAGATC  GAGCTGCCCG
451  ACGTGGAGCC  CCGAGCCTTC  CTGGCGCTGC  TGAGATTCT  ATATTCAGAT
501  GAAGTTCAAA  TTGGTCCAGA  AACAGTTATG  ACCACTCTTT  ATACTGCCAA
551  GAAATACGCA  GTCCCAGCCT  TGGGAAGACA  CTGTGTAGAA  TTTCTCACCA
601  AACATCTTAG  GGCAGATAAT  GCCTTTATGT  TACTTACTCA  GGCTCGATTA
651  TTTGATGAAC  CTCAGCTTGC  TAGTCTTTGT  CTAGATACAA  TAGACAAAAG
701  CACAAATGGAT  GCAATAAGTG  CAGAAGGGTT  TACTGATATT  GATATAGATA
751  CACTCTGTGC  AGTTTATAG  AGAGACACAC  TCAGTATTCT  AGAAAGTCGA
801  CTTTTTGGAG  CTGTTGTACG  CTGGGCAGAA  GCAGAATGTC  AGAGACAACA
851  ATTACTCTGT  ACTTTTGGGA  ATAAACAAAA  AGTTCTAGGA  AAAGCACTTT
901  CTTAATCCG  GTTCCCACTG  ATGACAATTG  AGGAATTGGA  AGCAGGTCCT
951  GCTCAATCTG  GAATTTTGTC  AGATCGTGAA  GTGGTAAACC  TCTTTCTTCA
1001  TTTTACTGTC  AACCTTAAAC  CCCGAGTTGA  ATACATTGAC  CGACCAAGAT
1051  GCTGTCTCAG  GGGAAAGGAA  TGCTGCATCA  ATAGATTCCA  GCAAGTAGAA
1101  AGCCGCTGGG  GTTACAGTGG  GACGAGTGAT  CGAATCAGAT  TCACAGTTAA
1151  TAGAAGGATC  TCTATAGTTG  GATTTGGCTT  GTATGGATCT  ATTCATGGCC
1201  CTACAGATTA  TCAAGTGAAT  ATACAGATCA  TTGAATATGA  GAAAAAGCAA
1251  ACCCTGGGAC  AGAATGATAC  CGGCTTTAGT  TGTGATGGGA  CAGCTAACAC
1301  ATTCAGGGTC  ATGTTCAAGG  AACCCATAGA  GATCCTGCCC  AATGTGTGCT
1351  ACACAGCATG  TGCAACACTC  AAAGGTCCAG  ATTCCCACCT  TGGCACAAAA
1401  GGATTGAAGA  AAGTAGTGCA  TGAGACACCT  GCTGCAAGCA  AGACTGTTTT
1451  TTTCTTTTTT  AGTTCCCTTG  GCAATAATAA  TGGCACTTCA  ATAGAAGATG
1501  GACAAATTCC  AGAAATCATA  TTTTATACAT  AATTTAGCAT  TATAATACAT
1551  CTTGGCTAAA  TAATACCATA  CAATCTAGTG  TCAAAAACAT  AAATGGCCAC
1601  AAAAAAGTAG  TTTGAGTGTT  ATGAATATTT  AAAATTGTAA  GATAAGAAAC
1651  AGTTTCTTAG  AGCAGATAGA  AAAATGCTTA  TTTAAATCTT  TGCATGATTT
1701  AAAAAACAGAT  TTTCCATTTT  CTTACAACCT  TAAGAGAAAA  GAACTGGGTT
1751  TAATGGTTTA  AAAAAAGGCA  CAGCTTTTTC  ACCTTCATCT  TGTATAATTT
1801  CATAGATTGG  CTGACTTAGG  GTCTTTCAAT  AGTTTGGGAA  TTGAAAGATT
1851  CTTGTATAT  ATAGCTAGTT  TGGGTTTGTT  TTTGTTTAA  CTATTTTGAA
1901  GGTTAGGTGA  GATGGGCAAA  TAGGCTTAAC  TATTTTGAAG  GTTGATGAA
1951  AAGAGATGGG  TCAGTATTCC  TACAGAATTC  TTATTAATCT  AAATAACTAA
2001  ATTCAGAAA  ATTAAGAAGC  TGACTTTATA  TTTGGTGGTT  TGAAGTATCT
2051  TGTTGTTAGC  ATTTGTAATA  ATGCTAAAAA  AGGCCTAATA  AAATGCCCAA
2101  GAAAAATATT  AGTGCATTTA  TAGAGAAGGA  TATTTTGTAG  TAGTATAGTA
2151  ATGTGTTATG  TAGTACAGTT  TTAAAGCTAT  AAATGGAATT  TTGTGTAAAT
2201  TCACAAAAAT  GTGATATAAA  CAGGATCTAA  GACTGGATTC  CCTGTCACCT
2251  AACTGCACCA  CTATACCTGT  CTCTCTGTGT  GGGGGACACT  GCTGATGATT
2301  CCCAAGATTG  AGATGATGAC  GGTGATGACG  ACTGGGTGAA  CAGCCATCAC
2351  TTCAACATTG  TGTAAATCCT  TCACAGCAAG  AAACCGAATA  AAATACTAAC
2401  ATTTCTAACA  ACTGCTCTGA  CATTGTAAAG  AGATCCAACA  GAATCACTCC
2451  TGCTGAAAAA  TACGCTTTCT  GCCACCTACA  CATTTCTATT  TAGGAAGTAA
2501  AATTTGCTTC  ATGGTCATGA  CCCCATTAGT  CAGTGTTACA  GCTGTGTTGG
2551  GGATAGGAAG  TATATCTGGC  AGATTGACAT  TTATACACTT  TTTTATAAAG
2601  CAGATTTTAA  AATATAGTAA  CATCCATTTT  TTCCCTTGA  AAGTGATTCT
2651  CTTATAAAAA  ATGAAAGTGG  AGTTTAAAGT  ATATCAAATC  GTTGTGGAAG
2701  GTGATTAAAA  ATCAAAATTC  TTTTAAATAT  CAACCTAATT  TTTTCTAAGT

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2751 AAGATACAAA AAATTTTCAT CTAAAGTAAT ATTTCACTTT ATATTGTAAA
2801 GAAGGTAGGT ATATTGGTGG CTGAGGTCTC TTGAAATTGC TAAAGGGAAA
2851 TTTTCTATG GTAATGCTCT TACGGATATA AGCCTCAGTT AAATGGAATT
2901 ATCTATGGGA TGTGTGGTTC TGGTTAACTA AAAATTAACC AGTAAACACT
2951 CTGTAGTAAC CATTACAGAA AATACTTCTG CCTTAAAAAA TATGATATGC
3001 CAGAGATGAG TTAGTGTTC TTGACGTTGG AGACCTATAA ATGCCTCATC
3051 TGTGTACTG AACAAATTGAA ACTGCATGCA GCCATAAAG GGACAAGAAA
3101 CAGAACTGTT TACTAACTTT GGGACATCCC CTGGAGTTT TAAAAATAAA
3151 TAAATATATA TATATATAAA AAAAAA

```

BLAST Results

Entry G37753 from database EMBL:
 SHGC-63477 Human Homo sapiens STS genomic.
 Score = 1627, P = 3.0e-66, identities = 327/329

Entry G37752 from database EMBL:
 SHGC-63476 Human Homo sapiens STS genomic.
 Score = 1578, P = 6.2e-64, identities = 320/324

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 84 bp to 1529 bp; peptide length: 482
 Category: similarity to unknown protein

```

1 MASLGPAAG EQASGAEE GPAGPPPPS PSSLGPLLPL QREPLYNWQA
51 TKASLKERFA FLFNSSELLSD VRFVLGKGRG AAAAGGPQRI PAHREVLAAAG
101 SAVFDAMFNG GMATTSAEIE LPDVEPA AFL ALLRFLYSDE VQIGPETVMT
151 TLYTAKKYAV PALEAHCVEF LTKHLRADNA FMLLTQARLF DEPQLASLCL
201 DTIDKSTMDA ISAEGFTDID IDTLCAVLER DTLISRESRL FGAVVRWAEA
251 ECQRQQLPVT FGNKQKVLGK ALSLIRFPLM TIEEFAAGPA QSGILSDREV
301 VNLFLHFTVN PKPRVEYIDR PRCCLRGKEC CINRFQQVES RWGYSCTSDR
351 IRETVNRRIS IVGFGLYGS I HGPTDYQVNI QIIIEYKKQT LGQNDTGFSC
401 DGTANTFRVM FKEPIEILPN VCYTACATLK GPDSHYGPKG LKKVVHETPA
451 ASKTVFFFFS SPGNNGT SI EDGQIPEIIF YT

```

BLASTP hits

Entry AC005306.2 from database TREMBL:
 product: "R27216_1"; Homo sapiens chromosome 19, cosmid R27216,
 complete sequence.
 Score = 1298, P = 1.9e-132, identities = 245/297, positives = 268/297

Entry CEF38H4.9 from database TREMBLNEW:
 gene: "F38H4.7"; Caenorhabditis elegans cosmid F38H4
 Score = 1237, P = 5.6e-126, identities = 248/446, positives = 322/446

Entry AC004678.1 from database TREMBL:
 product: "R34094_1"; Homo sapiens chromosome 19, cosmid R34094,
 complete sequence.
 Score = 555, P = 1.0e-53, identities = 112/137, positives = 123/137

Alert BLASTP hits for DKFZphtes3_35g6, frame 3

No Alert BLASTP hits found

Pendant information for DKFZphtes3_35g6, frame 3

Report for DKFZphtes3_35g6.3

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[LENGTH]      482
[MW]           52771.47
[pI]           5.79

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[HOMOL]          TREMBL:AC005306_2 product: "R27216_1"; Homo sapiens chromosome 19, cosmid
R27216, complete sequence. 1e-142
[BLOCKS]          BL01075D Acetate and butyrate kinases family proteins
[SUPFAM]          POZ domain homology 3e-08
[SUPFAM]          A55R protein middle region homology 5e-06
[SUPFAM]          A55R protein 5e-06
[SUPFAM]          A55R protein carboxyl-terminal homology 5e-06
[PROSITE]         MYRISTYL             6
[PROSITE]         CAMP_PHOSPHO_SITE      2
[PROSITE]         CK2_PHOSPHO_SITE       9
[PROSITE]         TYR_PHOSPHO_SITE       1
[PROSITE]         PKC_PHOSPHO_SITE       7
[PROSITE]         ASN_GLYCOSYLATION      2
[KW]              Alpha_Beta
[KW]              LOW COMPLEXITY         11.20 %
```

```

SEQ MASLGPAAAGEQASGAEEAPGPAGPPPPSPSSLLGPLLPLQREPLYNWQATKSLKERFA
SEG . . . xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD cccccccchhhhhhhccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhh

SEQ FLFNSELLSDVRFVLGKGRGAAAGGPQRIPAHRFVLAAGSAVFDAMFNGGMATTSAEIE
SEG . . . xxxxxxxxxxxxxxxx
PRD hhhccccccccccccccccccccccccchhhhhheeeccccchhhhhhhhhcchhhhhhee

SEQ LPDVEPAAFLLRLFLYSDEVQIGPETVMTTLYTAKKYAVPALEAHCFEFLTKHLRADNA
SEG . . .
PRD eccccchhhhhhhhhhhccccceechhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccch

SEQ FMLLTQARLFDEPQLASLCLDTIDKSTMDAISAEGFTDIDIDTLCVLERDTSIRESRL
SEG . . .
PRD hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhccccchhhhh

SEQ FGAVVRWAEACQRQQLPVTFGNKQKVLGKALSIRFPLMTIEEFAAGPAQSGILSDREV
SEG . . .
PRD hhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhccceccccccccccccchhhhh

SEQ VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGYSGTSDRIRFTVNRRI
SEG . . .
PRD hhhhhheeeccccceeeccccceeeccceehhhhhhhhhccccccccccchhhhhceee

SEQ IVGFGLYGSIHGPTDYQVNIQIIEYEKKQTLGQNDTGFS CDGTANTFRVMFKEPIEILPN
SEG . . .
PRD eeeeeccccccccchhhhhhhcchhhhhhhhhccccccccccccccccceeeccccceeecc

SEQ VCYTACATLKGPD SHYGTGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIPEIIF
SEG . . . xxxxxxxx
PRD cccccceccccccccccccceeeeeeccccceeeeeeccccccccccccccccceec

SEQ YT
SEG .
PRD CC

```

Prosites for DKFZphtes3_35g6.3

PS00001	394->398	ASN_GLYCOSYLATION	PDOC00001
PS00001	466->470	ASN_GLYCOSYLATION	PDOC00001
PS00004	357->361	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	387->391	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	54->57	PKC_PHOSPHO_SITE	PDOC00005
PS00005	154->157	PKC_PHOSPHO_SITE	PDOC00005
PS00005	234->237	PKC_PHOSPHO_SITE	PDOC00005
PS00005	296->299	PKC_PHOSPHO_SITE	PDOC00005
PS00005	348->351	PKC_PHOSPHO_SITE	PDOC00005
PS00005	406->409	PKC_PHOSPHO_SITE	PDOC00005
PS00005	428->431	PKC_PHOSPHO_SITE	PDOC00005
PS00006	14->18	CK2_PHOSPHO_SITE	PDOC00006
PS00006	54->58	CK2_PHOSPHO_SITE	PDOC00006
PS00006	115->119	CK2_PHOSPHO_SITE	PDOC00006
PS00006	206->210	CK2_PHOSPHO_SITE	PDOC00006
PS00006	217->221	CK2_PHOSPHO_SITE	PDOC00006
PS00006	234->238	CK2_PHOSPHO_SITE	PDOC00006
PS00006	281->285	CK2_PHOSPHO_SITE	PDOC00006
PS00006	296->300	CK2_PHOSPHO_SITE	PDOC00006
PS00006	468->472	CK2_PHOSPHO_SITE	PDOC00006
PS00007	430->437	TYR_PHOSPHO_SITE	PDOC00007
PS00008	80->86	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	365->371	MYRISTYL	PDOC00008

PS00008	392->398	MYRISTYL	PDOC00008
PS00008	402->408	MYRISTYL	PDOC00008
PS00008	463->469	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphtes3_35g6.3)

DKFZphtes3_35k16

group: metabolism

DKFZphtes3_35k16 encodes a novel 666 amino acid protein with weak similarity to fatty acid-CoA synthetases/ligases.

The novel protein contains a putative AMP-binding domain signature, which is present in enzymes, which act via an ATP-dependent covalent binding of AMP to their substrate. This domain is found in several CoA synthetases, such as acetate-CoA ligase (EC 6.2.1.1), long-chain-fatty-acid-CoA ligase (EC 6.2.1.3), bile acid-CoA ligase. Therefore it is a new fatty acid-CoA synthetases/ligase with unknown substrate.

The new protein can find application in modulation of fatty acid metabolism and as a new enzyme for biotechnologic production processes.

similarity to acyl-CoA synthetase

complete cDNA, complete cds, potential start codon at Bp 50, few EST hits, seems to be a testis specific cDNA, 5 of 6 EST hits are from testis derieved librarys

Sequenced by DKFZ

Locus: unknown

Insert length: 2520 bp

Poly A stretch at pos. 2510, polyadenylation signal at pos. 2490

```

1  CAGATGTCCC AGCTCCAGTG CTGTGGAGCA TGGTTTCTGC ACACCTGGAA
51  TGACTGGAAC CCCAAAGACT CAAGAAGGAG CTAAAGATCT TGAAGTAGAC
101  ATGAATAAAA CAGAAGTTAC TCCCAGGCTG TGGACCACCT GTCGAGATGG
151  AGAAGTCCTT CTGAGGCTAT CCAAACACGG ACCAGGCCAT GAGACCCCGA
201  TGACCATCCC TGAATTTTTT CGAGAGTCAG TCAACCGATT TGGAACTTAT
251  CCAGCCCTCG CATCCAAGAA TGGCAAAAAG TGGGAAATTC TGAATTTCAA
301  CCAGTACTAT GAGGCTTGTC GGAAGGCTGC AAAATCCTTG ATCAAGCTGG
351  GTTTGGAGCG TTTCCACGGA GTTGGTATCC TGGGGTTTAA CTCTGCAGAG
401  TGGTTTATCA CTGCTGTTGG TGCCATCCTA GCCGGGGGTC TTTGTGTTGG
451  TATTTATGCC ACCAACTCTG CCGAGGCTTG TCAATATGTC ATCACTCATG
501  CCAAAGTGAA CATCTTGCTG GTTGAGAATG ATCAACAGTT ACAGAAAATC
551  CTTTCGATTTC CACAGAGCAG CCTAGAGCCC CTAAAAGCGA TCATCCAGTA
601  CAGACTGCCA ATGAAGAAGA ACAACAACCT GTACTCTTGG GATGATTTCa
651  TGGAACTTGG CAGAAGTATC CCTGACACCC AACTGGAGCA GGTCACTGAG
701  AGCCAGAAGG CGAATCAATG CGCAGTGCTC ATCTACACTT CAGGGACCAC
751  AGGCATACCC AAGGGAGTGA TGCTCAGTCA TGACAACATC ACGTGGATTG
801  CAGGAGCAGT GACAAAGGAC TTTAAACTGA CAGACAAGCA TGAGACGGTG
851  GTTAGCTACC TCCCACCTCAG CCATATTGCA GCACAGATGA TGGACATCTG
901  GGTACCCATA AAGATTGGGG CGCTCACATA CTTTGCTCAA GCAGATGCTC
951  TCAAGGGGAC CTTGGTAAAT ACTCTAAAGG AGGTAAAACC TACTGTCTTC
1001  ATTTGGAGTG CTCAAAATTTG GGAGAAGATA CATGAGATGG TGAAGAAAAA
1051  TAGTGCCAAG TCCATGGGCT TGAAGAAGAA GGCATTCTGT TGGGCAAGAA
1101  ACATTTGGCT CAAGGTCAAC TCAAAAAAGA TGTTGGGGAA ATATAATACT
1151  CCGGTGAGTG ACCGCATGGC TAAGACTCTC GTGTTCAAGC AAGTCAAGAC
1201  ATCCCTTGGC TTGGATCACT GTCACTCTTT TATCAGTGGG ACTGCGCCCC
1251  TCAACCAAGA GACTGCCGAG TTCTTTCTAA GCTTGGACAT ACCTATAGGC
1301  GAGTTGTATG GGTGAGTGA GAGCTCGGGA CCCCACACGA TATCCAACCA
1351  GAATAACTAC AGGCTTCTAA GCTGTGGCAA GATCTTGACT GGGTGTAAGA
1401  ATATGCTGTT CCAGCAGAAC AAGGATGGCA TTGGGGAGAT CTGCCTCTGG
1451  GGTAGGCACA TCTTCATGGG CTATCTGGAA AGTGAGACTG AAACCTACAGA
1501  GGCCATCGAT GATGAAGGCT GGCTACACTC TGGGGATCTG GGCCAGCTGG
1551  ACGGTCTGGG TTTCTCTAT GTCAACGGCC ACATCAAAGA AATCCTTATC
1601  ACTGCTGGTG GTGAAAATGT GCCCCCCATT CCTGTTGAGA CCTTGGTTAA
1651  GAAGAAGATC CCCATCATCA GTAACGCCAT GTTAGTAGGA GATAAACTGA
1701  AGTTTCTGAG CATGTTGCTG ACGTGAAGT GTGAGATGAA TCAGATGAGC
1751  GGAGAACCCT TGGACAAGCT GAACCTCGAG GCCATCAACT TCTGTCGGGG
1801  TCTGGGCAGC CAGGCATCCA CCGTGAAGT GATGGTGAAG CAGCAAGACC
1851  CCCTGGTCTA CAAGGCCATC CAGCAAGGCA TCAATGCTGT GAACCAGGAA
1901  GCCATGAACA ATGCACAGAG GATTGAAAAG TGGGTCACTT TGGAGAAGGA
1951  CTTTTCATC TATGGTGGAG AGCTAGGTCC AATGATGAAA CTTAAGAGAC
2001  ATTTTGTAGC CCAGAAATAC AAAAAACAAA TTGATCACAT GTACCACTGA
2051  CTGCTTTGAT GGAGCTGCTC TCAGCTGTTT TGATGCCTTC AGCAGGAAGA
2101  CCTCATTTGA ATAAGTGAAA TGCTGCTCTA GGTAGAAGCT CTCCCTGCTG
2151  TTTTAAAGAA GCCACATTCC TCATTGGTCA GTTCTTGAT TGTTCGCTG
2201  TTGGAGAGGT GCTCCCTAGA AGAACCTGCC ATACGTTTCA AAGCAATAAA
2251  ATCACTGTAT ATCTTCTTAA GGACCTTCAA GTCATGACTC CAGGGAAGCC
2301  TATTGGGAAG TCTACTAAAA ACTGCCTGAT TTACAAGAAA GACCTGAAC

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2351 TGTGGGCTCC CATTGATTT TTTTCTCCTC AGGGGACTCA GACATTAGAA
2401 AGAAAAAGCC TCACAGATTT GAAGAACTGG ACCCCCAAAT CAACTCACCT
2451 GCCTGGAAGC AACTGGGAAA CCCTTCCAAT AAGTCCTGAT AATAAAGCAC
2501 TTCAGGGTCC AAAAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 50 bp to 2047 bp; peptide length: 666
 Category: similarity to known protein

```

1 MTGTPKTOEG AKDLEVDMNK TEVTPRLWTT CRDGEVLLRL SKHGPGHETP
51 MTIPEFFRES VNRFGTYPAL ASKNGKKWEI LNFNQYIEAC RKAAKSLIKL
101 GLERFHGVI LGFNSAEWFI TAVGAILAGG LCVGIYATNS AEACQYVITH
151 AKVNILLVEN DQQLQKILSI PQSSLEPLKA IIQYRLPMKK NNNLYSWDDF
201 MELGRSIPDT QLEQVIESQK ANQCAVLIYT SGTTGIPKGV MLSDHONITWI
251 AGAVTKDFKL TDKHETVVSY LPLSHIAAQM MDIWPVIKIG ALTYFAQADA
301 LKGTLVSTLK EVKPTVFIGV PQIWEKIHEN VKKNSAKSMG LKKKAFVWAR
351 NIGFKVNSKK MLGKYNTPTS YRMAKTLVFS KVKTSGLGLDH CHSFISGTAP
401 LNQETAFFEL SLDIPIGELY GLSESSGPHT ISNQNNYRL SCGKILTCK
451 NMLFQONKDG IGEICLWGRH IFMGYLESET ETTEAIDDEG WLHSGDLGQL
501 DGLGFLYVTG HIKEILITAG GENVPPIPVE TLVKKKIPII SNAMLVGDKL
551 KFLSMLLTLL CEMNQMSGEP LDKLNFEAIN FCRGLGSQAS TVTEMVKQOD
601 PLVYKAIQQG INAVNQEAMN NAQRIEKWVI LEKDFSIIYG ELGPMMLKLR
651 HFVAQKYKKQ IDHMYH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35k16, frame 2

TREMBL:AB014531.1 gene: "KIAA0631"; product: "KIAA0631 protein"; Homo sapiens mRNA for KIAA0631 protein, partial cds., N = 1, Score = 1641, P = 8.9e-169

PIR:E70937 probable fadD15 - Mycobacterium tuberculosis (strain H37RV), N = 2, Score = 532, P = 3.6e-62

PIR:H64041 long-chain-fatty-acid--CoA ligase homolog - Haemophilus influenzae (strain Rd KW20), N = 2, Score = 486, P = 6.5e-59

>TREMBL:AB014531.1 gene: "KIAA0631"; product: "KIAA0631 protein"; Homo sapiens mRNA for KIAA0631 protein, partial cds.
 Length = 634

HSPs:

Score = 1641 (246.2 bits), Expect = 8.9e-169, P = 8.9e-169
 Identities = 319/628 (50%), Positives = 440/628 (70%)

```

Query: 38 LRLSKHGPGHETPMTIPEFFRESVNRFGTYPALASKNGKKWEILNFNQYIEACRKAASKL 97
      LR+ P + P T+ F E++++G AL K KWE ++++QYY R+AAK
Sbjct: 2 LRIDPSCP--QLPYTVHRMFYEALDKYGDILALGFKRQDKWEHISYSQYLLARRAAKGF 59

Query: 98 IKLGLERFHGVIILGFNSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILL 157
      +KLGL++ H V ILGFNS EWF +AVG + AGG+ GIY T+S EACQY+ N+++
Sbjct: 60 LKLGLKQAHSAVAILGFNSPEWFFSAVGIVTFAGGIVTGIYTTSSPEACQYIAYDCCANVIM 119

Query: 158 VENDOQLOKILSIPQSSLEPLKAI IQYRLPM-KNNNNLYSWDDFMELGRSIPDTQLEQVI 216
      V+ +QL+KIL I L LKA++ Y+ P K N+Y+ ++FMELG +P+ L+ +I
Sbjct: 120 VDTQKQLEKILKI-WKQLPHLKAVVIYKEPPPNKMANVYTMEEFMELGNEVP EALDAII 178

Query: 217 ESQKANQCAVLIYTS GTTGIPKGVMLSDHONITWIA--GAVTKDFKLTD-KHETVVSYLPL 273

```

```

++Q+ NQC VL+YTS GTTG PKGVMLS DNITW A G+ D + + + E VVS YLPL
Sbjct: 179 DTQQPNQCCVLVYTS GTTGPNPKGVMLSQDNITWTARYGSQAGDIRPAEVQQE VVS YLPL 238

Query: 274 SHIAAQMMDIWVPIKIGALTYFAQADALKGTLVSTLKEVKPTVFIGVPQIWEKIHVMVK 333
SHIAAQ+ D+W I+ GA FA+ DALKG+LV+TL+EV+PT +GVP++WEKI E +++
Sbjct: 239 SHIAAQIYDLWTGIQWGAQVCFAEPDALKGSLVNTLREVEPTSHMGVPRVWEKIMERIQE 298

Query: 334 NSAKSMGLKKKAFVWARNIGFKVNSKKMLGKYNTPVSYRMAKTLVFSKVKTSGLDHC 393
+A+S +++K +WA ++ + N G P + R+A LV +KV+ +LG C
Sbjct: 299 VAAQSGFIRRKMLLWAMSVTLEQNLT-CPGSDLKPF TRLADYLV LAKVRQALGFAKCQK 357

Query: 394 FISGTAPLNQETAEEFLSLDIPIGELYGLSESSGPHTISNQNNYRLLSGKILTGCKNML 453
G AP+ ET FFL L+I + YGLSE+SGPH +S+ NYRL S GK++ GC+ L
Sbjct: 358 NFYGAAPMMAETQHFFLGLNIRLYAGYGLSETSGPHFMSSPYNYRLYSSGKLVPGCRVKL 417

Query: 454 FQONKDGIGEICLWGRHIFMGYLESETETEAIDDEGLHSGDLGQDGLGFLYVTGHIK 513
Q+ +GIGEICLWGR IFMGYL E +T EAID+EGWLH+GD G+LD GFLY+TG +K
Sbjct: 418 VNQDAEGIGEICLWGR TIFMGYLNMEDKTCEAIDEEGLWHTGDAGRLDADGFLYITGR LK 477

Query: 514 EILITAGGENVPPPIPVETLVKKKIPIISNAMLVGD KLFSLMLLTLKCEMNQMSGEPLDK 573
E++ITAGGENVPP+P+E VK ++PIISNAML+GD+ KFLSMLLTLKC ++ + + D
Sbjct: 478 ELIITAGGENVPPVPIEEAVKMELPIISNAMLIGDQRKFLSMLLTLKCTLDPDTSDQTDN 537

Query: 574 LNFEAINFCRGLGSQASTVTVMVKQDPLVYKAIQQGINAVNQEAMNNAQRIEKWVILEK 633
L +A+ FC+ +GS+A+TV+E++++D VY+AI++GI VN A I+KW ILE+
Sbjct: 538 LTEQAVEFCQRVGS RATTVSEIIEKKDEAVYQAIIEGIRRVNMNAAARPYHIQKWAILER 597

Query: 634 DFSIYG GELGPMMLKRHFVAQKYKKQIDHMY 665
DFSI GGELGP MKLKR V +KYK ID Y
Sbjct: 598 DFSISGGELGPTMKLRLTVLEKYKGIIDSFY 629

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Pedant information for DKFZphtes3_35k16, frame 2

Report for DKFZphtes3_35k16.2

```

[LENGTH] 666
[MW] 74344.97
[pI] 8.67
[HOMOL] TREMBL:AB014531_1 gene: "KIAA0631"; product: "KIAA0631 protein"; Homo sapiens
mRNA for KIAA0631 protein, partial cds. 1e-176
[FUNCAT] i lipid metabolism [H. influenzae, HI0002] 2e-55
[FUNCAT] 08.10 peroxisomal transport [S. cerevisiae, YER015w] 2e-29
[FUNCAT] 30.19 peroxisomal organization [S. cerevisiae, YER015w] 2e-29
[FUNCAT] 01.06.13 lipid and fatty-acid transport [S. cerevisiae, YER015w] 2e-29
[FUNCAT] 01.06.07 lipid, fatty-acid and sterol utilization [S. cerevisiae, YER015w]
2e-29
[FUNCAT] 01.06.01 lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YMR246w]
2e-23
[FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YMR246w] 2e-23
[BLOCKS] BL00455
[SCOP] dlci_ 5.19.1.1.1 Luciferase [Firefly (Photinus pyralis) 1e-49
[EC] 1.13.12.7 Photinus-luciferin 4-monooxygenase (ATP-hydrolysing) 9e-17
[EC] 6.2.1.3 Long-chain-fatty-acid--CoA ligase 4e-34
[EC] 5.1.1.11 Phenylalanine racemase (ATP-hydrolysing) 6e-08
[EC] 6.2.1.12 4-Coumarate--CoA ligase 8e-18
[PIRKW] duplication 6e-07
[PIRKW] phosphopantetheine 3e-12
[PIRKW] multifunctional enzyme 3e-06
[PIRKW] ligase 6e-08
[PIRKW] acid-thiol ligase 4e-34
[PIRKW] transmembrane protein 5e-22
[PIRKW] monooxygenase 9e-17
[PIRKW] hydrolase 4e-34
[PIRKW] peroxisome 9e-15
[PIRKW] antibiotic biosynthesis 3e-12
[PIRKW] isomerase 6e-08
[PIRKW] flavonoid biosynthesis 1e-17
[PIRKW] magnesium 9e-15
[PIRKW] ATP 5e-22
[PIRKW] oxidoreductase 9e-17
[PIRKW] liver 2e-31
[SUPFAM] alpha-aminoadipyl-cysteinyl-valine synthetase 3e-07
[SUPFAM] human long-chain-fatty-acid--CoA ligase 4e-34
[SUPFAM] gramicidin S synthetase I 6e-08
[SUPFAM] peptide synthetase ppsE 7e-06
[SUPFAM] gramicidin S synthetase I repeat homology 3e-12
[SUPFAM] peptide synthetase ppsD 2e-07

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[SUPFAM]    probable acyl-CoA ligase medium chain 2e-09
[SUPFAM]    acetate--CoA ligase 8e-10
[SUPFAM]    acetate--CoA ligase homology 4e-54
[SUPFAM]    surfactin synthetase 3e-12
[SUPFAM]    4-coumarate--CoA ligase 8e-18
[SUPFAM]    short-chain alcohol dehydrogenase homology 8e-07
[SUPFAM]    acyl carrier protein homology 2e-29
[PROSITE]   MYRISTYL      12
[PROSITE]   AMP_BINDING   1
[PROSITE]   AMIDATION     1
[PROSITE]   CAMP_PHOSPHO_SITE 1
[PROSITE]   CK2_PHOSPHO_SITE 9
[PROSITE]   TYR_PHOSPHO_SITE 3
[PROSITE]   PKC_PHOSPHO_SITE 10
[PROSITE]   ASN_GLYCOSYLATION 2
[PFAM]      AMP-binding enzymes
[KW]        Irregular
[KW]        3D
[KW]        LOW_COMPLEXITY 1.80 %

SEQ      MTGTPKQTQEGAKDLEVDMNKTEVTPRLWTTCRDGEVLLRLSKHGPGHETPMTIPEFFRES
SEG      .....
llci-    .....

SEQ      VNRFGTYPALASKNGKKWEILNFNQYYEACRKAASLIKGLERFHGVGILGFNSAEWFI
SEG      .....
llci-    .....

SEQ      TAVGAILAGGLCVGIYATNSAEACQYVITHAKVNI LLVENDQQLQKILSIPQSSLEPLKA
SEG      .....
llci-    .....

SEQ      IIQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGETTGIPKGV
SEG      .....
llci-    .....

SEQ      MLSHDNITWIAGAVTKDFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADA
SEG      .....
llci-    .....

SEQ      LKGTLVSTLKEVKPTVFIGVPQIWEKIHVMVKKNSAKSMGLKKKAFVWARNIGFKVNSKK
SEG      .....
llci-    .....

SEQ      MLGKYNTPVSYRMAKTLVFSKVKTSGLGDHCHSFISGTAPLNQETAEFFLSLDIPIGELY
SEG      .....
llci-    .....TTTTCEEETTTTCCCHHHHHHHHHHCCCCBCEE

SEQ      GLSESSGPHTISNQNNYRLSCGKILTCKNMLFQONKDGIGEICLWGRHIFMGYLESET
SEG      .....
llci-    ECGGGTTEEEECCEEEETTTTCEEEETTTTCEETEEEEETTTTCEETTTTHH

SEQ      ETTEAIDDEGWLHSGDLGLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPII
SEG      .....
llci-    HHHHHBTTTTCEEEEEEETTTTCEEE-----ECEEETTEEECHHHHHHHHHHT-TTE

SEQ      SNAMLVGDKLFLSMLLTLCCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEMVKQD
SEG      .....
llci-    EEEEEEE.....

SEQ      PLVYKAIQQGINAVNQEAMNNAQRIEKWVILEKDFSIIYGGEIGPMMLKLRHFVAQKYKKQ
SEG      .....
llci-    .....

SEQ      IDHMYH
SEG      .....
llci-    .....

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Prosites for DKFZphtes3_35k16.2

PS00001	19->23	ASN_GLYCOSYLATION	PDOC00001
PS00001	246->250	ASN_GLYCOSYLATION	PDOC00001
PS00004	332->336	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	4->7	PKC_PHOSPHO_SITE	PDOC00005
PS00005	24->27	PKC_PHOSPHO_SITE	PDOC00005
PS00005	30->33	PKC_PHOSPHO_SITE	PDOC00005
PS00005	218->221	PKC_PHOSPHO_SITE	PDOC00005
PS00005	261->264	PKC_PHOSPHO_SITE	PDOC00005

PS00005	308->311	PKC_PHOSPHO_SITE	PDOC00005
PS00005	335->338	PKC_PHOSPHO_SITE	PDOC00005
PS00005	358->361	PKC_PHOSPHO_SITE	PDOC00005
PS00005	370->373	PKC_PHOSPHO_SITE	PDOC00005
PS00005	558->561	PKC_PHOSPHO_SITE	PDOC00005
PS00006	30->34	CK2_PHOSPHO_SITE	PDOC00006
PS00006	52->56	CK2_PHOSPHO_SITE	PDOC00006
PS00006	173->177	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00006	206->210	CK2_PHOSPHO_SITE	PDOC00006
PS00006	210->214	CK2_PHOSPHO_SITE	PDOC00006
PS00006	308->312	CK2_PHOSPHO_SITE	PDOC00006
PS00006	478->482	CK2_PHOSPHO_SITE	PDOC00006
PS00006	591->595	CK2_PHOSPHO_SITE	PDOC00006
PS00007	659->666	TYR_PHOSPHO_SITE	PDOC00007
PS00007	658->666	TYR_PHOSPHO_SITE	PDOC00007
PS00007	597->605	TYR_PHOSPHO_SITE	PDOC00007
PS00008	3->9	MYRISTYL	PDOC00008
PS00008	65->71	MYRISTYL	PDOC00008
PS00008	124->130	MYRISTYL	PDOC00008
PS00008	130->136	MYRISTYL	PDOC00008
PS00008	134->140	MYRISTYL	PDOC00008
PS00008	235->241	MYRISTYL	PDOC00008
PS00008	239->245	MYRISTYL	PDOC00008
PS00008	303->309	MYRISTYL	PDOC00008
PS00008	387->393	MYRISTYL	PDOC00008
PS00008	421->427	MYRISTYL	PDOC00008
PS00008	498->504	MYRISTYL	PDOC00008
PS00008	586->592	MYRISTYL	PDOC00008
PS00009	74->78	AMIDATION	PDOC00009
PS00455	227->239	AMP_BINDING	PDOC00427

Pfam for DKFZphtes3_35k16.2

HMM_NAME	AMP-binding enzymes		
HMM	*TYRELNERANRLARHLRsekGIRPGDiVgIMMDRSMWMIVaMLGIWKAG		
Query	82	NFNQYYEACRKAAKSLI-KLGLERFHGVGILGFNSAEWFITAVGAILAG	129
HMM	GAYVPIDPeYPdERiQYMLEDSGARLLITQrh...HmqRIPdemwvvdH		
Query	130	GLCVGIYATNSAEACQYVITHAKVNILLVENDQQQLQKILSIPQSSLEPLK	179
HMM	IiviDWe.....WddlWWHedeeNpqpWvdPeDLAYIIY		
Query	180	AIQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIY	229
HMM	TSGTTGKPKGVMIEHRNIvNycqWMnWRYgmteeDDRILWFtSDpYWFda		
Query	230	TSGTTGIPKGVMLSHDNITWIAGAVTKDFKLTDKHETVVSYP-LSHIAA	278
HMM	SVWDMFWpLLnGaTLyIpPeEtRrDPerWWqYIqRHgITWwylTPSMFRM		
Query	279	QMMDIWPiKIGALTYFAQADAL--KGLVSTLKEVKPTVFIVGPQIWEK	326
HMM	Lmpd.....		
Query	327	IHEMVKKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKYNTPVSYRMAKT	376
HMMpsLRhVMFgGepLsPehWdWWRkrfgfkgRIINMYWPT		
Query	377	LVFSKVKTSGLGDHCHSFISGTAPLNQETAFFFL-SLD--IPIGELYGLS	423
HMM	ETTVWtTwMrIiPdepeqWrwiPIGRPIpNTqWYIMDdnMQLPiGViGE		
Query	424	ESSGPHTISNQNN--Y---RLLSCGKILTGCKNMLFQQN---KDG-IGE	463
HMM	LYIGWPGVARGYWNRPTELTEERfipNPFWPGEYrGWNrRMYRTGDLAR		
Query	464	ICLWG-RHIFMGYLESETETTEAIDDEGW-----LHSGDLGQ	499
HMM	WLPDgnIEYLGRID.DQVKIRGYRIELGEIEhqLr.qHPgIqEAVV*		
Query	500	LDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAML	545

DKF2phtes3_35k24

group: transmembrane protein

DKF2phtes3_35k24 encodes a novel 514 amino acid protein without similarity to known proteins.

The novel protein contains 5 transmembrane regions.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

unknown ;

membrane regions: 5

Summary DKF2phtes3_35k24 encodes a novel 514 amino acid protein.

No homologues found in bacteria yeast and C.elegans, specific for mammals?

unknown

complete cDNA, complete cds, few EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 2706 bp

Poly A stretch at pos. 2696, polyadenylation signal at pos. 2675

```
1 CCGTGTGCAG TCGCCCCGCG CCCCGCGCGA CCCTTCGGGT AAACACGAA
51 CTGGGAGTTC TGAAGAATGG GTAAAGACTT TCGTTACTAT TTCCAGCATC
101 CCTGGTCTCG CATGATTGTG GCTTACTTGG TGATCTTCTT TAACTTCTTA
151 ATATTTGCGG AGGACCCAGT TTCTCATAGC CAAACAGAAG CCAATGTTAT
201 TGTGTGTTGA AACTGTTTTT CATTTGTTAC AAATAAATAC CCTAGAGGAG
251 TTGGCTGGAG GATTTTGAAG GTGCTTCTAT GGCTACTTGC CATTCCTACA
301 GGAATAATAG CTGGCAAATT TCTGTTCCAT CAGCGTTTGT TTGGTCAGTT
351 GCTCCGATTA AAAATGTTTC GAGAAGATCA TGGGTCGTGG ATGACAATGT
401 TCTTCAGCAC AATTCTCTTT CTCTTCATAT TTTCTCACAT ATACAACACG
451 ATTCTTCTAA TGGATGGGAA CATGGGAGCA TATATCATT AAGACTATAT
501 GGGCATCCGA AATGAAAGTT TCATGAAATT AGCTGCAGTA GGGACCTGGA
551 TGGGGGACTT TGTACAGCTT TGGATGGTCA CTGATATGAT GCTTCAGGAC
601 AAACCCCTATC CTGACTGGGG AAAATCAGCA AGAGCTTTCT GGAAGAAAGG
651 AAATGTTAGG ATCACTTTAT TCTGGACAGT TCTTTTACT CTGACGCTG
701 TGTGTTGACT TGTGATTACA ACGGACTGGA TCAGCTGGGA CAAGCTGAAT
751 CGGGGATTTT TGCCCACTGA TGAAGTTTCC AGAGCATTCC TTGCTTCTTT
801 TATCTTGGTC TTTGACCTTC TTATTGTGAT GCAGGACTGG GAATTTCCAC
851 ATTTCATGGG AGATGTTGAT GTAAATCTCC CTGGTTTGCA CACCCCTCAC
901 ATGCAGTTCA AGATTCTTT CTTCAGAAA ATCTTCAAGG AGGAATATCG
951 TATTCACATA ACAGGCAAAT GGTTTAACTA TGAATTATC TTCTCTGCT
1001 TGATTTTGA TCTTAATATG TGAAGAACC AAATATTTTA TAAACCTCAT
1051 GAATATGGCG AATATATCGG CCCGGGGCAG AAGATATATA CAGTGAAAGA
1101 CTCAGAAAGT TTTAAAGATT TGAACAGAAC CAAGCTATCC TGGGAATGGA
1151 GGTCCAATCA CACTAACCTT CGGACTAATA AAACATATGT TGAGGGAGAC
1201 ATGTTCTTAC ACAGCAGGTT CATAGGAGCC AGTCTTGATG TCAAGTGTCT
1251 GGCCTTTGTT CCAAGCCTGA TAGCCTTTGT GTGGTTTGGG TTCTTTATT
1301 GGTCTTTTGG ACGATTTTGG AAAAATGAGC CACGCATGGA GAATCAAGAC
1351 AAAACTTACA CTCGCATGAA AAGAAAATCT CCATCAGAAC ATAGCAAAGA
1401 CATGGGAATC ACTCGAGAAA ACACCCAGGC TTCAGTAGAA GACCCCTTGA
1451 ATGACCCCTT TTTGGTTTGC ATCAGGCTCT ACTTCAATGA GATCGTCTAC
1501 AAGTCTTCCC ACCTAACCTC GGAAAACCTG AGCTCAGAGT TGAACGAATC
1551 TACTAGTGCA ACAGAAGCTG ATCAAGACCC AACGACTTCT AAAAGTACAC
1601 CTACGAACCT GACTCGGAGA TAGACTTGGA GATAACACAA AAAGCAAGCT
1651 TGAGTGTAAC TTTAAAAAAT TAGTCTTTCC TTTTGATATAT GTAAGGTTTA
1701 CGTAGTGTAA GGTAAAAATA TGAACAATGC CACAACGGTG CTCAACATGC
1751 TTTTCTTAGG ATTCATTGTT TTCTATTTGT ATTATAATAC ACGTGCCTAC
1801 TGTATACTCA ACAGTCTCT AGAGATTGCT TTTCACAATT GCACAAGCTA
1851 TTAGTGACTT TACAGCATAG TGAAGATTA GCTGATGACC CATGTATCTG
1901 ATGTTCAACC ATAGTGGTGC CTTGAGACAT TAACTGTTT TTAACGTAC
1951 CAGAAATGAA GTGTGGAACA GTTACCTAAC CTATTTCACA TGGGCGTTTT
2001 GTATACAACCT ATTTTGATCT AACTTTGATG TCTGAGCAGA AAACAGAAAT
2051 AGCTAAATGT GACTCAGGAA GTATCTCTTG GTTCTTATT CAGCAGCAGA
2101 GTTGGTGACT TTGACAACCT GACTGCAGAG AAACATGGTG ATCACCTTTT
2151 AATTTTTTAT GGTGTCTGTC CAAATATAAA TACAGATGCA AAATTCAGTA
2201 ATAGGAGATC CATAACCCAA CATGGGTCAC TACTCGTGAA ATGTGACTT
2251 CTCCCAACAG TAATTGAAAT GAGGTGATGA TACCTAATTA TGTTTCTCTA
2301 ATTAAAGATA AATTGCTACT TGATTAAAAA TCCTGCCCTT CACCTTTGGG
```

```

2351 AACAAAGGTT AAGAGACACA GTTGGGCGAA CTCTCAAATT TATTGGCATT
2401 TACACAAAGT CCCAGACAAC CAAGGAAGT AAGTTTTCAT CATATGAGAG
2451 CAGCACATCC CACCATTTC AATATTCGTA TATCTTCTG CAAATATGGC
2501 TCTGGATAGT GAAAATTGAA AAACATATGC CAACCCTGAG CAAGGGAAGT
2551 CCTCAAAAAA TCATGCAGCG GAACCTGTC AGGTAGAGAA GCCGTGCATG
2601 AAAGAATTTG TTTAATGTCT TGTTTTGCGT ATGTGTTTTT TGTTTTTGTT
2651 TTTTAAGAAC TAAATATTGC ACATTAATAA ATAAGAATTA TACAGCAAAA
2701 AAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 67 bp to 1608 bp; peptide length: 514
 Category: putative protein

```

1 MGKDFRYFQ HPWSRMIVAY LVIFFNFLIF AEDPVSHSQT EANVIVVGNC
51 FSFVTNKYPR GVGWRILKVL LWLLAILTGL IAGKFLFHQR LFGQLRLKLM
101 FREDHGSWMT MFFSTILFLF IFSHIYNTIL LMDGNMGAYI ITDYMGIENE
151 SFMKLAAGVT WMGDFVTAWM VTDMLQDKP YPDWGKSARA FWKKGNVRIT
201 LFWTVLFTLT SVVVLVITTD WISWDKLNRG FLPSDEVSRV FLASFILVFD
251 LLIVMQDWEF PHFMGDVDVN LPGLHTPHMQ FKIPFFQKIF KEEYRIHITG
301 KWFNYGIIFL VLILDLMWVK NQIFYKPHEY GQYIGPGQKI YTVKDSLSLK
351 DLNRTKLSWE WRSNHTNPRT NKTYVEGDMF LHSRFIGASL DVKCLAFVPS
401 LIAFVWFQFF IWFFGRFLKN EPRMENQDKT YTRMKRKSPP EHSKDMGITR
451 ENTQASVEDP LNDPSLVCIR SDFNEIVYKS SHLTSENLSL QLNESSTATE
501 ADQDPTTSKS TPTN

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35k24, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3_35k24, frame 1

Report for DKFZphtes3_35k24.1

```

[LENGTH]      514
[MW]           60185.03
[pI]           8.67
[PROSITE]      MYRISTYL           5
[PROSITE]      CAMP_PHOSPHO_SITE 1
[PROSITE]      CK2_PHOSPHO_SITE   8
[PROSITE]      TYR_PHOSPHO_SITE   1
[PROSITE]      PKC_PHOSPHO_SITE   7
[PROSITE]      ASN_GLYCOSYLATION  6
[KW]           SIGNAL PEPTIDE 32
[KW]           TRANSMEMBRANE 5
[KW]           LOW_COMPLEXITY     15.37 %

```

```

SEQ  MGKDFRYFQHPWSRMIVAYLVIFFNFLIFAEDPVSHSQT EANVIVVGNCFSFVTNKYPR
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....
SEQ  GVGWRILKVLWLLWLLAILTGLIAGKFLFHQR LFGQLRLKMFREDHGSWMTMFFSTILFLF
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM  .....

```

Prosites for DKFZphtes3 35k24.1

(No Pfam data available for DKFZphtes3 35k24.1)

DKFZphtes3_35n12

group: metabolism

DKFZphtes3_35n12 encodes a novel 315 amino acid protein with strong similarity to ADP,ATP carrier T (ANT) proteins.

The novel protein contains three mitochondrial energy transfer signatures and is closely related to the ADP/ATP translocator, or adenine nucleotide translocator (ANT), a protein most abundant in mitochondria. In its functional state, it is a homodimer of 30-kD subunits embedded asymmetrically in the inner mitochondrial membrane. The dimer forms a gated pore through which ADP is moved from the matrix into the cytoplasm.

The new protein can find application in modulation of ADP-transport and energy metabolism in cells/mitochondria.

strong similarity to ADP/ATP carrier proteins

EST hits to mouse and drosophila

Sequenced by DKFZ

Locus: unknown

Insert length: 1803 bp

Poly A stretch at pos. 1793, polyadenylation signal at pos. 1772

```
1 AGCGTCCCAA GAGCCACTTT CTCGCCAGTA CGATGCTGCA GCGGTTTTCC
51 GGTTCCTCCG TCCCTTCAT CGTAGCTCCC GTACTCATT TTAGCCACTG
101 CTGCCGGTTT TTATATCCTT CTCCATCATG CATCGTGAGC CTGCGAAAAA
151 GAAGGCAGAA AAGCGGCTGT TTGACGCTC ATCCTTCGGG AAGGACCTTC
201 TGGCCGCGCG AGTCGCGGCA GCTGTGTCCA AGACAGCGGT GCGCGCCATC
251 GAGCGGGTGA AGCTGCTGCT GCAGGTGCAG GCGTCGTCGA AGCAGATCAG
301 CCCCAGGCGC CGGTACAAAG GCATGGTGGA CTGCCTGGTG CGGATTCTTC
351 GCGAGCAGGG TTCTTTCAGT TTTTGGCGTG GCAATTTGGC AAATGTTATT
401 CGGTATTTTC CAACACAAGC TCTAACTTT GCTTTAAGG ACAATAACAA
451 GCAGCTATTC ATGTCTGGAG TTAATAAAGA AAAACAGTTC TGGAGGTGGT
501 TTTTGGCAAA CCTGGCTTCT GGTGGAGCTG CTGGGGCAAC ATCCTTATGT
551 GTAGTATATC CTCTAGATT TTGCGCAACC CGATTAGGTG TCGATATTGG
601 AAAAGGTCCT GAGGAGCGAC AATTCAAGGG TTTAGGTGAC TGTATTATGA
651 AAATAGCAAA ATCAGATGGA ATTGCTGGTT TATACCAAGG GTTTGGTGTG
701 TCAGTACAGG GCATCATTGT GTACCGAGCC TCTATTTTG GAGCTTATGA
751 CACAGTTAAG GGTTTATTAC CAAAGCCAAA GAAAACCTCA TTTCTTGCTC
801 CCTTTTTCAT TGCTCAAGTT GTGACTACAT GCTCTGGAAT ACTTCTTAT
851 CCCTTTGACA CAGTTAGAAG ACGTATGATG ATGCAGAGTG GTGAGGCTAA
901 ACGGCAATAT AAAGGAACCT TAGACTGCTT TGTGAAGATA TACCAACATG
951 AAGGAATCAG TTCTTTTCTT CGTGGCGCCT TCTCCAATGT TCTTCGCGGT
1001 ACAGGGGGTG CTTTGGTGTG GGTATTATAT GATAAAATTA AAGAATTCTT
1051 TCATATTGAT ATTGGTGGTA GGTAAATCGG AGAGTAAAT AAGAAATAAC
1101 ATGGATTAA CTGTGTTAAAC ATACAAATTA CATAGCTGCC ATTTGCATAC
1151 ATTTTGATAG TGTATTGTC TGTATTTTGT TAAAGTGCTA GTTCTGCAAT
1201 AAAGCATACA TTTTTCAG AATTAAATA CTAAATCA GATAAATGTG
1251 GATTTTCCTC CCACCTTAGAC TCAAACACAT TTTAGTGTGA TATTTCATT
1301 ATTATAGGTA GTATATTTA ATTTGTTAGT TTAATAATCT TTTTATGATT
1351 AAAAATTAAT CATATAATCC TAGATTAATG CTGAAATCTA GGAAATCAAA
1401 GTAGCGTCTT TAAATTTGCT ATTCATTTAA TATACCTGTT TTCCCATCTT
1451 TTGAAGTCAT ATGGTATGAC ATATTTCTTA AAAGCTTATC AATAGATGTC
1501 ATCATATGTG TAGGCAGAAA TAAGCTTTGT TCTATATCTC TTCTAAGACA
1551 GTTGTTATTA CTGTGTATAA TATTTACAGT ATCAGCCTTT GATTATAGAT
1601 GTGATCATTT AAAAATTTGAT AATGACTTTA GTGACATTAT AAAACTGAAA
1651 CTGGAATAA AAATGGCTTA TCTGCTGATG TTTATCTTTA AAATAAATAA
1701 AATCTTGCTA GTGTGAATAT ATCTTAGAAC AAAAGGTATC CTCTTGAAAA
1751 TTAGTTTGTA TATTTTGTG ACAATAAAGG AAGCTTAACT GTTAAAAAAA
1801 AAA
```

BLAST Results

No BLAST result

Medline entries

96289608:

Molecular biological and quantitative abnormalities of ADP/ATP carrier protein in cardiomyopathic hamsters.

Peptide information for frame 2

ORF from 128 bp to 1072 bp; peptide length: 315
 Category: strong similarity to known protein
 Classification: Metabolism
 Prosite motifs: MITOCH_CARRIER (40-50)
 MITOCH_CARRIER (145-155)
 MITOCH_CARRIER (242-252)

```

1 MHREPAKKKA EKRLFDASSF GKDLLAGGVA AAVSKTAVAP IERVKLLLQV
51 QASSKQISPE ARYKGMVDCL VRIPREQGFF SFWRGNLANV IRYFPTQALN
101 FAFKDKYKQL FMSGVNKEKQ FWRWFLANLA SGGAAGATSL CVVYPLDFAR
151 TRLGVDIGKG PEERQFKGLG DCIMKIAKSD GIAGLYQGFG VSVQGIIVYR
201 ASYFGAYDTV KGLLPKPKKT PFLVSFFIAQ VVTTCSGILS YPFDTVRRRM
251 MMQSGEAKRQ YKGTLDCEVK IYQHEGISSF FRGAFSNVLR GTGGALVLVL
301 YDKIKEFFHI DIGGR

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35n12, frame 2

PIR:S37210 ADP,ATP carrier protein T1 - mouse, N = 1, Score = 1127, P = 2.7e-114

PIR:A44778 ADP,ATP carrier protein T1 - human, N = 1, Score = 1125, P = 4.4e-114

TREMBL:DMADPATPT_2 product: "ADP/ATP translocase"; Drosophila melanogaster gene encoding ADP/ATP translocase, N = 1, Score = 1124, P = 5.6e-114

PIR:XWBO ADP,ATP carrier protein T1 - bovine, N = 1, Score = 1121, P = 1.2e-113

>PIR:S37210 ADP,ATP carrier protein T1 - mouse
 Length = 298

HSPs:

Score = 1127 (169.1 bits), Expect = 2.7e-114, P = 2.7e-114
 Identities = 214/293 (73%), Positives = 248/293 (84%)

```

Query: 17 ASSEFGKDLLAGGVAAVSKTAVAPIERVKLLLQVQASSKQISPEARYKGMVDCLVRIPRE 76
      A SF KD LAGG+AAVSKTAVAPIERVKLLLQVQ +SKQIS E +YKG++DC+VRIP+E
Sbjct: 5 ALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE 64

Query: 77 QGFFSFWRGNLANVIRYFPTQALNFAFKDKYKQLFMSGVNKEKQFWRWFLANLASGGAAG 136
      QGF SFWRGNLANVIRYFPTQALNFAFKDKYKQ+F+ GV++ KQFWR+F NLASGGAAG
Sbjct: 65 QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG 124

Query: 137 ATSLC VVYPLDFARTRLGVLDIGKGPEERQFKGLGDCIMKIAKSDGIAGLYQGFGVSVQGI 196
      ATSLC VYPLDFARTRL D+GKG +R+F GLGDC+ KI KSDG+ GLYQGF VSVQGI
Sbjct: 125 ATSLCFVYPLDFARTRLAADVKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFVSVQGI 184

Query: 197 IVYRASVYFGAYDTVKGLLPKPKKTPFLVSFFIAQVVTTCSGILSYPFDTVRRRMMMQSGE 256
      I+YRA+YFG YDT KG+LP PK +VS+ IAQ VT +G++SYPFDTVRRRMMMQSG
Sbjct: 185 IYRAAYFGVYDTAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMMQSGR 244

Query: 257 --AKRQYKGTLDCEVKIYQHEGISSFRRGAFSNVLRGTGGALVLVLVDKIKEF 307
      A Y GTLDC+ KI + EG ++FF+GA+SNVLRG GGA VLVLYD+IK++
Sbjct: 245 KGADIMYGTLDCEVKIAKDEGANAFKCAWSNVLRGMGGAFLVLVLYDEIKKY 297

```

Pedant information for DKFZphtes3_35n12, frame 2

Report for DKFZphtes3_35n12.2

[LENGTH] 315

Prosites for DKFZphtes3_35n12.2

PS00215	40->50	MITOCH_CARRIER	PDOC00189
PS00215	145->155	MITOCH_CARRIER	PDOC00189
PS00215	242->252	MITOCH_CARRIER	PDOC00189

Pfam for DKFZphtes3_35n12.2

HMM_NAME	Mitochondrial carrier proteins		
HMM	*pFwkDFLAGGIAGmMeHTvMFPIDtIKTRMQlQgEMpM..ahpRYkGMI +F+KD+LAGG+A++++T+++PI+++K+++Q+Q +++ RYKGM+		
Query	19	SFGKDLLAGGVAAVSKTAVAPIERVKLLQVQASSKQISPEARYKGMV	67
HMM	dCFRwIwkNEGWRGLWRGLgANvIRYIPqWaIRFGFYEFMKemFiDyfg DC+ +I++++G++++WRG++ANVIRY+P++A++F+F++ +K +F + +++		
Query	68	DCLVRIPREQGFFSFWRGNLANVIRYFPTQALNFAFKDKYKQLFMSGVNV	117
HMM	ddnyWmWfwmnYMaGsmAGEwisvIitYPMWvVKTRLQaDqkHphsQp.R ++W+WF+ N+++G++AG ++S+ ++YP+++++TRL D +++++ R		
Query	118	EKQFWRWFLANLASGGAAG-ATSLCVVYPLDFARTRLGVD--IGKGPEER	164
HMM	hYNGvWNcWkIYReEGgFkGLYRGWtPTWMMIPYqmiYFfvYEtLKeW +++G+ +C KI +++G ++GLY+G++ +++++I+Y++ YF++Y+T K +		
Query	165	QFKGLGDCIMKIAKSDG-IAGLYQGFGVSVQGIIVYRASVFAYD TVKGL	213
HMM	lynYtgYnPgprelCMddsPwWhwiIgWmIAGMiaWivSYPFdVVRTRMM L +++ + ++++++I++ ++ +++++I+SYPFd+VR+RMM		
Query	214	LP-----KPK--KTPFLVSFFIAQVVT-TCSGILSYPFDTVRRRMM	251
HMM	Mdsm.edhkYqSmlDCWMqIYKnEGFkGFWKGFWRPRIMRiMPWtAIMFmI M+S+ ++++Y+++LDC+++IY++EG+ +F++G+ +++R+ ++A+++++		
Query	252	MQSGEAKRQYKGTLD CFVKIYQHEGISSFFRGAFSNVLRGT-GGALVVLV	300
HMM	YEqMKwFL* Y+ +K+F+		
Query	301	YDKIKEFF	308

DKFZphtes3_35n24

group: testes derived

DKFZphtes3_35n24 encodes a novel 365 amino acid protein without similarity to known proteins.

The novel protein contains a Prosite Ig(Immunoglobulin)-MHC pattern. This pattern represents a domain, approximately one hundred amino acids long and including a conserved intra-domain disulfide bond (Ilg domain). Thus, the novel protein is a new member of the Ig-superfamily. No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 1589 bp

Poly A stretch at pos. 1579, polyadenylation signal at pos. 1560

```
1 CGATCGTCAC GTGACGCCGG GGTTCAGCGT ATCCTTGCTG GGCAACCGTC
51 TTAGAGACCA GCACTGCTGG CTGCACCATG AATGTGATCT ACCCACTGGC
101 AGTCCCAAG GGGCGCAGAC TCTGCTGTGA GGTGTGCGAA GCCCCAGCCG
151 AGCGGGTGTG CGCGGCCTGC ACAGTCACTT ATTACTGTGG GGTGGTACAT
201 CAGAAGGCTG ACTGGGACAG CATCCATGAG AAAATATGTC AGCTCTTGAT
251 TCCACTGCGC ACTTCCATGC CCTTCTACAA TTCAGAGGAA GAACGGCAGC
301 ATGGCCTGCA GCAGCTGCAG CAGCGGCAGA AGTATTGTAT TGAATTCTGC
351 TACACCATAG CCCAGAAATA CCTCTTTGAA GGGAAACACG AAGATGCTGT
401 ACCAGCAGCT TTGCAGTCCC TTCGCTTCCG TGTGAAGCTG TATGGCCTGA
451 GCTCCGTAGA GCTTGTGCCT GCTTACCCGC TGTGGCCGA GGCAGCCCTT
501 GGTCTGGGCC GAATCGTTCA GGCTGAAGAA TATCTATTCC AAGCCAGTGA
551 GACAGTCTCT AAATCAACTG ACTGTAGTAA TGCCACCCAC TCTTTACTGC
601 ATCGGAATCT GGGACTTCTC TATATAGCTA AGAAAACTA TGAAGAGGCC
651 CGTTATCATC TGGCCAATGA TATTTATTTT GCCAGTGTG CATTGGGAAC
701 AGAGGACATT AGGACTTCAG GAGGCTACTT CCACCTGGCT AATATATTCT
751 ATGACCTTAA AAAGTTGGAC CTGGCAGACA CATTGTACAC CAAGGTCTCT
801 GAGATCTGGC ATGCATATTT GAACAATCAC TATCAAGTCC TCTCAGGC
851 TCACATCCAA CAAATGGATT TACTGGGCAA ACTATTGAG AATGACACTG
901 GCTTGGATGA AGCCCAAGAA GCAGAAGCCA TTCGCATCCT GACTTCAATC
951 TTGAACATTG GAGAATCTAC ATCTGACAAA GCCCCCCAAA AAACCATCTT
1001 TGTTCTGAAG ATCCTGGTCA TGCTTTACTA CCTGATGATG AATTCTTCAA
1051 AGGCACAGGA ATATGGCATG AGGGCCCTCA GTCTAGCCAA AGAACAACAG
1101 CTTGATGTCC ATGAGCAAAG CACCATTCAA GAGTTATTAA GTCTCATTTT
1151 AACTGAAGAC CATCCATTA CTTAGTGACC CATGAGCTCT GCATCAAGGG
1201 TTATTCCAGG GGCTACTGAA GATCTAATAT ATTCCAGCCT TGCACAACCTG
1251 CTTTGAGGTA CTGTAGACTG CTGAAGTTTC CACCCCTTTC CCCTGGGATT
1301 GCACACATAG CTGTTATTTT TTTCTTACAC AGCATATTAA GGGGAATATAA
1351 AGCTTTAGGC ATAGAAATCA CTAAAACTG TGTTTGTCAT GACCTTTGTA
1401 CTTGATTTAT CATGACTTTG TATGACTGAG TAATATGTAG TCAGATCACT
1451 AATATGGTAT TTGTAATTAA ACTACAAATA GTTTGTGATT TCCCAGAAAGT
1501 CTTCCAACGA TGCATGTTTC ATACACTTTT GCTAAAGGAG GGGTAAAGGA
1551 GGGGGTAGGG AATAAAGCTA TATTGGAACA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 78 bp to 1172 bp; peptide length: 365
Category: putative protein

Prosites motifs: IG_MHC (35-42)

```
1 MNVIYPLAVP KGRRLCCEVC EPAERVCAA CTVTYCGVV HQKADWDSIH
51 EKICQLLIPL RTSMFPYNSE EERQHGLQQL QORQKYLIEF CYTIAQKYLE
101 EGKHEDAVPA ALQSLRFRVK LYGLSSVELV PAYPLAEAS LGLGRIVQAE
151 EYLFQAQWTV LKSTDCSNAT HSLLRNLGL LYIAKKNYEE ARYHLANDIY
201 FASCAFGTED IRTSGGYFHL ANIFYDLKKL DLADTLYTKV SEIWHAYLNN
251 HYQVLSQAH I QMDLLGKLF ENDTGLDEAQ EAEAIRILTS ILNIRESTSD
301 KAPQKTIFVL KILVMLYYLM MNSSKAQEG MRALSLAKEQ QLDVHEQSTI
351 QELLSLISTE DHPIT
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35n24, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_35n24, frame 3

Report for DKFZphtes3_35n24.3

```
{LENGTH} 365
{MW} 41768.24
{pI} 5.82
{BLOCKS} BL00273 Heat-stable enterotoxins proteins
{PROSITE} MYRISTYL 1
{PROSITE} IG_MHC 1
{PROSITE} AMIDATION 1
{PROSITE} CK2_PHOSPHO_SITE 7
{PROSITE} TYR_PHOSPHO_SITE 4
{PROSITE} PKC_PHOSPHO_SITE 3
{PROSITE} ASN_GLYCOSYLATION 3
{KW} Alpha_Beta
{KW} LOW_COMPLEXITY 4.11 %
```

```
SEQ MNVIYPLAVPKGRRLCCEVCEAPAERVCAACTVTYTCGVVHQKADWDSIHEKICQLLIPL
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
```

```
SEQ RTSMFPYNSEERQHGLQQLQORQKYLIEFCYTIAQKYLEFEGKHEDAVPAALQSLRFRVK
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
```

```
SEQ LYGLSSVELVPAYPLAEASLGLGRIVQAEYLFQAQWTVLKSTDCSNATHSLLRNLGL
SEG .....
PRD hcccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
```

```
SEQ LYIAKKNYEEARYHLANDIYFASCAFGTEDIRTSGGYFHLANIFYDLKKLDLADTLYTKV
SEG .....
PRD eeeeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
```

```
SEQ SEIWHAYLNNHYQVLSQAHIQMDLLGKLFENDTGLDEAQEAEAIRILTSILNIRESTSD
SEG .....
PRD hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
```

```
SEQ KAPQKTIFVLKILVMLYYLMNNSKAQEGMRALSLAKEQQLDVHEQSTIQELLSLISTE
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
```

```
SEQ DHPIT
SEG .....
PRD ccccc
```

Prosites for DKFZphtes3_35n24.3

PS00001	168->172	ASN_GLYCOSYLATION	PDOC00001
PS00001	272->276	ASN_GLYCOSYLATION	PDOC00001
PS00001	322->326	ASN_GLYCOSYLATION	PDOC00001
PS00005	114->117	PKC_PHOSPHO_SITE	PDOC00005
PS00005	299->302	PKC_PHOSPHO_SITE	PDOC00005
PS00005	323->326	PKC_PHOSPHO_SITE	PDOC00005

PS00006	48->52	CK2_PHOSPHO_SITE	PDOC00006
PS00006	69->73	CK2_PHOSPHO_SITE	PDOC00006
PS00006	125->129	CK2_PHOSPHO_SITE	PDOC00006
PS00006	274->278	CK2_PHOSPHO_SITE	PDOC00006
PS00006	297->301	CK2_PHOSPHO_SITE	PDOC00006
PS00006	349->353	CK2_PHOSPHO_SITE	PDOC00006
PS00006	358->362	CK2_PHOSPHO_SITE	PDOC00006
PS00007	85->93	TYR_PHOSPHO_SITE	PDOC00007
PS00007	186->194	TYR_PHOSPHO_SITE	PDOC00007
PS00007	186->194	TYR_PHOSPHO_SITE	PDOC00007
PS00007	185->194	TYR_PHOSPHO_SITE	PDOC00007
PS00008	275->281	MYRISTYL	PDOC00008
PS00009	11->15	AMIDATION	PDOC00009
PS00290	35->42	IG_MHC	PDOC00262

(No Pfam data available for DKFZphtes3_35n24.3)

DKFZphtes3_35n9

group: metabolism

DKFZphtes3_35n9 encodes a novel 607 amino acid protein which is a splice variant of human carboxylesterase (EC 3.1.1.1).

The novel protein contains both, one carboxylesterase B1 and one B2 pattern. In comparison to EC 3.1.1.1, DKFZphtes3_35n9 shows a N-terminal extension and aa 458-474 are missing.

The new protein can find application in modulation of carboxylester metabolism and as a new enzyme for biotechnologic production processes.

carboxylesterase, splice variant

5' extension of mRNA and N-terminal elongation of protein (64 aa), missing exon! aa 458-474 of JC5408 are missing

Sequenced by DKFZ

Locus: unknown

Insert length: 2888 bp

Poly A stretch at pos. 2878, no polyadenylation signal found

```
1 CTCGGCCTGA GGTGCGAGAG AAGCGGTGAC CGCGGCCCTG GCTGCTCGGA
51 CCCGGGAACA TGATGGTTCG TGGAGCAGAA GCGCCTGAGA AGGGACCACG
101 GCGGCGCTGG GTCTGTGCGAG CCAGTAGCGG GCTGAAACGT AGAGGCCAGA
151 ACCAGGTCTC AGGGGGCACT AAAGGCGGTC GGAGGTAATC CCCACACCCG
201 TTCCTCCTGG AAGTCAGGCT GGCCGGGAGC TCCCGTATCC AGGACGGTTG
251 GTCCGCTCTG GCTGTGCGAG GATCCTAGTG TCTCGGGACC TCCCGGTGAC
301 CGCGCTGCCT CCCCTGCTGC ACCATAGGCC CGGGAGTACG GCGTCCCCAC
351 AGCTTGGACC GGCAGGGGCT CGTGAAATGT TTGTCAAAGT GATAAATGAC
401 CATGGCCGTG GTCTCCGCGG GAGGTGAGGA AACTGAAAGC CACCGAGGAA
451 AAGGGGGGCG CTCCTTAAGA AGTGCCGCGG TCACGTGTAC GTTTCAAAAG
501 AATGGCGTGA CTGAGTAGGG AGGGGACCGC GGAGACCCCT AGACCCCTGA
551 CTGTAAGGAG ATGAGGGGCC GTGAAGGGGA ACCCAGGAAA CTGAGTCCTG
601 AAAGCAAGGA GGAACCTCCA GAATGAAGGG CGCCGACACT CCTTCCTGCC
651 TTTGCTCAAG CGGTTCCTTC ACCCCGATCA AGTTCCTTCC CATTCTCCA
701 TCTGGGGGAT CCTGAACGTG CACATCCTCA GAGAAGCCCT CCTGGGGTCT
751 CCAATTCTAG TTTATTGCCC CCTCCTATCG ATCCCCCAGC GCGCTCATCG
801 GGCCTGTGGA CAAGACAGAG TTTGAAGAGA GGATTCCCTG GATCGCGGAA
851 GGGCTGCAGG AATGGCACAG CCCCTTCCGA GGATGCCAAA GGAGCCCGGG
901 CAAAGGAAAG TGGCCGTGCC CGGGCCTGCC TACCACTAGA TCCCCACCCA
951 CCTATGACTG CTCAGTCCCG CTCTCCTACC ACACCCACCT TTCCCGGCCC
1001 AAGCCAGCGC ACCCGCTGTA CTCCCTGCCC AGTCCAAACT CCAAGGCTGG
1051 GCAAGGCACT GATCCACTGC TGGACAGACC CGGGGCAGCC TCTGGGTGAA
1101 CAGCAGCGTG TCCGCCGGCA GCGAACCAGG ACCAGCGAGC CGACCATGCG
1151 GCTGCACAGA CTTGCTGCGC GGCTGAGCGC GGTGGCCTGT GGGCTTCTGC
1201 TGCTTCTTGT CCGGGGCCAG GGCCAGGACT CAGCCAGTCC CATCCGACC
1251 ACACACACCG GGCAGGTGCT GGGGAGTCTT GTCCATGTGA AGGGCGCCAA
1301 TGCCGGGGTC AATACCTTCC TGGGAATTCC ATTTGCCAAG CCACCTCTAG
1351 GTCGCTGCGG CATTGCACCC CTTGAGCCCC CTGAATCTTG GAGTGGTGTG
1401 AGGGATGGAA CCACCCATCC GGCCATGTGT CTACAGGACC TCACCGCAGT
1451 GGAGTCAGAG TTTCTTAGCC AGTTCACAT GACCTTCCCT TCCGACTCCA
1501 TGTCTGAGGA CTGCCTGTAC CTCAGCATCT ACACGCCGGC CCATAGCCAT
1551 GAAGGCTCTA ACCTGCCCGT GATGCTCTGG ATCCACGCTG GTGCGCTTGT
1601 TTTTGGCATG GCTTCCTTGT ATGATGGTTC CATGCTGGCT GCCTTGGAGA
1651 ACGTGGTGGT GGTTCATCAT CAGTACCGCC TGGGTGTCTT GGGCTTCTTC
1701 AGCACTGGAG ACAAGCACGC AACCGGCAAC TGGGGCTACC TGGACCAAGT
1751 GGTGTCACFA CGCTGGGTCC AGCAGAATAT CGCCCACTTT GGAGGCAACC
1801 CTGACCGTGT CACCAATTTT GCGGAGTCTG CGGGTGGCAC GAGTGTGTCT
1851 TCGCTTGTTC TGTCCTCCAT ATCCCAAGGA CTCTCCACG GAGCCATCAT
1901 GGAGAGTGGC GTGGCCCTCC TGCCCGGCCCT CATTGCCAGC TCAGCTGATG
1951 TCACTCTCCAC GGTGGTGGCC AACCTGTCTG CCTGTGACCA AGTTGACTCT
2001 GAGGCCCTGG TGGGCTGCCT GCGGGGCAAG AGTAAAGAGG AGATTCTTGC
2051 AATTAAACAAG CCTTTCAAGA TGATCCCCGG AGTGGTGGAT GGGGTCTTCC
2101 TGCCCAAGGA AGTCCAGGAG CTGCTGGCCT CTGCCGACTT TCAGCCTGTC
2151 CCTAGCATTG TTGGTGTCAA CAACAATGAA TTCGGCTGGC TCATCCCCAA
2201 GGTCATGAGG ATCATATGATA CCCAGAAGGA AATGGACAGA GAGGCCTCCC
2251 AGGCTGCTCT GCAGAAAATG TTAACGCTGC TGATGTTGCC TCCTACATT
2301 GGTGACCTGC TGAGGGAGGA GTACATTGGG GACAATGGGG ATCCCCAGAC
2351 CCTCCAAGCG CAGTTCAGG AGATGATGGC GGAATCCATG TTTGTGATCC
2401 CTGCACTCCA AGTAGCACAT TTTCACTGTT CCGGGGCCCC TGTGACTTTC
2451 TACGAGTTCC AGCATCAGCC CAGCTGGCTC AAGAACATCA GGCCACCGCA
2501 CATGAAGGCA GACCATGTTA AATTCACTGA GGAAGAGGAG CAGCTAAGCA
2551 GGAAGATGAT GAAGTACTGG GCCAACTTTG CGAGAAATAG GAACCCCAAT
2601 GGCAGGGGTC TGCCACACTG GCCGCTGTTC GACCAGGAGG AGCAATACCT
```

```

2651 GCAGCTGAAC CTACAGCCTG CGGTGGGCGG GGCTCTGAAG GCCCACAGGC
2701 TCCAGTTCTG GAAGAAGGCG CTGCCCCAAA AGATCCAGGA GCTCGAGGAG
2751 CCTGAAGAGA GACACACAGA GCTGTAGCTC CCTGTGCCGG GGAGGAGGGG
2801 GTGGGTTCGC TGACAGGCGA GGGTCAGCCT GCTGTGCCCA CACACACCCA
2851 CTAAGGAGAA AGAAGTTGAT TCCTTCATAA AAAAAAAA

```

BLAST Results

Entry D50579 from database EMBL:
Homo sapiens mRNA for carboxylesterase, complete cds.
Score = 7197, P = 0.0e+00, identities = 1441/1443

Entry JC5408 from database PIR:
carboxylesterase (EC 3.1.1.1) - human
Score = 2808, P = 1.2e-291, identities = 542/559, positives = 543/559,
frame +3

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 954 bp to 2774 bp; peptide length: 607
Category: known protein
Classification: Metabolism
Prosite motifs: CARBOXYLESTERASE_B_1 (279-295)
CARBOXYLESTERASE_B_2 (185-196)

```

1 MTAQSRSPPT PTFPGPSQRT PLTPCPVQTP RLKALIHCV TDPGQPLGEQ
51 QRVRRQRTET SEPTMRLHRL RARLSAVACG LLLLVLVRGQG QDGASPIRTT
101 HTGOVLGSLV HVKGANAGVQ TFLGIPFAKP PLGPLRFAPP EPPESWSGVR
151 DGTTHPAMCL QDLTAVESEF LSQFNMTFPS DSMSEDCLYL SIYTPAHSHE
201 GSNLPMVMWI HGGALVFGMA SLYDGSMLAA LENVVVVVIQ YRLGVLGFFS
251 TGDKHATGNW GYLDQVAALR WVQONIAHFG GNPDRVTIFG ESAGGTSVSS
301 LUVSPISQGL FHGAIMESGV ALLPGLIASS ADVISTVVAN LSACDQVDSE
351 ALVGCLRGKS KEEILAINKP FKMIPGVVDG VFLPRHPQEL LASADFQVPV
401 SIVGVNNNEF GWLIPKVMRI YDTQKEMDRE ASQAALQKML TLLMLPPTFG
451 DLLREEYIGD NGDPQTLQAO FQEMMADSMF VIPALQVAHF QCSRAPVYFY
501 EFQHQPSWLK NIRPPHMKAD HVKFTEEEEQ LSRKMMKYWA NFARNGNPNG
551 EGLPHWPLFD QEEQYLQLNL QPAVGRALKA HRLQFWKKAL PQKIQELEEP
601 EERHTEL

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35n9, frame 3

PIR:JC5408 carboxylesterase (EC 3.1.1.1) - human, N = 1, Score = 2808,
P = 1.9e-292

TREMBL:HSU60553_1 gene: "hCE-2"; product: "carboxylesterase"; Human
carboxylesterase (hCE-2) mRNA, complete cds., N = 1, Score = 2761, P =
1.8e-287

PIR:A34329 60K esterase (EC 3.1.1.-) isoform 2 - rabbit, N = 1, Score =
1985, P = 3.1e-205

TREMBL:D50580_1 product: "carboxylesterase precursor"; Rattus
norvegicus mRNA for carboxylesterase, partial cds., N = 1, Score =
1984, P = 4e-205

>PIR:JC5408 carboxylesterase (EC 3.1.1.1) - human
Length = 559

HSPs:

Score = 2808 (421.3 bits), Expect = 1.9e-292, P = 1.9e-292

Identities = 542/559 (96%), Positives = 543/559 (97%)

Query: 65 MRLHRLRLRLSAVACGLLLLLLVRRGQGQDSASPIRTHHTGQVLGSLVHVKGANAGVQTFLG 124
 MRLHRLRLRLSAVACGLLLLLLVRRGQGQDSASPIRTHHTGQVLGSLVHVKGANAGVQTFLG
 Sbjct: 1 MRLHRLRLRLSAVACGLLLLLLVRRGQGQDSASPIRTHHTGQVLGSLVHVKGANAGVQTFLG 60

Query: 125 IPFAKPPLGPLRFAPPEPPESWSGVRDGTTHPAMCLODLTAVESEFLSQFNMTFPSDSMS 184
 IPFAKPPLGPLRFAPPEPPESWSGVRDGTTHPAMCLODLTAVESEFLSQFNMTFPSDSMS
 Sbjct: 61 IPFAKPPLGPLRFAPPEPPESWSGVRDGTTHPAMCLODLTAVESEFLSQFNMTFPSDSMS 120

Query: 185 EDCLYLSIYTPAHSHEGSNLPVMVWIHGGALVFGMASLYDGSMLAALENVTVVVIQYRLG 244
 EDCLYLSIYTPAHSHEGSNLPVMVWIHGGALVFGMASLYDGSMLAALENVTVVVIQYRLG
 Sbjct: 121 EDCLYLSIYTPAHSHEGSNLPVMVWIHGGALVFGMASLYDGSMLAALENVTVVVIQYRLG 180

Query: 245 VLGFFSTGDKHATGNWGYLDQVAALRWVQONIAHFGGNPDRVTIFGESAGGTSVSSSLVVS 304
 VLGFFSTGDKHATGNWGYLDQVAALRWVQONIAHFGGNPDRVTIFGESAGGTSVSSSLVVS
 Sbjct: 181 VLGFFSTGDKHATGNWGYLDQVAALRWVQONIAHFGGNPDRVTIFGESAGGTSVSSSLVVS 240

Query: 305 PISQGLFHGAINESSGVALLPGLIASSADVISTVVANLSACQVDSEALVGCLRGKSKEEI 364
 PISQGLFHGAINESSGVALLPGLIASSADVISTVVANLSACQVDSEALVGCLRGKSKEEI
 Sbjct: 241 PISQGLFHGAINESSGVALLPGLIASSADVISTVVANLSACQVDSEALVGCLRGKSKEEI 300

Query: 365 LAINKPFKMI PGVVDGVFLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQ 424
 LAINKPFKMI PGVVDGVFLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQ
 Sbjct: 301 LAINKPFKMI PGVVDGVFLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQ 360

Query: 425 KEMDREASQAALQKMLTLLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPA 484
 KEMDREASQAALQKMLTLLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPA
 Sbjct: 361 KEMDREASQAALQKMLTLLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPA 420

Query: 485 LQVAHFQCSRAPVYFYEFOHQPSWLKNIRPPHMKADH-----VKFTEEE 528
 LQVAHFQCSRAPVYFYEFOHQPSWLKNIRPPHMKADH +KFTEEE
 Sbjct: 421 LQVAHFQCSRAPVYFYEFOHQPSWLKNIRPPHMKADHGDDELFPVFRSFFGGNYIKFTEEE 480

Query: 529 EQLSRKMMKYWANFARNGNPNGEGLPHWPLFDQEEQYLQNLQPAVGRALKAHRLQFWKK 588
 EQLSRKMMKYWANFARNGNPNGEGLPHWPLFDQEEQYLQNLQPAVGRALKAHRLQFWKK
 Sbjct: 481 EQLSRKMMKYWANFARNGNPNGEGLPHWPLFDQEEQYLQNLQPAVGRALKAHRLQFWKK 540

Query: 589 ALPQKIQELEEEPEERHTEL 607
 ALPQKIQELEEEPEERHTEL
 Sbjct: 541 ALPQKIQELEEEPEERHTEL 559

Pedant information for DKFZphtes3_35n9, frame 3

Report for DKFZphtes3_35n9.3

{LENGTH} 607
 {MW} 67051.20
 {PI} 6.11
 {HOMOL} PIR:JC5408 carboxylesterase (EC 3.1.1.1) - human 0.0
 {BLOCKS} BL01173A Lipolytic enzymes "G-D-X-G" family, histidine
 {BLOCKS} BL00122G
 {BLOCKS} BL00122F
 {BLOCKS} BL00122E
 {BLOCKS} BL00122D Carboxylesterases type-B serine proteins
 {BLOCKS} BL00122C Carboxylesterases type-B serine proteins
 {BLOCKS} BL00122B Carboxylesterases type-B serine proteins
 {BLOCKS} BL00122A Carboxylesterases type-B serine proteins
 {SCOP} dlakn 3.56.1.1.4 Bile-salt activated lipase [Bovine (Bos taurus 1e-158
 {SCOP} d2ack 3.56.1.1.1 Acetylcholinesterase [Electric ray (Torped 1e-170
 {SCOP} dlthg 3.56.1.9.7 type-B carboxylesterase/lipase [fungu 1e-149
 {EC} 3.1.1.13 Sterol esterase 1e-52
 {EC} 3.1.1.7 Acetylcholinesterase 5e-74
 {EC} 3.1.1.1 Carboxylesterase 0.0
 {EC} 3.1.1.8 Cholinesterase 5e-68
 {EC} 3.1.1.59 Juvenile-hormone esterase 1e-34
 {EC} 3.1.1.3 Triacylglycerol lipase 3e-52
 {PIRKW} duplication 2e-47
 {PIRKW} homotetramer 3e-67
 {PIRKW} transmembrane protein 9e-44
 {PIRKW} microsome 1e-130
 {PIRKW} pancreas 3e-52
 {PIRKW} endoplasmic reticulum 1e-134
 {PIRKW} homotrimer 1e-134
 {PIRKW} phosphatidylinositol linkage 5e-74
 {PIRKW} synapse 3e-73
 {PIRKW} liver 1e-131
 {PIRKW} heparin binding 3e-52

[PIRKW] phosphoprotein 7e-25
 [PIRKW] glycoprotein 1e-134
 [PIRKW] thyroid hormone biosynthesis 2e-47
 [PIRKW] carboxylic ester hydrolase 0.0
 [PIRKW] monomer 2e-42
 [PIRKW] disulfide bond 2e-31
 [PIRKW] mammary gland 3e-52
 [PIRKW] alternative splicing 5e-74
 [PIRKW] iodine 2e-47
 [PIRKW] pyroglutamic acid 6e-39
 [PIRKW] hydrolase 1e-135
 [PIRKW] muscle 3e-73
 [PIRKW] thyroid gland 2e-47
 [PIRKW] membrane protein 3e-73
 [PIRKW] neurotransmitter degradation 3e-73
 [PIRKW] cholesterol 3e-52
 [PIRKW] homodimer 2e-47
 [PIRKW] nerve 3e-73
 [SUPFAM] cholinesterase 0.0
 [SUPFAM] triacylglycerol lipase 1e-32
 [SUPFAM] cholinesterase homology 0.0
 [SUPFAM] thyroglobulin 2e-47
 [SUPFAM] thyroglobulin type I repeat homology 2e-47
 [SUPFAM] juvenile-hormone esterase 2e-35
 [SUPFAM] probable lipolytic protein ybaC 1e-07
 [PROSITE] CARBOXYLESTERASE_B_2 1
 [PROSITE] CARBOXYLESTERASE_B_1 1
 [PFAM] Carboxylesterases
 [KW] Alpha_Beta
 [KW] 3D
 [KW] LOW_COMPLEXITY 3.95 %

SEQ MTAQSRSPPTTPTFPGPSQRTPLTPCPVQTPRLGKALHCWTDPGQPLGEQQRVRRQRTET
 SEGXXXXXXXXX...
 lacj-

 SEQ SEPTMRLHRLRLRLSAVACGLLLLLLVRGQGQDSASPIRTHHTGQVLGSLVHVKGANAGVQ
 SEGXXXXX.....
 lacj-ETTEEECEEEEEETTEE--EE

 SEQ TFLGIPFAKPLPLGRFAPPEPPESWSGVRDGTTHPAMCLQDLTAVESEFLSQFNMTFPS
 SEG
 lacj- EEEEECEETTTGGGTTTCCEECCEEECEEECCCEEECCCTTTTTT-HHHHHCCCC

 SEQ DSMSEDCLYLSIYTPAHSHEGSNLPVMVWIHGGALVFGMASLYDGSMLAALENVVVVIQ
 SEG
 lacj- CCBTTTTCEEEEEET--TTTTTTEEEEEECTTTTTTCTTTTGCHHHHHHHHCCEEEEC

 SEQ YRLGVLGFFSTGDKHATGNWGYLDQVAALRWVQONIAHFGGNPDRVTIFGESAGGTSVSS
 SEG
 lacj- CCCCCGGCCCTTTTTTTCCHHHHHHHHHHHHHHCGGGGCEEEEEEEEEECCHHHHHHHH

 SEQ LVVSPISQGLFHGAIMESGVALLPGLIASSADVISTVVANLSACDQVDSEALVGCLRGKS
 SEG
 lacj- HHHCGGGTTTTCEEEEEETTTTTTTTTTTCCHHHHHHHHHHHHC-CCCCCHHHHHHHHHHC

 SEQ KEEILAINKPKFMIPGVVDGVFLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRI
 SEG
 lacj- HHHHHHHHTCCCTTTTCBTTTTTTTTTHHHHHHHHTTCCCEEEEEETBTTHHHHHHTTTT

 SEQ YDTQKEMDREASQAALQKMLTLMLPPTFGDLLREYIGDNGDPQTLOAQFQEMMADSMF
 SEG
 lacj- TTTCCCCCHHHHHHHHHHHHTTTTCHHHHHHHHHHCTTTTTTTHHHH-HHHHHHHHHHHH

 SEQ VIPALQVAHFQCSRAPVYFYEFQHQPSWLKNIRPPHMKADHVKFTEEEEQLSRKMMKYWA
 SEG
 lacj- HHHHHHHHHHHHCCCCEEEEECCECGGTTBTTHHHHCGGGCCCHHHHHHHHHHHHHH

 SEQ NFARNGNPNGEGLPHWPLFDQEEQYLQNLQPAVGRALKAHRLQFWKKALPQKIQELEEP
 SEGXXXXX
 lacj- HHHHHCCCCC--CCCBTTTTBEEEECCCCCEETTTTHHHHHHHHHHHHH.....

 SEQ EERHTEL
 SEG
 lacj-

Prosites for DKF2phtes3_35n9.3

PS00122 279->295 CARBOXYLESTERASE_B_1 PDOC00112
 PS00941 185->196 CARBOXYLESTERASE_B_2 PDOC00112

Pfam for DKFZphtes3_35n9.3

HMM_NAME	Carboxylesterases	
HMM	*MfMnwlImFLLwmItWii.WheqaprpPdPyiVdtnnCGkIRGmNedtD + +L+++ ++++++ ++Q+++P I T+ G + G ++ +	
Query	69 RLRARLSAVACGLLLLLVRGQGQDSASP---IRTTHT-GQVLGSLVHVK	113
HMM	NG..pYYvFLGIPYAEPVGNLRFKePQPYhePwTNVWNATnYPPMCMQW + + +FLGIP+A+PP+G LRF +P+P +E W++V++ T+ P MC+Q+	
Query	114 GANAGVQTFGLGIPFAKPLGLRFAPPEP-PESWSGVRDGTTHPAMCLQD	162
HMM	ndFGFWlFdmieMWNeniP..eMSEDCLYLNVWTPWnrkPnsKLPVMVWI +++ +++N++ P +MSEDCLYL++TP+ + ++S+LPVMVWI	
Query	163 LTAV--ESEFLSQFNMTFSPDSMSEDCLYLSIYTPAHSHEGSNLPVMVWI	210
HMM	HGGGFMFGSGhsYPliqYDgeylMeeNVIVVtINyRLGPFGLSTgDid HGG+++FG + ++YDG+ L++ ENV+VV I+YRLG++GF+STGD +	
Query	211 HGGALVFGMA-----SLYDGSMLAALENVVVVIQYRLGVLGFFSTGDKH	255
HMM	lPPHGNWGLWDQRMALQWVQDNIAFGGDPNNITIFGESAGGMSVHlHML + GNWG++DQ++AL+WVQ+NIA+FGG+P+++TIFGESAGG+SV+ ++	
Query	256 AT--GNWGYLDQVAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLV	303
HMM	SYGGDNPPmfKqLFHRAIMQSGsAmcPwvIQsnyNaRqRafRfArimGCN S P + +LFH AIM+SG A+ P++I S++ + +A++ C+	
Query	304 S-----PISQGLFHGAIMESGVALLPGLIASSA--DVISTVVANLSACD	345
HMM	rmDsseMIqCLRsKPweELWdAtWnFwmWfYfPflPWFFgPVIDGDDaPE + DS++++ CLR K+ EE+++++ +F + + +DG+	
Query	346 QVDSEALVGCLRGKSKEILAINK----PFKMIPGV-----VDGV----	381
HMM	aFIPDHPeemIKEGkFnDVPWIIgYNnDEGiWfapMmMnfnWfdEDeWId F+P+HP+E++++ F VP I+G+NN E++W++P M + + +E++	
Query	382 -FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDT-QKEMDR	429
HMM	itNedWyeWMPYIlFYrddmsNikDMDDYiDkvyEeYPgWWDrfPqESYW ++ + ++ M +L + + + D ++EEY+G+ + PQ	
Query	430 EASQAALQKMLTLMLPPT-F-----GDLLREEYIGDNGD-PQTLQA	469
HMM	nLqDMFTDYLFWCpTRihadnHRkHwgsPVYMYeFDHPPsFGYgQFFmWR ++Q+M+ D F++P + ++H++ +PVY+YEF+H PS +	
Query	470 QFQEMMADSMFVIP--ALQVAHFQCSRAPVYFYEFQHQPsw-----LKN	511
HMM	WWPpWMgvdH* +PP+M++DH	
Query	512 IRPPHMKADH	521
HMM	*tEEEiissMRmMMNYWINFAKhGNPNnthnglCWWPqYTsnEQYdMIME TEEE+ +S R MM+YW+NFA++GNPN++ GL++WP ++++EQY++ +	
Query	525 TEEEEQLS-RKMMKYWANFARNGNPNGE--GLPHWPLFDQEEQYLQLNL	570
HMM	tIImiQmCrMrDPYCNEW* + +++++ + EW	
Query	571 QPAVGRALKAHR--LQFW	586

DKF2phtes3_35p17

group: testes derived

DKF2phtes3_35p17 encodes a novel 505 amino acid protein with weak similarity to Proteins of the armadillo family.

Proteins of the armadillo family are involved in diverse cellular processes in higher eukaryotes. Some of them, like armadillo, beta-catenin and plakoglobins have dual functions in intercellular junctions and signalling cascades. Others, belonging to the importin-alpha-subfamily are involved in NLS recognition and nuclear transport, while some members of the armadillo family have as yet unknown functions. The novel protein shows similarity to S. cerevisiae protein Yel013p (VAC8) and Danio rerio b-catenin, but contains no armadillo (arm) repeats.

No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to S.cerevisiae VAC8

complete cDNA, complete cds, few EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 1966 bp

Poly A stretch at pos. 1956, polyadenylation signal at pos. 1935

```
1 AAGTCAAATG TAAGATTGGT TCATTAAAAA TACTGAAGGA AATCAGTCAT
51 AATCCTCAAA TCAGACAGAA TATTGTTGAC CTGGGGGGCT TACCAATTAT
101 GGTGAATATA CTTGATTCTC CACACAAGAG TCTAAATGT TTGGCAGCCG
151 AGACTATCGC GAATGTTGCC AAGTTTAAAA GAGCACGGCG GGTGGTGAGG
201 CAGCACGGGG GTATCACCAA ACTGGTTGCT CTACTAGACT GTGCACATGA
251 TTCCACAAAA CCTGCCCAAT CGAGTCTGTA TGAGGCCAGA GACGTGGAAG
301 TGGCTCGCTG TGGGGCACTG GCCCTGTGGA GCTGCAGTAA GAGTCATACG
351 AATAAAGAAG CCATCCGCAA AGCTGGGGGC ATTCCTCTGT TGGCTCGGCT
401 GCTGAAGACT TCTCATGAAA ACATGCTAAT TCCAGTGGTG GGGACATTGC
451 AAGAGTGTGC ATCAGAGGAA AACTACCGGG CTGCAATCAA AGCAGAAAGG
501 ATCATTGAAA ACCTTGTCOA GAACCTAAAT AGTGAGAATG AGCAGCTGCA
551 GGAGCACTGC GCCATGGCCA TTTACCAAGT TGCTGAAGAT AAGGAAACCC
601 GGGACCTCGT TAGGCTGCAC GGAGGACTTA AGCCCTTGGC CAGTCTACTC
651 AATAACACTG ACAATAAAGA GCGGTTAGCT GCTGTACAG GGGCTATATG
701 GAAATGTTCC ATCAGCAAAG AGAATGTTAC CAAGTTTCGG GAATACAAAG
751 CCATTGAAAC CTTGGTGGGA CTCTAACAG ATCAGCCTGA AGAAGTACTT
801 GTGAATGTGG TTGGGGCCTT GGGAGAATGC TGCCAAGAAC GTGAAAACCG
851 AGTCATTGTC CGGAAATGTG GTGGCATTCA ACCACTTGTG AACCTCCTTG
901 TTGGAATAAA CCAAGCTCTT CTGTGAAATG TTACAAAAGC AGTTGGTGCT
951 TGTGCAGTAG AACCTGAAAG TATGATGATA ATGATCGCT TAGATGGAGT
1001 TCGTTTGTG TGGTCCCTGC TGAAAATCC TCACCCAGAC GTGAAGGCCA
1051 GCGCAGCATG GGCACCTCTG CCATGCATCA AAAATGCAAA GGATGCTGGG
1101 GAAATGGTTC GTTCCTTTGT TGGTGGTTTG GAACTTATTG TCAATTTACT
1151 GAAATCAGAT AACAAAGAAG TTCTGGCAAG TGTATGTGCT GCCATTACCA
1201 ACATAGCAAA AGATCAAGAA AATTTAGCTG TTATCACAGA TCATGGAGTT
1251 GTTCCTTTAT TGTCCAAACT GGCAAAATCA AATAACAATA AATTGAGACA
1301 TCATCTAGCA GAAGCTATTT CACGTTGCTG TATGTGGGCG AGGAATAGAG
1351 TGGCCTTCGG TGAGCACAAA GCAGTGGCTC CACTAGTGGC TTATCTGAAA
1401 TCAAATGACA CCAACGTGCA TCGGGCGACA GCTCAGGCCT TGTACCAACT
1451 CTCAGAAGAC GCCGATAACT GCATCACCAT GCATGAGAAT GGTGCAGTAA
1501 AGCTTCTACT GGATATGGTT GGGTCCCTCG ACCAGGATCT CCAGGAAGCT
1551 GCAGCTGGTT GTATATCCAA TATCCGAGG CTGGCTCTTG CTACAGAGAA
1601 GGCAAGATAC ACTTGAAATT TAAATGGACA TTACAAGCTA TCAAATTCTA
1651 CATGACACAG GACATGTCAC TCCCATGGCC AGAAAGCCTA AATTGGGAAA
1701 CATGTTGTAG CAAACCCCTT CAACCATCTA AATGAAAACA CACAAATTGA
1751 AATGCACAG AATGTTTTTC ATCTGAAAT TGATGGAGA CTTTGTGTTT
1801 TATTTAATGT TTTCGAGATA TGACATGTGA TAAGATGGAA AGCCAATAAA
1851 CATTGATAA GTTCTAAGA ATATGAGAAT ATACGTATAT GATGATTTT
1901 TAGTTCAGTG ATGCTTTTGT ATTTGTGGCG ATTTTAATAA AGGATATGGC
1951 CTTCCCAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

98413148:

Yel013p (Vac8p), an armadillo repeat protein related to plakoglobin and importin alpha is associated with the yeast vacuole membrane.

98330438:

YEB3/VAC8 encodes a myristylated armadillo protein of the *Saccharomyces cerevisiae* vacuolar membrane that functions in vacuole fusion and inheritance.

98158703:

Vac8p, a vacuolar protein with armadillo repeats, functions in both vacuole inheritance and protein targeting from the cytoplasm to vacuole.

Peptide information for frame 3

ORF from 99 bp to 1613 bp; peptide length: 505
Category: similarity to known protein
Classification: unset

```

1 MVNILDSPHK SLKCLAAETI ANVAKFKRAR RVVRQHGGIT KLVALLDCAH
51 DSTKPAQSSL YEARDVEVAR CGALALWSCS KSHTNKEAIR KAGGIPLLAR
101 LLKTSHEMML IPVVGTLQEC ASEENYRAAI KAERIENLV KNLNSENQQL
151 QEHCAAIYQ CAEDKETRDL VRLHGGLKPL ASLLNNTDNK ERLAAVTGAI
201 WKCSISKENV TKFREYKAIE TLVGLLTDQP EEVLNVVGA LGECCQEREN
251 RVIVRKCGGI QPLVNLLVGI NQALLVNVTK AVGACAVEPE SMMIIDRLDG
301 VRLLWSLLKN PHPDVKASAA WALCPCIKNA KDAGEMVRSF VGGLELIVNL
351 LKSDNKEVLA SVCAAITNIA KDQENLAVIT DHGVVPLLSK LANTNNKLR
401 HHLAEAISRC CMWGRNRVAF GEHKAVAPLV RYLKSNNTNV HRATAQALYQ
451 LSEDADNCIT MHENGAVKLL LDMVGSPDQD LQEAAGCIS NIRRLALATE
501 KARYT

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35p17, frame 3

PIR:S50446 VAC8 protein - yeast (*Saccharomyces cerevisiae*), N = 1,
Score = 237, P = 7.8e-17

PIR:T00403 T13E15.9 protein - *Arabidopsis thaliana*, N = 1, Score = 215,
P = 4.9e-14

TREMBL:DR41081_1 product: "b-catenin"; *Danio rerio* b-catenin mRNA,
complete cds., N = 1, Score = 195, P = 5.8e-12

>PIR:S50446 VAC8 protein - yeast (*Saccharomyces cerevisiae*)
Length = 578

HSPs:

Score = 237 (35.6 bits), Expect = 7.8e-17, P = 7.8e-17
Identities = 106/401 (26%), Positives = 177/401 (44%)

```

Query:   92 AGGIPLLARLLKTSHEMMLIPVVGTLQECASEENYRAAIKAERIENLVKNLSENQQL 151
      +GG PL A      +N+ +      L      E Y      + E ++E ++ L S++ Q+Q
Sbjct:   45 SGG-PLKALTTLVYSDNLNLQRSAALAFAEITEKYVRQVSRE-VLEPILILLQSQDPQIQ 102

Query:   152 EHCAMAIYQCAEDKETRDLVRLHGGLKPLASLLNNTDNKERLAAVTGAIWKCSISKENV 211
      A+      A + E + L+      GGL+PL + +      DN E      G I      + +N
Sbjct:   103 VAACAALGNLAVNNENKLLIVEMGGLEPLINQMMG-DNVEVQCNAVGCITNLATRDDNKH 161

Query:   212 KFREYKAIEITLVGLLTDQPEEVLNVVVGALGECCQERENRVIVRKCGGIQPLVNLLVGIN 271
      K      A+ L L      + V N GAL      ENR +      G + LV+LL +
Sbjct:   162 KIATSGALIPLTKLAKSKHIRVQRNATGALLNMTHSEENRKELVNAGAVPVLVSLLSSTD 221

Query:   272 QALLVNVTKAVGACAVEPESMMIIDRLDG--VRLLWSLLKNPHPDVKASAAWALCPCIKN 329
      +      T A+ AV+ +      + + + V L SL+ +P VK A AL      +

```

Sbjct: 222 EDVQYYCTTALSNIADVDEANRKKLAQTEPRLVSKLVSLMDSPSSRVKQCATLALRNLASD 281

Query: 330 AKDAGEMVRSFVGGLLELIVNLLKSDNKE-VLASVCAAITNIAKDQENLAVITDHGVV-PL 387
 E+VR+ GGL +V L++SD+ VLASV A I NI+ N +I D G + PL

Sbjct: 282 TSYQLEIVRA--GGLPHLVKLIQSDSIPLVLASV-ACIRNISIHLNEGLIVDAGFLKPL 338

Query: 388 LSKLANTNNKLRHHLAEAISRCCMWG-RNRVAFGEHKAVAPLVRYLKSNDTNVHRATAQ 446
 + L ++ +++ H + +NR F E AV + +V ++

Sbjct: 339 VRLLDYKDSEEIQCHAVSTLRNLAASSEKNRKEFFESGAVEKCKELALDSPVSV-QSEIS 397

Query: 447 ALYQLSEAD-NCITMHENGAVKLLLDVMGSPDQDLQEEAAAGCISNI 492
 A + + AD + + + E + L+ M S +Q++ AA ++N+

Sbjct: 398 ACFAILALADVSKLDLLEANILDALIPMTFSQNEVSGNAAAALANL 444

Score = 213 (32.0 bits), Expect = 3.6e-14, P = 3.6e-14
 Identities = 81/341 (23%), Positives = 163/341 (47%)

Query: 163 EDKETRDVRLHGGKPLASLLNNTD-NKERLAAVTGAIWKCSISKENVTKFREYKAIET 221
 EDK+ D G LK L +L+ + + N +R AA+ A I+++ V + + +E

Sbjct: 36 EDKQDLDFYS-GGPLKALTTLVSDNLNQRSAAALFA----EITEKYVRQVSR-EVLEP 89

Query: 222 LVGLLTDQPEEVLVNVVVGALGECCQERENRVIVRKCGLIQLVNLVGINQALLVNVTKA 281
 ++ LL Q ++ V ALG EN++++ + GG++PL+N ++G N + N

Sbjct: 90 ILILLQSQDPQIQVAACAALGNLAVNNENKLLIVEMGGLEPLINQMMGDNVEVQCNVAVGC 149

Query: 282 VGACAVEPESMMIIDRLDGVRLLSLLKNPHDPVKASAALWALCPCIKNAKDAGEMVRSFV 341
 + A ++ I + L L K+ H V+ +A AL + ++ E+V +

Sbjct: 150 ITNLATRDDNKHKIATSGALIPLTAKLAKSKHIRVQRNATGALLNMTHSEENRKELVNA-- 207

Query: 342 GGLLELIVNLLKSDNKEVLASVCAAITNIAKDQENLAVI--TDHGVVPLLSKLANTNNK 399
 G + ++V+LL S + +V A++NIA D+ N + T+ +V L L ++ +++

Sbjct: 208 GAVPVLVSLSSSTDPOVQYYCTTALSNIADVDEANRKKLAQTEPRLVSKLVSLMDSPSSRV 267

Query: 400 RHHLAEAISRCCMWGRNRVAFGEHKAVAPLVRYLKSNDTNVHRATAQALYQLSEADNCI 459
 + A+ ++ + LV+ ++S+ + A+ + +S N

Sbjct: 268 KCQATLALRNLASDTSYQLEIVRAGGLPHLVKLIQSDSIPLVLASVACIRNISIHLNEG 327

Query: 460 TMHENGAVKLLLDVMGSPDQDLQEEAAAGCISNIRLALATEKAR 503
 + + G +K L+ ++ D + E +S +R LA ++EK R

Sbjct: 328 LIVDAGFLKPLVRLLDYKDSE--EIQCHAVSTLRNLAASSEKNR 369

Score = 180 (27.0 bits), Expect = 1.6e-10, P = 1.6e-10
 Identities = 80/346 (23%), Positives = 142/346 (41%)

Query: 145 SENEQLQEHCAIAIYQCAEDKETRDVRLHGGKPLASLLNNTDNKERLAAVTGAIWKCS 204
 S+N LQ A+A + E K R + R L+P+ LL + D + ++AA A+ +

Sbjct: 58 SDNLNQRSAAALFAEITE-KYVRQVSR--EVLEPILILLQSQDPQIQVAACA-ALGNLA 113

Query: 205 ISKENVTKFREYKAIETLVGLLTDQPEEVLVNVVVGALGECCQERENRVIVRKCGLIQLV 264
 ++ EN E +E L+ + EV N VG + +N+ + G + PL

Sbjct: 114 VNNENKLLIVEMGGLEPLINQMMGDNVEVQCNVAVGCITNLATRDDNKHKIATSGALIPLT 173

Query: 265 NLLVGINQALLVNVTKAVGACAVEPESMMIIDRLDGVRLLSLLKNPHDPVKASAALWALC 324
 L + + N T A+ E+ + V +L SLL + PDV+ AL

Sbjct: 174 KLAKSKHIRVQRNATGALLNMTHSEENRKELVNAGAVPVLVSLSSSTDPOVQYYCTTALS 233

Query: 325 PCIKNAKDAGEMVRSFVGGLLELIVNLLKSDNKEVLASVCAAITNIAKDQENLAVITDHGV 384
 + + ++ ++ + +V+L+ S + V A+ N+A D I G

Sbjct: 234 NIAVDEANRKKLAQTEPRLVSKLVSLMDSPSSRVKQCATLALRNLASDTSYQLEIVRAGG 293

Query: 385 VPLLSKLANTNNKLRHHLAEAISRCCMWGRNRVAFGEHKAVAPLVRYLKSNDTNVHRAT 444
 +P L KL +++ L I + N + + PLVR L D+ +

Sbjct: 294 LPHLVKLIQSDSIPLVLASVACIRNISIHLNEGLIVDAGFLKPLVRLLDYKDSEEIQCH 353

Query: 445 A-QALYQLSEAD-NCITMHENGAVKLLLDVMGSPDQDLQEEAAAGCIS 490
 A L L+ ++ N E+GAV+ ++ +Q + C +

Sbjct: 354 AVSTLRNLAASSEKNRKEFFESGAVEKCKELALDSPVSVQSEISACFA 401

Score = 155 (23.3 bits), Expect = 8.8e-08, P = 8.8e-08
 Identities = 88/401 (21%), Positives = 175/401 (43%)

Query: 60 LYEAR--VEVARCGALALWSCSKSHTNKEAIRKAGGI-PLLARLLKTSHEENMLIPVVG 116
 L +++D ++VA C AL + + ++ NK I + GG+ PL+ +++ + E + VG

Sbjct: 93 LLQSQDPQIQVAACAALG--NLAVNNENKLLIVEMGGLEPLINQMMGDNVE-VQCNVAVGC 149

Query: 117 LQECASEENYRAAIIKAERIIENLVKNLNSENEQLQEHCAIAIYQCAEDKETR-DLVRLHG 175
 + A+ ++ + I + L K S++ ++Q + A+ +E R +LV G

Sbjct: 150 ITNLATRDDNKHKIATSGALIPLTAKLAKSKHIRVQRNATGALLNMTHSEENRKELVNA-G 208

Query: 176 GLKPLASLLNNTDNKERLAAVTGAIWKCSISKENVTKFR--EYKAIETLVGLLTDQPEEV 233
 + L SLL++TD + T A+ ++ + N K E + + LV L+ V

Sbjct: 209 AVPVLVSLLSSTDPDVQYYCTT-ALSNIADVDEANRKKLAQTEPRLVSKLVSLMDSPPSSRV 267

Query: 234 LVNVVVGALGECCQERENRIVRKCGGIQPLVNLVGINQALLVNVTKAVGACAVEPESMM 293
AL + ++ + + GG+ LV L+ + L++ + ++ P +

Sbjct: 268 KCQATLALRNLASDTSYQLEIVRAGGLPHLVKLIQSISIPLVLASVACIRNISIHPLNEG 327

Query: 294 IIDRLDGVRLWLSLK-NPHDPVKASAAWALCPCIKNA-KDAGEMVRSFVGGLELIVNLL 351
+I ++ L LL +++ A L ++ K+ E S G +E L

Sbjct: 328 LIVDAGFLKPLVRLLDYKDSEEIQCHAVSTLRNLAASSEKNRKEFFES--GAVEKCKELA 385

Query: 352 KSDNKEVLA--SVCAAITNIAKDQENLAVITDHGVVPLLSKLANTNNKLRHHLAEAISR 409
V + S C AI +A D L ++ + ++ L + + N ++ + A A ++

Sbjct: 386 LDSPVSVQSEISACFAILALA-DVSKDLL-EANILDALIPMTFSQNEVSGNAAAALAN 443

Query: 410 CCMWGRNRVAFGE-----HKAVAP-LVRYLKSNDTNVHRATAQALYQLSE 453
C N E ++ + L+R+LKS+ + QL E

Sbjct: 444 LCSRNNYTKIIEAWDRPNEGIRGFLIRFLKSDYATFEHIALWTILQLE 493

Score = 139 (20.9 bits), Expect = 5.0e-06, P = 5.0e-06
Identities = 80/329 (24%), Positives = 142/329 (43%)

Query: 37 GGITKLVALLDCAHD-STKPAQ---SSLYEARDVEVARCGALWSCSKSHTNKEAIRKA 92
G I T L D H +T A + L +++ + V R AL + + S N++ + A

Sbjct: 148 GCITNLATRDDNKHKIATSGALIPLTKLAKSKHIRVQRNATGALLNMTHSEENRKELVNA 207

Query: 93 GGIPLLARLLKTSHENMLIPVVGTLQECASEE-NYRAAIKAE-RIENLVKNLNSENEQL 150
G +P+L LL ++ ++ L A +E N + + E R++ LV ++S + ++

Sbjct: 208 GAVPVLVSLLSSTDPDVQYYCTTALSNIADVDEANRKKLAQTEPRLVSKLVSLMDSPPSSRV 267

Query: 151 QEHCAIAIYQCAEDKETR-DLVRLHGGGLKPLASLLNNTDNKERLAAVTGAIWKCSISKEN 209
+ +A+ A D + ++VR GGL L L+ + D+ + A I SI N

Sbjct: 268 KCQATLALRNLASDTSYQLEIVRA-GGLPHLVKLIQS-DSIPLVLASVACIRNISIHPLN 325

Query: 210 VTKFREYKAJETLVGLLT-DQPEEVLVNVVVGALGECCQERE-NRVIVRKCGGIQPLVNL 267
+ ++ LV LL EE+ + V L E NR + G ++ L

Sbjct: 326 EGLIVDAGFLKPLVRLLDYKDSEEIQCHAVSTLRNLAASSEKNRKEFFESGAVEKCKELA 385

Query: 268 VG--INQALLVNVTKAVGACA-VEPESMMIIDRLDGVRLWLSLKPNPHDPVKASAAWA-L 323
+ ++ ++ A+ A A V ++ + LD + + + +N A+AA A L

Sbjct: 386 LDSPVSVQSEISACFAILALADVSKDLLEANILDAL-IPMTFSQNEVSGNAAAALANL 444

Query: 324 CPCIKN-AKDAGEMVRSFVGGLELIVNLLKSD 354
C + N K R G ++ LKSD

Sbjct: 445 CSRNNYTKIIEAWDRPNEGIRGFLIRFLKSD 476

Score = 136 (20.4 bits), Expect = 1.1e-05, P = 1.1e-05
Identities = 72/304 (23%), Positives = 133/304 (43%)

Query: 58 SSLYEARDVEVARCGALWSCSKSHTNKEAIRKAGGIPLARLLKTSHENMLIPVVGTL 117
+ L +++ + V R AL + + S N++ + AG +P+L LL ++ ++ L

Sbjct: 173 TKLAKSKHIRVQRNATGALLNMTHSEENRKELVNAGAVPVLVSLLSSTDPDVQYYCTTAL 232

Query: 118 QECASEE-NYRAAIKAE-RIENLVKNLNSENEQLQEHCAIAIYQCAEDKETR-DLVRLH 174
A +E N + + E R++ LV ++S + +++ +A+ A D + ++VR

Sbjct: 233 SNIADVDEANRKKLAQTEPRLVSKLVSLMDSPPSSRVKCQATLALRNLASDTSYQLEIVRA- 291

Query: 175 GGLKPLASLLNNTDNKERLAAVTGAIWKCSISKENVTKFREYKAJETLVGLLT-DQPEEV 233
GGL L L+ + D+ + A I SI N + ++ LV LL EE+

Sbjct: 292 GGLPHLVKLIQS-DSIPLVLASVACIRNISIHPLNEGLIVDAGFLKPLVRLLDYKDSEEI 350

Query: 234 LVNVVVGALGECCQERE-NRVIVRKCGGIQPLVNLVGINQALLVNVTKAVGACA-VEP 289
+ V L E NR + G ++ L + ++ ++ A+ A A V

Sbjct: 351 OCHAVSTLRNLAASSEKNRKEFFESGAVEKCKELALDSPVSVQSEISACFAILALADVSK 410

Query: 290 ESMMIIDRLDGVRLWLSLKPNPHDPVKASAAWA-LCPCIKN-AKDAGEMVRSFVGGLELI 347
++ + LD + + + +N A+AA A LC + N K R G +

Sbjct: 411 LDLLEANILDAL-IPMTFSQNEVSGNAAAALANLCSRNNYTKIIEAWDRPNEGIRGFL 469

Query: 348 VNLLKSD 354
+ LKSD

Sbjct: 470 IRFLKSD 476

Score = 114 (17.1 bits), Expect = 2.7e-03, P = 2.7e-03
Identities = 71/335 (21%), Positives = 132/335 (39%)

Query: 1 MVNILDSPHSLKCLAAETIANVAKFKRARRVVRQHGGITKLVALLDCAHDSTKPAQSSSL 60
+ + S H ++ A + N+ + R+ + G + LV+LL ST P

Sbjct: 172 LTKLAKSKHIRVQRNATGALLNMTHSEENRKELVNAGAVPVLVSLLS-----STDP----- 222

Query: 61 YEARDVEVARCGALWSCSKSHTNKEAIRKAGGIPLARLLKTSHENMLIPVVGTLQEC 120
DV+ AL+ + +++ K A + + L L+ + + L+

Score = 106 (15.9 bits), Expect = 2.0e-02, P = 2.0e-02
Identities = 49/204 (24%), Positives = 89/204 (43%)

Pedant information for DKFZphtes3 35p17, frame 3

Report for DKF2phtes3 35p17.3

```
SEQ      MVNILDSPHKSCLKLAAETIANVAKFKRARRVVVRQHGGITKLVALLDCAHDSTKPAQSSL
SEG      .....XXXXXXXXXXXXX.....
2bct-    .....HH

SEQ      YEARDVEVARCGALALWSCSKSHTNKEAIRKAGGIPLLARLLKTSHENMLIPVVGTLQEC
SEG      .....
2bct-    HRCCHHHHHHHHHHHHHHHHHHHHCCHHHHHHHHHHGGGCCCHHHHHHHHHHHHHHHHHHH

SEQ      ASEENYRAAIKAERI IENLVKNLSENEQLQEHCCAMAIYQCAEDKETRDVLRLHGLGKPL
SEG      .....
2bct-    HHTTTTNNNNNNNNNNHCNNNNNNNNNNCCCCNNNNNNNNNNNNNNNNNNNTTNNNNNNNNNNHCNNNN
```


SEQ ASLLNNTDNKERLAAVTGAIWKCSISKENVTKFREYKAIETLVGLLTDQPEEVLNVVGA
SEG
2bct- HHHHH-HCCCHHHHHHHHHHHHHHCCCHHHHHHHHHCHHHHHHTTTTCCHHHHHHHHHH

SEQ LGECQERENRVIVRKCGGIQPLVNLLVGINQALLVNVTKAVGACAVEPESMMIIDRLDG
SEG
2bct- H-----HHHHHCCCCTTTHHHHHHHHHHHCTTTHHHHHHHHTTTHHHHHHHH-HHCH

SEQ VRLLWSLLKNPHPDVKASAAWALCPCIKNAKDAGEMVRSFVGGLIVNLLKSDNKEVLA
SEG
2bct- HHHHHHHHTTTHHHHHHHHHHHHHHCCCHH-HHHHHHHHHHHHHHHCTTTTTHHHH

SEQ SVCAAITNIAKDQENLAVITDHGVVPLLSKLANTNNKLRHHLAEAISRCCMWGRNRVAF
SEG
2bct- HHHHHHHHHHCGGGHHHHHHHHCHHHHHHHHHHHHTTCCHHHHHHHHHHCHHHHH

SEQ GEHKAVAPLVRYLKSNDTNVHRATAQALYQLSEADNCITMHENGAVKLLLDVMGSPDQD
SEG
2bct- HTTTHHHHHHHHHCCCHHHHHHHHHHHHTTTHHHHHHHHCCCHHHHHHTTTTTHH

SEQ LQEAAAGCISNIRRLALATEKARYT
SEG
2bct- HHHHHHHHH.....

(No Prosite data available for DKFzphtes3_35p17.3)

(No Pfam data available for DKFzphtes3_35p17.3)

DKFZphtes3_35p22

group: cell cycle

DKFZphtes3_35p22 encodes a novel 549 amino acid protein, with similarity to oncogene 1 (tre-2 locus).

The novel protein is closely related to human tre-2 and other enzymes involved in the degradation of ubiquitinated proteins. The human tre-2 oncogene encodes a deubiquitinating enzyme, indicating a role for the ubiquitin system in mammalian growth control.

The novel protein can find application in cancer diagnostics and treatment, and in regulating protein stability and growth control via regulation of ubiquitination.

strong similarity to oncogene 1 (tre-2 locus)

membrane regions: 1

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: map="17"

Insert length: 2072 bp

Poly A stretch at pos. 2062, polyadenylation signal at pos. 2039

```

1  GTTACACACA GGCAGTGGTA TCTGTGAGCA GCTCTGTGGA CTCAAAGGTT
51 TTCTCCCTGA GAGGCATGAC CCAGGCCAGC TGATTCATCA GAATCAGGAT
101 GGACGTGGTA GAGGTCGCGG GCAGTTGGTG GGCACAAGAG CGAGAGGACA
151 TCATTATGAA ATACGAAAAG GGACACCGAG CTGGGCTGCC AGAGGACAAG
201 GGGCCTAAGC CTTTTCGAAG CTACAACAAC AACGTCGATC ATTTGGGGAT
251 TGTACATGAG ACGGAGCTGC CTCCTCTGAC TGCGCGGGAG GCGAAGCAAA
301 TTCGGCGGGA GATCAGCCGA AAGAGCAAGT GGGTGGATAT GCTGGGAGAC
351 TGGGAGAAAT ACAAAGCAG CAGAAAGCTC ATAGATCGAG CGTACAAGGG
401 AATGCCCATG AACATCCGGG GCCCGATGTG GTCAGTCCTC CTGAACACTG
451 AGGAAATGAA GTTGA AAAAC CCCGGAAGAT ACCAGATCAT GAAGGAGAAG
501 GGCAAGAAGT CATCTGAGCA CATCCAGCGC ATCGACCGGG ACGTAAGCGG
551 GACATTAAGG AAGCATATAT TCTTCAGGGA TCGATACGGA ACCAAGCAGC
601 GGGAACTACT CCACATCCTC CTGGCATATG AGGAGTACAA CCCGGAGGTG
651 GGCTACTGCA GGGACCTGAG CCACATCGCC GCCTTGTTCC TCCTCTATCT
701 TCCTGAGGAG GATGCATTCT GGGCACTGGT GCAGCTGCTG GCCAGTGAGA
751 GGCATCCCTC GCAGGGATTT CACAGCCCAA ATGGCGGGAC CGTCCAGGGG
801 CTCCAAGACC AACAGGAGCA TGTGGTAGCC ACGTCACAAC CCAAGACCAT
851 GGGGCATCAG CACAAGAAAG ATCTATGTGG GCAGTGTTCC CCGTTAGGCT
901 GCCTCATCCG GATATTGATT GACGGGATCT CTCTCGGGCT CACCTTGCGC
951 CTGTGGGACG TGTATCTGGT AGAAGGCGAA CAGGCGCTGA TGCCGATAAC
1001 AAGAATCGCC TTTAAGGTTT AGCAGAAGCG CCTCACGAAG ACGTCCAGGT
1051 GTGGCCCGTG GGCACGTTTT TGCAACCGGT TCGTTGATAC CTGGGCCAGG
1101 GATGAGGACA CTGTGCTCAA GCATCTTAGG GCCTCTATGA AGAACTAAC
1151 AAGAAAGAAG GGGGACCTGC CACCCCCAGC CAAACCCGAG CAAGGGTCGT
1201 CGGCATCCAG GCCTGTGCCG GCTTCACGTG GCGGGAAGAC CCTCTGCAAG
1251 GGGGACAGGC AGGCCCTCC AGGCCACCA GCCCGGTTCC CGCGGCCAT
1301 TTGGTCAAGT TCCCGGCCAC GGGCACCTCG TTCTTCCACA CCCTGTCTTG
1351 GTGGGGCTGT CCGGGAAGAC ACCTACCCTG TGGGCACTCA GGGTGTGCCC
1401 AGCCCGGCC C TGGCTCAGGG AGGACCTCAG GGTTCCTGGA GATTCTTGCA
1451 GTGGAATCC ATGCCCGGCC TCCCAACGGA CCTGGACGTA GAGGGCCCTT
1501 GGTTCGCCCA TTATGATTTT AGACAGAGCT GCTGGGTCCG TGCCATATCC
1551 CAGGAGGACC AGCTGGCCCC CTGCTGGCAG GCTGAACACC CTGCGGAGCG
1601 GGTGAGATCG GCTTTCGCTG CACCCAGCAC TGATTCCGAC CAGGGCACCC
1651 CCTTCAGAGC TAGGGACGAA CAGCAGTGTG CTCCACCTC AGGGCCTTGC
1701 CTCTGCGGCC TCCACTTGGA AAGTTCTCAG TTCCCTCCAG GCTTCTAGAA
1751 GCATCTGGGC CAGGGCTCAT GGCTGGATAA TTTCCCTAGG CTTAACAACC
1801 CAAGCAAGCT TCGCATCCTC GTTTTATTTT TGGTTAAACT TATGAAAATG
1851 TATTAAGAAA GAGTGCAGCT CGAGAGAGAT TCAGAGATGG AACACACCAG
1901 ACCCCAGATC ACAAAGCCAA CCATGCCCGC CCCCTCCAG CACCCCCAGC
1951 CCCACGACCA TCGTTCTGAA TTCTGACGAC ACCGTGAGCC TGCTTTGTA
2001 CTTCAAACCT ATGGAAGGAT AACCACCTTC ATGTTTGTAA ATAAATGTTT
2051 CCTGTTGAAA TGAAAAAAA AA

```

BLAST Results

Entry AC003976 from database EMBL:
Homo sapiens chromosome 17, clone hCIT.91 J.4, complete sequence.
Score = 4385, P = 0.0e+00, identities = 881/886

14 exons

Entry HSG19723 from database EMBL:

human STS A001W35.

Score = 850, P = 1.9e-32, identities = 170/170

Medline entries

92228503:

A novel transcriptional unit of the tre oncogene widely expressed in human cancer cells.

94067315:

The yeast DOA4 gene encodes a deubiquitinating enzyme related to a product of the human tre-2 oncogene.

95176708:

UBP5 encodes a putative yeast ubiquitin-specific protease that is related to the human Tre-2 oncogene product.

Peptide information for frame 3

ORF from 99 bp to 1745 bp; peptide length: 549
Category: strong similarity to known protein

```
1 MDVVEVAGSW WAQEREDIIM KYEKGHRAGL PEDKGPKPFR SYNNNVVDHLG
51 IVHETELPPL TAREAQIRR EISRKSKWVD MLGDWEKYKS SRKLIDRAYK
101 GMPMNIRGPM WSVLLNTEEM KLKNPGRYQI MKEKGKKSSE HIQRIDRDVS
151 GTLRKHIFFR DRYGTKQREL LHILLAYEY NPEVG YCRDL SHIAALFLLY
201 LPEEDAFWAL VQLLASERHS LQGFHSPNGG TVOGLQDQQE HVVATSQPKT
251 MGHQDKKDLG GQCSPLGCLI RILIDGISLG LTLRLWDVYL VEGEQALMPI
301 TRIAFKVQQK RLTKTSRCGP WARFCNRFVD TWARD ETVL KHLRASMKKL
351 TRKKGDLPPP AKPEQGSSAS RVPVPSRGGK TLCKGDRQAP PGPPARFPRP
401 IWSASPPRAP RSSTPCPGGA VREDTYPVGT QGVPSPALAQ GGPQGSWRFL
451 QWNSMPRLPT DLDVEGPWFR HYDFRQSCWV RAISQEDQLA PCWQAEHPAE
501 RVRSAFAAPS TDS DQGTFFR ARDEQQCAPT SGPCLCGLHL ESSQFPFPGF
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_35p22, frame 3

PIR:S22155 oncogene 1 (tre-2 locus) (clone 210) - human, N = 1, Score = 2181, P = 5.5e-226

PIR:S57867 oncogene 1 - human, N = 1, Score = 1536, P = 1.2e-157

>PIR:S22155 oncogene 1 (tre-2 locus) (clone 210) - human
Length = 786

HSPs:

Score = 2181 (327.2 bits), Expect = 5.5e-226, P = 5.5e-226
Identities = 405/500 (81%), Positives = 440/500 (88%)

```
Query: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60
MD+VE A S AQER+DI+MKY+K GHRAGLPEDKGP+P N+++D GI+HETELPP+
Sbjct: 1 MDMVENADSLQAQERKDILMKYDKGHRAGLPEDKGPEPV-GINSSIDRFGILHETELPPV 59

Query: 61 TAREAQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM 120
TAREAK+IRRE++R SKW++MLG+WE YK S KLIDR YKG+PMNIRGP+WSVLLN +E+
Sbjct: 60 TAREAKIRREMTRTSKWMEMLGEWETKYHSSKLIDRVYKGIPMNIRGPVWSVLLNIQEI 119

Query: 121 KLKNPGRYQIMKEKGKKSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEY 180
KLKNPGRYQIMKE+GK+SSEHI ID DV TLR H+FFRDRYG QREL +ILLAY EY
Sbjct: 120 KLKNPGRYQIMKERGKRSSEHIHHIDLVDVTTLRNHVFFRDRYGAKQRELFYILLAYSEY 179

Query: 181 NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVOGLQDQQE 240
NPEVG YCRDL SHI ALFLLYLPEEDAFWALVQLLASERHSL GFHSPNGGTVOGLQDQQE
Sbjct: 180 NPEVG YCRDL SHITALFLLYLPEEDAFWALVQLLASERHSLPGFHSPNGGTVOGLQDQQE 239
```

Query:	241	HVVATSQPKTMGHQDKKDLCGQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI	300
		HVV SQPKTM HQDK+ LCGQC+ LGCL+R LIDGISLGLTLRLWDVYLVEGEQ LMPI	
Sbjct:	240	HVVPKSQPKTMWHQDKEGLCGQCASLGCLLRNLIDGISLGLTLRLWDVYLVEGEQVLMPI	299
Query:	301	TRIAFKVQQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKKHLRASMKKLTTRKKGDLPPP	360
		T IA KVQQKRL KTSRCG WAR N+F DTWA ++DTVLKKHLRAS KKLTRK+GDLPPP	
Sbjct:	300	TSIALKVQKRLMKTSRCGLWARLRNQFFDTWAMNDDTVLKKHLRASTKKLTKRKQDGLPPP	359
Query:	361	AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPAPRFPRIWSASPPRAPRSSTPCPGGA	420
		AK EGGS A RVPASRGGKTLCKG RQAPPGPPA+F RPI SASPP A R STPCPGGA	
Sbjct:	360	AKREQGSLAPRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICASPPWASRFSTPCPGGA	419
Query:	421	VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV	480
		VREDTYPVGTQGVPS ALAQGGPQGSWRFL+W SMPRLPTDLD+ GPWF HYDF +SCWV	
Sbjct:	420	VREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMPRLPTDLDIGGPWFPHYDFERSCWV	479
Query:	481	RAISQEDQLAPCWQAEHPAE	500
		RAISQEDQLA CWQAEH E	
Sbjct:	480	RAISQEDQLATCWQAEHCGE	499

Pedant information for DKFZphtes3 35p22, frame 3

Report for DKFZphtes3 35p22.3

```

[LENGTH]      549
[MW]           62159.16
[pI]           9.23
[HOMOL]        PIR:S22155 oncogene 1 (tre-2 locus) (clone 210) - human 0.0
[FUNCAT]       11.01 stress response [S. cerevisiae, YGR100w] 2e-16
[FUNCAT]       04.05.01.04 transcriptional control [S. cerevisiae, YGR100w] 2e-16
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YNL293w] 3e-15
[PIRKW]        transmembrane protein 6e-14
[PROSITE]      MYRISTYL 6
[PROSITE]      AMIDATION 1
[PROSITE]      CAMP_PHOSPHO_SITE 3
[PROSITE]      CK2_PHOSPHO_SITE 4
[PROSITE]      TYR_PHOSPHO_SITE 2
[PROSITE]      PKC_PHOSPHO_SITE 10
[KW]           TRANSMEMBRANE 1
[KW]           LOW COMPLEXITY 5.28 %

```

```
SEQ      MDVVEVAGSWWAQEREDIIMKYEKGRHAGLPEDKGPKPFRSYNNNDVHLGIVHETELPPL
SEG      .....
PRD      cccceecocchhhhhhhhhhhhhhhhhhhccccccccccccccccceeecccccccccccccccc
MEM
```

```
SEQ      TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLLIDRAYKGMPMNIRGPMWSVLLNTEEM
SEG      .....
PRD      chhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhhhccccccccccceeeccccc
MEM
```

```
SEQ      KLKNPGRYQIMKEKGKKSSEHIQRIDRDVSGTLRKHIFFRDRYGTQRELLHILLAYEY
SEG      .....
PRD      cccccchhhhhhhccccchhhhhhhhhhhhhccccccccccccccccchhhhhhhhhhhhhc
MEM
```

```
SEQ      NPEVGYCRDLSHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVQGLDQQDE
SEG      .....
PRD      ccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM
```

```
SEQ      HVVATSQPKTMGHGQDKKDLGCQCSPLGLIRILIDGISLGLTLRLWDVYLVGEQALMPI
SEG
PRD      hhhhhhhhhchhhhhhhhhccccccccchhhhhhhhhhhccccchhhhhhhhhccccceeehh
MEM      .MMMMMMMMMMMMMMMMMMMMMM
```

SEQ	TRIAFKVQQRLLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKKGDLPPP
SEG
PRD	hhhhhhhhhhhhhhhhcccchhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhcccc
MEM

```
SEQ      AKPEQGSASRPVPASRGGKTLCKGDRAQP GP PARFPRPIWSASP RPAPRSSTPCPGA
SEG      .....XXXXXXXXXXXXXXXXXXXXX..
PRD      CCCCCCCCCCCCCCCCCCCeccccccccccccc cccccccccccccccccccc
MEM
```

```

SEQ    VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV
SEG    .....
PRD    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
MEM    .....

SEQ    RAISQEDQLAPCWQAEPVRSFAFAAPSTDSDQGTFFRARDEQQCAPTSGLCLGLHL
SEG    .....
PRD    cchhhhhhhhhhhhhhhcchhhhhhhhhccccccccccccccccchhhhhccccccccccceee
MEM    .....

SEQ    ESSQFPFPGF
SEG    .....
PRD    ccccccccc
MEM    .....

```

Prosites for DKFZphtes3_35p22.3

PS00004	136->140	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	310->314	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	348->352	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	61->64	PKC_PHOSPHO_SITE	PDOC00005
PS00005	73->76	PKC_PHOSPHO_SITE	PDOC00005
PS00005	90->93	PKC_PHOSPHO_SITE	PDOC00005
PS00005	152->155	PKC_PHOSPHO_SITE	PDOC00005
PS00005	216->219	PKC_PHOSPHO_SITE	PDOC00005
PS00005	282->285	PKC_PHOSPHO_SITE	PDOC00005
PS00005	315->318	PKC_PHOSPHO_SITE	PDOC00005
PS00005	346->349	PKC_PHOSPHO_SITE	PDOC00005
PS00005	351->354	PKC_PHOSPHO_SITE	PDOC00005
PS00005	446->449	PKC_PHOSPHO_SITE	PDOC00005
PS00006	61->65	CK2_PHOSPHO_SITE	PDOC00006
PS00006	460->464	CK2_PHOSPHO_SITE	PDOC00006
PS00006	484->488	CK2_PHOSPHO_SITE	PDOC00006
PS00006	511->515	CK2_PHOSPHO_SITE	PDOC00006
PS00007	93->100	TYR_PHOSPHO_SITE	PDOC00007
PS00007	92->100	TYR_PHOSPHO_SITE	PDOC00007
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	101->107	MYRISTYL	PDOC00008
PS00008	230->236	MYRISTYL	PDOC00008
PS00008	276->282	MYRISTYL	PDOC00008
PS00008	366->372	MYRISTYL	PDOC00008
PS00008	441->447	MYRISTYL	PDOC00008
PS00009	134->138	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_35p22.3)

DKFZphtes3_4b4

group: testes derived

DKFZphtes3_4b4 encodes a novel 497 amino acid protein similar to SCP proteins and a human trypsin inhibitor.

The novel protein contains an extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2, predicted by Prosite and Pfam. This domain is found in a variety of extracellular proteins from eukaryotes that have been found to be evolutionary related. The exact function of these proteins is not yet known. In addition, the protein is similar to a human trypsin inhibitor.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes or as a new protease inhibitor.

strong similarity to trypsin inhibitor

might be a new protease inhibitor?

Sequenced by AGOWA

Locus: /map="333.4 cR from top of Chr16 linkage group"

Insert length: 4574 bp

Poly A stretch at pos. 4551, polyadenylation signal at pos. 4539

```
1  GCGGGCTGCT  CCCATTGAGC  TGTCTGCTCG  CTGTGCCCGC  TGTGCCCTGCT
51  GTGCCCCGCG  TGTCCGCGCT  GCTACCGCGT  CTGCTGGACG  CGGGAGACGC
101 CAGCGAGCTG  GTGATTGGAG  CCCTGCGGAG  AGCTCAAGCG  CCCAGCTCTG
151 CCCGAGGAGC  CCAGGCTGCC  CCGTGAGTCC  CATAGTTGCT  GCAGGAGTGG
201 AGCCATGAGC  TGCCTCCTGG  GTGGTGTCTC  CCCCTTGGGG  CTGCTGTTCC
251 TGGTCTGCGG  ATCCCAAGGC  TACCTCCTGC  CCAACGTCAC  TCTCTTAGAG
301 GAGCTGCTCA  GCAAATACCA  GCACAACGAG  TCTCACTCCC  GGGTCCGCAG
351 AGCCATCCCC  AGGGAGGACA  AGGAGGAGAT  CCTCATGCTG  CACAACAAGC
401 TTCGGGGCCA  GGTGCAGCCT  CAGGCCCTCA  ACATGGAGTA  CATGACCTGG
451 GATGACGAAC  TGGAGAAGTC  TGCTGCAGCG  TGGGCCAGTC  AGTGCATCTG
501 GGAGCACGGG  CCCACCACTC  TGCTGGTGTC  CATCGGGCAG  AACCTGGGCG
551 CTCCTGGGG  CAGGTATCGC  TCTCCGGGGT  TCCATGTGCA  GTCCTGGTAT
601 GACGAGGTGA  GAGACTACAC  CTACCCCTAC  CCGAGCGAGT  GCAACCCCTG
651 GTGTCCAGAG  AGGTGCTCGG  GGCCTATGTG  CACGCACTAC  ACACAGATAG
701 TTTGGGCCAC  GACCAACAAG  ATCGGTTGTG  CTGTGAACAC  CTGCCGGAAG
751 ATGACTGTCT  CCGGAGAAAGT  TTGGGAGAAC  GCGGTCTACT  TTGTCTGCAA
801 TTATTCTCCA  AAGGGGAAGT  GGATTGGAGA  AGCCCCCTAC  AAGAATGGCC
851 GGCCCTGTCT  TGAGTGCCCA  CCCAGCTATG  GAGGCAGCTG  CAGGAACAAC
901 TTGTGTTACC  GAGAAGAAAC  CTACACTCCA  AAACCTGAAA  CGGACGAGAT
951 GAATGAGGTT  GAAACGGCTC  CCATTCTCTG  AGAAAACCAT  GTTTGGCTCC
1001 AACCGAGGGT  GATGAGACCC  ACCAAGCCCA  AGAAAACCTC  TCGGGTCAAC
1051 TACATGACCC  AAGTCGTCAG  ATGTGACACC  AAGATGAAGG  ACAGGTGCAA
1101 AGGGTCCACG  TGTAACAGGT  ACCAGTGCCC  AGCAGGCTGC  CTGAACCACA
1151 AGGCCAAGAT  CTTTGGAACT  CTGTTCTATG  AAAGCTCGTC  TAGCATATGC
1201 CGCGCCGCCA  TCCACTACGG  GATCCTGGAT  GACAAGGGAG  GCCTGGTGGA
1251 TATCACCAGG  AACGGGAAGG  TCCCTTCTT  CGTGAAGTCT  GAGAGACACG
1301 GCGTGCAGTC  CCTCAGCAAA  TACAAACCTT  CCAGCTCATT  CATGGTGTCA
1351 AAAGTGAAG  TGCAGGATTT  GGACTGCTAC  ACGACCGTTG  CTCAGCTGTG
1401 CCCGTTTGAA  AAGCCAGCAA  CTCACGCCCC  AAGAATCCAT  TGTCGGGCAC
1451 ACTGCAAGA  CGAACCTTCC  TACTGGGCTC  CGGTGTTTGG  AACCACATC
1501 TATGCAGATA  CCTCAAGCAT  CTGCAAGACA  GCCGTGCACG  CGGGAGTCAT
1551 CAGCAACGAG  AGTGGGGGTG  ACGTGGACGT  GATGCCCGTG  GATAAAAAGA
1601 AGACCTACGT  GGGCTCGCTC  AGGAATGGAG  TTCAGTCTGA  AAGCCTGGGG
1651 ACTCCTCGGG  ATGGAAGGCG  CTTCCGGATC  TTTGCTGTCA  GGCAGTGAAT
1701 TTCCAGCACC  AGGGGAGAAG  GGGCGTCTTC  AGGAGGGCTT  CGGGGTTTTG
1751 CTTTATTATT  TATTTTGTCA  TTGCGGGGTA  TATGGAGAGT  CAGGAACTT
1801 CCTTTGACTG  ATGTTCACTG  TCCATCACTT  TGTGGCCTGT  GGGTGAGGTG
1851 ACATCTCATC  CCTCACTGTA  AGCAACAGCA  TCCCAAGGTG  CTCAGCCGGA
1901 CTCCCTGGTG  CCTGATCCTG  CTGGGGCCCC  GGGGTCTCCA  TCTGGACGTC
1951 CTCTCTCCTT  TAGAGATCTG  AGCTGTCTCT  TAAAGGGGAC  AGTTGCCCAA
2001 AATGTTCTCT  GCTATGTGTT  CTTCTGTTGG  TGGAGGAAGT  TGATTTCAAC
2051 CTCCCTGCCA  AAAGAACAAC  CCATTGGAAG  CTCACAATTG  TGAAGCATT
2101 ACGGCGTCGG  AAGAGGCCTT  TTGAGCAAGC  GCCAATGAGT  TTCAGGAATG
2151 AAGTAGAAGC  TAGTTATTTA  AAAATAAAAA  ACACACTCCC  TCCCTACCAA
2201 TAGAGAAAAA  TGTTTAAAT  GTTTGCTGGT  CAGACAGACA  AATGGGCTAG
2251 AGTAAGAGGG  CTGCGGGTAT  GAGAGACCCC  GGCTCCGCCC  TGGCACGTGT
2301 CCTTGCTGGC  GGGCCGCCAC  AGGCCCTTCT  CAATGGCCCG  ATTGAGGATG
2351 GCTCTATACA  CAGCAGTGCT  GGTTTATGTA  GAGTTCAGCA  GTCACTTCAG
2401 AGATGTATCT  TGTCTTTGTC  AGGCCCTTCA  TCTTCATGGC  CCACCTGTTT
2451 TCTGCCGTGA  CCTTTGGTCC  CATTGAGGAC  TAAGGATCGG  GACCCCTTCT
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2501 TTACCCCTTA CCCATTGTGG CTCCCACCCT GCCTCGGACT GGTTTACGTG
2551 TCCTGGTTCA CACCCAGGAC TTTTCTTTGC AAGCGAACCT GTTTGAAGCC
2601 CAAGTCTTAA CTCCTGGTCT CGTAAGGTTC CACTGAGACG AGATGTCTGA
2651 GAACAACCAA AGAAGGCCTG CTCTTTGCTG CTTTAAAAA ATGACAATTA
2701 AATGTGCAGA TTCCCCACGC ACCCGATGAC CTATTTTTTC AGCCGTGGGA
2751 GGAATGGAGT CTTTGGTACA TTCTCACCG AGGTTAGCAG CTCAGTTTGT
2801 GGTTATGAAA CCGTCTGTGG CCTCATGACA GCGAGAGATG GGAATACACT
2851 AGAAGGATCT CTTTTCCTGT TTTCGTGAAA CGACTCTTGC CAAACGTTCC
2901 CGAGGCGCCA AGGAGTGTAG TACACCCTGG CTGCCATCAC TCTATAAAG
2951 TGCTTCATGA GCCCAGACCA AAAGCCCACA GTGAAATGAA GTACCCTTTT
3001 GTAAATAGCA TTTTTTGTCA GAAGGTGAAA ATTCCACTCT CTACCACCGG
3051 GCCAGCCAAT AGATCACTTT GGTGAATGCT AGTTTCAAAT TTGATTCAAA
3101 ATATTTCTTA GGTGAAAGAA CTAGCAGAAA GTCAAAAACT AAGATACTGT
3151 AGACTGGACA AGAAATCTA CCTGGGCACC TAGGTGATGC CTTCTTTCTT
3201 TGATTGCTTT TCTAATAAAT GCAGAATCTG AAGGTAATA GGTTTAAAC
3251 AAAACAAAAA CCCACCCTT TAAGGAGTTG GTAAAAAGCA GTCAACTCT
3301 TAGCTTGACT GAGCTAAAAA TCACAGGACT ACGTGCTTTG TGCATTGTAG
3351 TCTAGTCGTA ATTCATAGGT ACTGACTCCT CAGCCCCAAA TGTCGGAGAG
3401 GAAGAATTCG GTCAGCCTGT CAGGTCGTGA GTCCAGTTAC CACCAACAT
3451 CTGGGAAACT TCTGGGTGCT GGTGCTCTG CTGCTGGACT TTTGTGGCTG
3501 TGTCTGTGTC TGCAAGATAA ATTAGATCGC CTGTGGGGT TTGCAGAATT
3551 AGTGAAGGGT CCAGGACGAT CCCAGTGGGC TCCTTCCAA AGCATCCAC
3601 TCAAGGGAGA CTTGAACTT CCAGTGTGAG TTGACCCAT CATTTAAAAA
3651 TAAAGTCCCC GGGTTCCCTTA ATGCCCTCCT CACTGGGCCT TCCTAGCAGG
3701 ATAGAAAGTC CTTGCCAGA GCAGGACCTG GCTGTCTTT TTTTTTTTTT
3751 TTTCCCGAGA CCAAGTTTCA CTCTGTTGCC CAAGGTAGAG TGCAGTGGCG
3801 TGATCTCTGC TCATTGCAAC TGCCGCCCTC CGGGTTCAAG CAATTCTCAT
3851 GCATCAGCCT CCAAGTACC TGGGACTACA GGCGTGAGCT ACCATGCCCG
3901 GCTAATTTTT GTATTTTATG TAGAGATGGG GTTTCATTAT GTTGGCCAGG
3951 CTGGTCTCGA ACTCCTTACC TCAGGTGATC CACCCACCTT GGCTCCCGA
4001 AGTGCTGGGA TTACAGGCAT GAGCCACTGC GCCCGGCCAT GGACCTGGCT
4051 GTCTTTATCA TCCCCACAAA CATTTTGAAA CTGGAATATT TGTCTTCAGA
4101 AAATGGAAAC AAGACTATAA ATGATAAGCC CTGTCCCTAG CACCACCTCT
4151 CCTGTGTGTG GAATAGAGGC CCCTCGTGCT ACCAACACTT ACCCTGTGTT
4201 TAAAAAGATC TTGTACCAAG CCAACGGCGT TCCTGGCTCT CCTGCCACA
4251 GGATGAACAT TTTCGGCTTC CTTAGGAGTT TTGCCCTACC GTATTCCAAA
4301 GCGTGTGTGT GTTTCTCATA TTGTCTGTAG GCTCACTCAG CCCGCAGTTT
4351 ATGTGTGTGT TTTTCTCTAT GAAAAATGAT GTATTTTGCT ACTTCTGTG
4401 TACAAAGTTT TATTGTAAAT GTTTTGTGT CTTTGCATGA ACAGGGGCCA
4451 CGTTGTTGCA ATTGTTTCAG TAGAAGTGGT TTGATTCTA AAATGTTCTT
4501 GTAACATATC TTTTATGAAC AAATCTGAAC AATTTGTGAA ATAAACATT
4551 GAAAACAAA AAAAAAAAAA AAAA

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BLAST Results

Entry HS834352 from database EMBL:
human STS WI-15502.
Score = 1331, P = 5.4e-54, identities = 287/301

Medline entries

98146272:
cDNA cloning of a novel trypsin inhibitor with similarity to
pathogenesis-related proteins, and its
frequent expression in human brain cancer cells.

Peptide information for frame 1

ORF from 205 bp to 1695 bp; peptide length: 497
Category: strong similarity to known protein

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1 MSCVLGGVIP LGLLFLVCGS QGYLLPNVTL LEELLSKYQH NESHRSVRRA
51 IPREDKEEIL MLHNKLRGQV QPQASNMEYM TWDDELEKSA AAWASQCIWE
101 HGPTSLVLSI GQNLGAHWGR YRSPGFHVQS WYDEVKDYTY PYPSECNPWC
151 PERCSGPMCT HYTQIVWATT NKIGCAVNTC RKMTVWGEVW ENAVYFVCNY
201 SPKGNWIGEA PYKNGRPCSE CPPSYGGSCR NNLCYREETY TPKPETDEMN
251 EVETAPIPEE NHVWLQPRVM RPTKPKKTSV VNYMTQVVRV DTKMKDRCKG
301 STCNRYQCPA GCLNHHKAKIF GTLFYESSSS ICRAAIHYGI LDDKGGGLVDI
351 TRNGKVPFFV KSERHGVQSL SKYKPSSSFM VSKVKVDLD CYTTVAQLCP
401 FEKPATHCPR IHCPAHCKDE PSYWAPVFGT NIYADTSSIC KTAVHAGVIS

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451 NESGGDVDVM PVDKKKTYVG SLRNGVQSES LGTPRDGKAF RIFAVRQ

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_4b4, frame 1

TREMBLNEW:AF109674_1 gene: "Lg11"; product: "late gestation lung protein 1"; Rattus norvegicus late gestation lung protein 1 (Lg11) mRNA, complete cds., N = 1, Score = 968, P = 1.9e-97

TREMBL:D45027_1 product: "25 kDa trypsin inhibitor"; Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds., N = 1, Score = 738, P = 4.5e-73

TREMBL:AB009609_1 gene: "HrTT-1"; Halocynthia roretzi HrTT-1 mRNA, complete cds., N = 1, Score = 345, P = 2e-31

PIR:JC5308 testis-specific, vespid, and pathogenesis-related protein 1 precursor - human, N = 1, Score = 337, P = 1.7e-30

>TREMBLNEW:AF109674_1 gene: "Lg11"; product: "late gestation lung protein 1"; Rattus norvegicus late gestation lung protein 1 (Lg11) mRNA, complete cds.

Length = 188

HSPs:

Score = 968 (145.2 bits), Expect = 1.9e-97, P = 1.9e-97
Identities = 160/185 (86%), Positives = 170/185 (91%)

Query: 61 MLHNKLRGQVQPQASNMEYMTWDELEKSAAAWASQCIWEHGPTSLVLSIGQNLGAHWGR 120
MLHNKLRGQV P ASNMEYMTWD+ELE+SAAAWA +C+WEHGP SLLVLSIGQNL HWGR
Sbjct: 1 MLHNKLRGQVYPASNMEYMTWDEELERSAAAWAQRCLWEHGPPASLLVLSIGQNLAVHWGR 60

Query: 121 YRSPGFHVQSWYDEVKDYTYPPYSECNPWCPERCSPGPMCTHYTQIVWATTNKIGCAVNTC 180
YRSPGFHVQSWYDEVKDYTYPPY ECNPWCPCPCSG MCTHYTQ+VWATTNKIGCAV+TC
Sbjct: 61 YRSPGFHVQSWYDEVKDYTYPPYHECNPWCPERCSCGAMCTHYTQMWWATTNKIGCAVHTC 120

Query: 181 RKMTVWGEVWENAVYFVCNYSKGNWIGEAPYKNGRPCSECPSPSYGGSCRNNLCYREETY 240
R M+VWG++WENAVY VCNYSKGNWIGEAPYK+GRPCSECP SYGG CRNNLCYREE Y
Sbjct: 121 RSMVWGDWENAVYLVNYSKGNWIGEAPYKHGRPCSECPSSYGGGCRNNLCYREEHY 180

Query: 241 TPKPE 245
KPE
Sbjct: 181 HQKPE 185

Pedant information for DKFZphtes3_4b4, frame 1

Report for DKFZphtes3_4b4.1

{LENGTH} 497
{MW} 55920.00
{pI} 8.36
{HOMOL} TREMBL:D45027_1 product: "25 kDa trypsin inhibitor"; Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds. 6e-78
{FUNCAT} 99 unclassified proteins [S. cerevisiae, YJL078c] 8e-12
{BLOCKS} BL01009E Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins
{BLOCKS} BL01009D Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins
{BLOCKS} BL01009C Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins
{BLOCKS} BL01009A Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins
{PIRKW} glycoprotein 5e-22
{PIRKW} blocked amino end 5e-13
{PIRKW} brain 9e-30
{PIRKW} hydrolase 4e-09
{PIRKW} hemolymph coagulation 4e-09
{PIRKW} zymogen 4e-09
{PIRKW} alternative splicing 4e-09
{PIRKW} sperm 5e-22
{PIRKW} viroid-induced protein 2e-11
{PIRKW} venom 6e-18
{PIRKW} pyroglutamic acid 2e-11
{PIRKW} transmembrane protein 2e-10
{PIRKW} serine proteinase 4e-09
{SUPFAM} C-type lectin homology 4e-09
{SUPFAM} trypsin homology 4e-09


```

[SUPFAM] complement factor H repeat homology 4e-09
[SUPFAM] cysteine-rich secretory protein 1 6e-24
[SUPFAM] pathogenesis-related leaf protein 7e-15
[PROSITE] MYRISTYL 8
[PROSITE] CAMP_PHOSPHO_SITE 3
[PROSITE] CK2_PHOSPHO_SITE 6
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] PKC_PHOSPHO_SITE 8
[PROSITE] ASN_GLYCOSYLATION 3
[PROSITE] SCP_AG5_PRI_SC7_2 1
[PFAM] SCP-like extracellular Proteins
[KW] All Beta
[KW] SIGNAL_PEPTIDE 23
[KW] LOW_COMPLEXITY 1.21 %

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SEQ MSCVLGGVIFLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEIL
SEG .....xxxxxx.....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ MLHNKLRGQVQPQASNMEYMTWDELEKSAAAWASQCIWEHGPTSLLSIGQNLGAHWGR
SEG .....
PRD hhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ YRSPGFHVQSWYDEVKDYTYYPSECNPWCPCPERCSGPMCTHYTQIVWATTNKIGCAVNTC
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ RKMTVWGEVWENAVYFVCNYSKGNWIGEAPYKNGRPCSECPPSYGGSCRNNLCYREETY
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ TPKPETDEMNEVETAPIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTMKDRCKG
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ STCNRYQCPAGCLNHKAKIFGTLFYESSSSICRAAIHYGILDDKGGGLVDITRNGKVPFFV
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ KSERHGVQSLSKYKPSSSFMVSKVKVDLDCYTTVAQLCPFEKPATHCPRIHCPAHCKDE
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ PSYWAPVFGTNIYADTSSICKTAVHAGVISNESGGDVDMPVDKKKTYVGLRNGVQSES
SEG .....
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ LGTPRDGKAFRIFAVRQ
SEG .....
PRD ccccccccccccccccccc

```

Prosites for DKFZphtes3_4b4.1

PS00001	27->31	ASN_GLYCOSYLATION	PDOC00001
PS00001	41->45	ASN_GLYCOSYLATION	PDOC00001
PS00001	451->455	ASN_GLYCOSYLATION	PDOC00001
PS00004	181->185	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	276->280	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	464->468	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	170->173	PKC_PHOSPHO_SITE	PDOC00005
PS00005	179->182	PKC_PHOSPHO_SITE	PDOC00005
PS00005	201->204	PKC_PHOSPHO_SITE	PDOC00005
PS00005	228->231	PKC_PHOSPHO_SITE	PDOC00005
PS00005	241->244	PKC_PHOSPHO_SITE	PDOC00005
PS00005	362->365	PKC_PHOSPHO_SITE	PDOC00005
PS00005	471->474	PKC_PHOSPHO_SITE	PDOC00005
PS00005	483->486	PKC_PHOSPHO_SITE	PDOC00005
PS00006	29->33	CK2_PHOSPHO_SITE	PDOC00006
PS00006	75->79	CK2_PHOSPHO_SITE	PDOC00006
PS00006	81->85	CK2_PHOSPHO_SITE	PDOC00006
PS00006	130->134	CK2_PHOSPHO_SITE	PDOC00006
PS00006	453->457	CK2_PHOSPHO_SITE	PDOC00006
PS00006	483->487	CK2_PHOSPHO_SITE	PDOC00006
PS00007	385->393	TYR_PHOSPHO_SITE	PDOC00007
PS00008	111->117	MYRISTYL	PDOC00008
PS00008	115->121	MYRISTYL	PDOC00008
PS00008	174->180	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008

PS00008	227->233	MYRISTYL	PDOC00008
PS00008	300->306	MYRISTYL	PDOC00008
PS00008	447->453	MYRISTYL	PDOC00008
PS00008	470->476	MYRISTYL	PDOC00008
PS01010	195->207	SCP_AG5_PR1_SC7_2	PDOC00772

Pfam for DKFZphtes3_4b4.1

HMM_NAME	SCP-like extracellular Proteins		
HMM	*PQDEQDEWLKHNDFRQQVGRGLETRGNPGPQPPAsNMnPMVWNDELAt		
		P + ++E+L HN +R QV	P ASNM M+W+DEL +
Query	52	PREDKEEILMLHNKLRGQVQ-----PQASNMEYMTWDDELEK	88
HMM	IAQnWANQCiFDHHDCCWNHsnYPYGQNIAWWSsTANnPWnWssMIQMwY		
		A WA+QCI +H ++ + S GQN+ + + +++++ +Q+WY	
Query	89	SAAAWASQCIWEHGPTSLVSI---GQNLGAHWG---RYRSPGFHVQSWY	132
HMM	NEvkDYNYNWNTCKGG....NNFmVCGHYTQMVRnTfrIGCGRYICYC		
		+EVKDY Y + + +C HYTQ+VW+ T +IGC+ C+	
Query	133	DEVKDYTYPPSECNPWCPERCSPMCTHYTQIVWATTNKIGCAVNTCRK	182
HMM	NNNWrkPDPWKkKwYYVCNYCPpGNYmN*		
		+ W + W+ +Y VCNY P+GN+++	
Query	183	MTVW--GEVWENAVYFVCNYSKGNWIG	208

DKFZphtes3_4f17

group: testes derived

DKFZphtes3_4f17 encodes a novel 656 amino acid protein with weak similarity to methyl-CpG-binding proteins.

Methylation at the DNA sequence 5'-CpG is required for mammalian development. Methyl-CpG-binding proteins bind specifically to methylated DNA via a related amino acid motif and can repress transcription. The novel protein does not contain such a motif.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to methyl-CpG-binding protein

extension of HS557771/HSZ78337,
there are some differences to these sequences

Sequenced by AGOWA

Locus: /map="18"

Insert length: 2320 bp

Poly A stretch at pos. 2266, polyadenylation signal at pos. 2251

```
1 GGCAGGTTTCG CGGGTCGCTG GCGGGGGTCG TGAGGGAGTG CCGCGGGAGC
51 GGAGATATGG AGGGAGATGG TTCAGACCCA GAGCCTCCAG ATGCCGGGGA
101 GGACAGCAAG TCCGAGAATG GGGAGAATGC GCCCATCTAC TGCATCTGCC
151 GCAAACCGGA CATCAACTGC TTCATGATCG GGTGTGACAA CTGCAATGAG
201 TGGTTCCATG GGGACTGCAT CCGGATCACT GAGAAGATGG CCAAGGCCAT
251 CCGGGAGTGG TACTGTCTGG AGTGACAGAGA GAAAGACCCC AAGCTAGAGA
301 TTCGCTATCG GCACAAGAAG TCACGGGAGC GGGATGGCAA TGAGCGGGAC
351 AGCAGTGAGC CCCGGGATGA GGGTGGAGGG CGCAAGAGGC CTGTCCCTGA
401 TCCAGACCTG CAGCGCCGGG CAGGGTCAGG GACAGGGGTT GGGGCCATGC
451 TTGCTCGGGG CTCTGCTTCG CCCACAAAT CCTCTCCGCA GCCCTTGGTG
501 GCCACACCCA GCCAGCATCA CCAGCAGCAG CACCAGCAGA TCAAACGGTC
551 AGCCCGCATG TGTGGTGAGT GTGAGGCATG TCGGCGCACT GAGGACTGTG
601 GTCACGTGTA TTTCTGTCTG GACATGAAGA AGTTCTGGGG CCCCAACAAG
651 ATCCGGCAGA AGTGCCGGCT GCGCCAGTGC CAGCTGCGGG CCCGGGAATC
701 GTACAAGTAC TTCCCTTCCT CGCTCTCACC AGTGACGCCC TCAGAGTCCC
751 TGCCAAGGCC CCGCCGGCCA CTGCCACCCC AACAGCAGCC ACAGCCATCA
801 CAGAAGTTAG GGGCATCCG TGAAGATGAG GGGGCAGTGG CGTCATCAAC
851 AGTCAAGGAG CCTCTGAGG CTACAGCCAC ACCTGAGCCA CTCTCAGATG
901 AGGACCTACC TCTGGATCCT GACCTGTATC AGGACTTCTG TGCAGGGGCC
951 TTTGATGACC ATGGCCTGCC CTGGATGAGC GACACAGAAG AGTCCCCATT
1001 CCTGGACCCC GCGCTGCGGA AGAGGGCAGT GAAAGTGAAG CATGTGAAGC
1051 GTCGGGAGAA GAAGCTGAG AAGAAGAAGG AGGAGCGATA CAAGCGGCAT
1101 CGGCAGAAGC AGAAGCACA GGATAAATGG AAACACCCAG AGAGGGCTGA
1151 TGCCAAGGAC CCTGCGTCAC TGCCCCAGTG CCTGGGGCCC GGCTGTGTGC
1201 GCCCCGCCCA GCCCAGCTCC AAGTATTGCT CAGATGACTG TGGCATGAAG
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1351 GCATTTCGCC AGAGCAGCAG AGTGCCCGCA CCGCCTTCA GGAATGGAA
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1451 TGTGCGCGAG GATGAGGAGA GCAACGAGGG TGACAGTGAT GACACAGACC
1501 TGCAGATCTT CTGTGTTTCC TGTGGGCACC CCATCAACCC ACGTGTTCCT
1551 TTGCGCCACA TGGAGCGCTG CTACGCCAAG TATGAGAGCC AGACGTCTTT
1601 TGGGTCCATG TACCCACAC GCATTGAAGG GGCCACACGA CTCTTCTGTG
1651 ATGTGTATAA TCCTCAGAGC AAAACATACT GTAAGCGGCT CCAGGTGCTG
1701 TGCCCCGAGC ACTCACGGGA CCCCAGAGTG CCAGCTGAGC AGGTATGCGG
1751 GTGCCCCCTT GTACGTGATG TCTTTGAGCT CACGGGTGAC TTETGCCGCC
1801 TGCCCCAGCG CCAGTGCAAT CGCCATTACT GCTGGGAGAA GCTGCGCGCT
1851 GCGGAAGTGG ACTTGGAGCG CGTGCGTGTG TGGTACAAGC TGGACGAGCT
1901 GTTTGAGCAG GAGCGCAATG TGCGCACAGC CATGACAAAC CGCGCGGGAT
1951 TGTGCGCCTT GATGCTGCAC CAGACGATCC AGCAGATCCC CCTCACTACC
2001 GACCTGCGCT CCAGTGCCGA CCGCTGAGCC TCCTGGCCCG GACCCCTTAC
2051 ACCCTGCATT CCAGATGGGG GAGCCGCCCG GTGCCCCTGT GTCCGTTCTT
2101 CCACTCATCT GTTCTCCCGG TTCTCCCTGT GCCCATCCAC CGGTTGACCG
2151 CCCATCTGCC TTTATCAGAG GGACTGTCCC CGTCGACATG TTCAGTGCTT
2201 GGTGGGGCTG CCGAGTCCAC TCATCCTTGC CTCCTCTCCC TGGGTTTTGT
2251 TAATAAAATT TTGAAGAAAC CAAAAAATAA AAAAAAATAA AAAAAAATAA
2301 AAAAAAATAA AAAAAAATAA
```

BLAST Results

 Entry HS557771 from database EMBLEST:
 Human chromosome 18 clone 2 mRNA sequence.
 Score = 7582, P = 0.0e+00, identities = 1560/1598

Entry HSZ78337 from database EMBLEST:
 H.sapiens mRNA, expressed sequence tag ICRFp507H02194 (5')
 Score = 6339, P = 9.0e-281, identities = 1307/1347

Entry HS095149 from database EMBL:
 human STS WI-6941.
 Score = 1210, P = 2.2e-49, identities = 246/251

Medline entries

98449942:
 Identification and characterization of a family of mammalian methyl-CpG
 binding proteins.

9824997:
 Gene silencing by methyl-CpG-binding proteins.

Peptide information for frame 3

ORF from 57 bp to 2024 bp; peptide length: 656
 Category: similarity to known protein

```

1 MEGDGSDEPEP PDAGEDSKSE NGENAPIYCI CRKPDINCFM IGCDNCNEWF
51 HGDCIRITEK MAKAIREWYC RECREKDPKL EIRYRHKKS ERDGNERDSS
101 EPRDEGGGRK RPVPDPDLQR RAGSGTGVGA MLARGSASEH KSSPQPLVAT
151 PSQHHQOQQQ QIKRSARMCG ECEACRRTED CGHCDFCRDM KKFGGPNKIR
201 QKCRLRQCQL RARESYKYFP SSLSPVTPSE SLPRPRRPLP TQQQPQPSQK
251 LGRIREDEGA VASSTVKEPP EATATPEPLS DEDLPLDPDL YQDFCAGAFD
301 DHGLPWMSDT EESPFLLDPAL RKRAVKVKHV KRREKKSEKK KEERYKRHRQ
351 KQKHKDKWKH PERADAKDPA SLPQCLGPGC VRPAQPSSKY CSDDCGMKLA
401 ANRIYEILPQ RIQQWQQSPC IAEHGGKLL ERIRREQQA RTRLQEMERR
451 FHELEAILR AKQAVREDE ESNEGSDDT DLQIFCVSCG HPINPRVALR
501 HMERCYAKYE SQTSGSMYP TRIEGATRLF CDVYNPQSKT YCKRLQVLCF
551 EHSRDPKVPV DEVCGPLVR DVFELTGDFC RLPKRQCNRH YCWEKLRRAE
601 VDLERVRVWY KLDELFEQER NVRTAMTNRA GLLALMLHQT IQHDPLTTDL
651 RSSADR
  
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_4f17, frame 3

TREMBL:CEF52B11_4 gene: "F52B11.1"; Caenorhabditis elegans cosmid
 F52B11, N = 2, Score = 316, P = 8.8e-27

TREMBL:HSAB2331_1 gene: "KIAA0333"; Human mRNA for KIAA0333 gene,
 partial cds., N = 2, Score = 163, P = 2.8e-13

TREMBL:SPCC594_5 gene: "SPCC594.05c"; product: "putative
 transcriptional regulatory protein, phd finger containing"; S.pombe
 chromosome III cosmid c594., N = 3, Score = 168, P = 3.6e-12

TREMBL:AF072240_1 gene: "Mbd1"; product: "methyl-CpG binding protein
 MBD1"; Mus musculus methyl-CpG binding protein MBD1 (Mbd1) mRNA,
 complete cds., N = 2, Score = 189, P = 7.6e-11

>TREMBL:CEF52B11_4 gene: "F52B11.1"; Caenorhabditis elegans cosmid F52B11
 Length = 523

HSPs:

Score = 316 (47.4 bits), Expect = 8.8e-27, Sum P(2) = 8.8e-27
 Identities = 100/336 (29%), Positives = 167/336 (49%)

Score = 53 (8.0 bits), Expect = 8.8e-27, Sum P(2) = 8.8e-27
Identities = 24/100 (24%), Positives = 41/100 (41%)

Score = 48 (7.2 bits), Expect = 2.9e-26, Sum P(2) = 2.9e-26
Identities = 13/39 (33%), Positives = 19/39 (48%)

Pedant information for DKFZphtes3_4f17, frame 3

Report for DKFZphtes3_4f17.3

```
[LENGTH]          656
[MW]               75711.71
[pI]               8.61
[HOMOL]            TREMBL:CEF52B11_4 gene: "F52B11.1"; Caenorhabditis elegans cosmid F52B11 3e-25

[FUNCAT]           99 unclassified proteins          [S. cerevisiae, YPL138c] 3e-10
[FUNCAT]           04.05.01.04 transcriptional control [S. cerevisiae, YNL097c] 2e-04
[PROSITE]          MYRISTYL          6
[PROSITE]          AMIDATION         2
[PROSITE]          CK2_PHOSPHO_SITE   8
[PROSITE]          TYR_PHOSPHO_SITE   3
[PROSITE]          GLYCOSAMINOGLYCAN  1
[PROSITE]          PKC_PHOSPHO_SITE   9
[KW]               All_Alpha
[KW]               LOW_COMPLEXITY      18.75 %
[KW]               COILED_COIL        4.57 %
```

```
SEQ      MEGDGSDEPPPDAGEDSKSENGENAPIYCI CRKPDINCFMIGDCNCNEWFHGDCIRITEK  
SEG      .....  
PRD      cccccccccccccccccccccccceeeeeeccccceeeeecccccccccccchhhhhh  
COILS    .....
```

```
SEQ      MAKAIREWYC RECREKD PKLEI RYRHK SRERDGN ERDSSEP RDEGGGRKR PVPDPDLQR  
SEG      .....  
PRD      hhhhhh hhhhhc cccccccc hhhhhhh hhcccccccccccccccccccccccccccccc  
COILS    .....
```

```
SEQ      RAGSGTGV GAMLARG SASPHKSSPQPLVATPSQH HQQQQQ QIKRSARMCGECEACRRTED  
SEG      ..... xxxxxxxxxx .....  
PRD      cccccccceeecccccccccccccccccccc chhhhhhhhhhhhhhhhhhhcccccccccc  
COILS    .....
```

```

SEQ    CGHCDFCDRMKKFEGGPNKIRQKCLRQCQLRARES YKYFPSSLSPVTPSESLPRPRRPLP
SEG    .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD    cccccccccccccccccchhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccc
COILS  .....

SEQ    TQQQPQPSQKLGRIREDEGAVASSTVKEPPEATATPEPLSDEDLPLDPDLYQDFCAGAFD
SEG    xxxxxxxx.....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS  .....

SEQ    DHGLPWMSDTEESPFDPALRKRAVKVKHVREKKSEKKKEERYKRHRQKQHKDKWKH
SEG    .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD    cccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchh
COILS  .....

SEQ    PERADAKDPASLPQCLGPGCVRPAQPSSKYCSDDCGMKLAANRIYEILPQRIQQWQQSPC
SEG    .....
PRD    hhhhhccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhccch
COILS  .....

SEQ    IAEEHGKLLERIRREQQSARTRLQEMERRFHELEAILRAKQAVREDEESNEGDSDDT
SEG    .....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc
COILS  .....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....

SEQ    DLQIFCVSCGHPINPRVALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT
SEG    x.....
PRD    ceeeeeeccccccccchhhhhhhhhhhhhhhhhhhhhccccccccccccceeeeeccccccc
COILS  .....

SEQ    YCKRLQVLCPEHSRDPKVPADDEVCGCPLVRDVFELTGDFCRLPKRQCNRHYCWEKLRRAE
SEG    .....
PRD    cchhhhhhhccccccccccccceeeccccchhhhhccccccccccccccccchhhhhhhhhhh
COILS  .....

SEQ    VDLERVRVWYKLDELFEQERNVRTAMTNRAGLLALMLHQTIQHDPLTTDLRSSADR
SEG    .....
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc
COILS  .....

```

Prosites for DKFZphtes3_4f17.3

PS00002	124->128	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	58->61	PKC_PHOSPHO_SITE	PDOC00005
PS00005	165->168	PKC_PHOSPHO_SITE	PDOC00005
PS00005	215->218	PKC_PHOSPHO_SITE	PDOC00005
PS00005	248->251	PKC_PHOSPHO_SITE	PDOC00005
PS00005	265->268	PKC_PHOSPHO_SITE	PDOC00005
PS00005	337->340	PKC_PHOSPHO_SITE	PDOC00005
PS00005	387->390	PKC_PHOSPHO_SITE	PDOC00005
PS00005	439->442	PKC_PHOSPHO_SITE	PDOC00005
PS00005	627->630	PKC_PHOSPHO_SITE	PDOC00005
PS00006	6->10	CK2_PHOSPHO_SITE	PDOC00006
PS00006	17->21	CK2_PHOSPHO_SITE	PDOC00006
PS00006	227->231	CK2_PHOSPHO_SITE	PDOC00006
PS00006	265->269	CK2_PHOSPHO_SITE	PDOC00006
PS00006	280->284	CK2_PHOSPHO_SITE	PDOC00006
PS00006	308->312	CK2_PHOSPHO_SITE	PDOC00006
PS00006	521->525	CK2_PHOSPHO_SITE	PDOC00006
PS00006	652->656	CK2_PHOSPHO_SITE	PDOC00006
PS00007	339->346	TYR_PHOSPHO_SITE	PDOC00007
PS00007	500->507	TYR_PHOSPHO_SITE	PDOC00007
PS00007	211->219	TYR_PHOSPHO_SITE	PDOC00007
PS00008	42->48	MYRISTYL	PDOC00008
PS00008	123->129	MYRISTYL	PDOC00008
PS00008	125->131	MYRISTYL	PDOC00008
PS00008	129->135	MYRISTYL	PDOC00008
PS00008	259->265	MYRISTYL	PDOC00008
PS00008	396->402	MYRISTYL	PDOC00008
PS00009	107->111	AMIDATION	PDOC00009
PS00009	425->429	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_4f17.3)

DKFZphtes3_4f5

group: signal transduction

DKFZphtes3_4f5.3 encodes a novel 790 amino acid protein similar to beta-transducins.

The protein contains 3 WD-40 repeats, which are typical for the beta-transducin subunit of G-proteins. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. In addition, a Cytochrome C family heme-binding site signature is present. The protein is larger (790 amino acids) than the usual eukaryotic G-beta transducins (about 340 amino acids).

The new protein can find application in modulating/blocking G-protein-dependent pathways.

similarity to *S.pombe* "beta-transducin"

complete cDNA, EST hits

complete cds,

on genomic level encoded by HS313D11, at least 7 exons these exons

match

only partially with the predicted transcripts in HS313D11

Sequenced by AGOWA

Locus: /map="16p13.3"

Insert length: 3166 bp

No poly A stretch found, no polyadenylation signal found

```
1  GCGCGCTTCC GCGCGGCGCG TTCCGGACAA CCGTGGCGCTT TTAGTAAAAG
51  ATTTGGGGTTC GCGCGGGGGA GAAGGGCTGC CCCGGGCCCT CTGGTTCTCG
101 TCCCGCAGCG TCCGCTCCCC CGCGCCACTG CGCGCTCCC AGGAACCCTG
151 TACTCCGGGG TCGCCGGCTT CTCTCCTGCC TCCGGTCCCG CCAGACACCT
201 CGAGCTCCTT AAGTAGCTCG GTCTTGACG TCCCTCTGGG CCCTTCCCGC
251 GTCTATCGCC TGAGTCCCCG GGCCCTCTA GCCCTCTGTT CCCTCCCTCT
301 TTTTGTTCCT CCCTAGAGCC CCGCCGCCCT CAGGGCTGAC AGTGTGGACG
351 GCGGGAGTCT CCTCGCTCCC CTGCTGGGAT TGACTGACCG AGCGTTTAGT
401 GACTGCCCAAG ATCTGGCTGA TGGGGGTACC GAGAGGTGGC CTGGGCCCGG
451 AATGTCCAGC TAGAGTCTTC CGTGGAAGTC AGACATGAAA CTGACAGGCC
501 TAAGGGAAGC TAGGAAGTCC CCTCACCCTG CAGCCAGGGT GATGGGCTGG
551 ACTGACAGAC TCCAGTGAAT TTGAGCTTGC CTGTCAAGGT GATTGGCTGA
601 TAGACAGCCC TGGATTGGCT CACTAAGACT GACCAGCCCG GGACCAAGCA
651 GTTCTGGGGT CCCAACCTGG GTGGAAGGTC TGAAGTATG ACCCACCAG
701 GCTGACCAGG TCAGCCCAAC TCACTGACCT CCTGACCCCT GACCTCATCA
751 CCTGTGCAGC CATGGAGAAG ATGTCCCGTG TGACCACAGC CCTGGGTGGC
801 AGCGTGCTGA CAGGCCGCAC CATGCACTGC CACCTGGATG CTCCCGCCAA
851 TGCCATCACT GTGTGCCGCG ACGCAGCCCA GGTGGTCTGT GCAGGCCGTA
901 GCATCTTCAA GATCTATGCC ATCGAGGAGG AACAGTTCTG GGAAGAGCTG
951 AACCTGCGTG TGGGGCGCAA GCCTTCGCTT AACCTGAGCT GTGCTGACGT
1001 GGTCTGGCAC CAGATGGATG AGAACCTGCT GGCCACAGCA GCCACCAATG
1051 GCGTGGTGGT CAGTGGAAC CTGGGCCGGC CATCCGCAA CAAGCAGGAC
1101 CAGCTGTTC AAGAACACAA GCGCACGGTA AACAAAGTCT GCTTCCACCC
1151 CACCGAAGCC CAGCTGCTGC TCAGTGGCTC CCAGGATGGC TTCTATGAAGT
1201 GCTTTGACCT CCGCAGAAAG GACTCTGTCA GCACCTTCTC GGGCCAGTCG
1251 GAGAGCGTGC GGGACGTGCA GTTCAATATC CGGGACTACT TCACCTTCGC
1301 CTCCACCTTT GAGAACGGCA ATGTGCAGCT CTGGGACATC CGGCGTCCCG
1351 ACCGCTGCGA GAGGATGTTT ACAGCCACA ACGGACCCGT CTTCTGCTGC
1401 GACTGGCACC CCGAGGACAG GGGCTGGTTG GCCACTGGAG GCGCGACAA
1451 GATGGTGAAG GTCTGGGACA TGACCACGCA CCGTGCCAAG GAGATGCACT
1501 GTGTGCAGAC CATCGCCTCG GTGGCCCGTG TGAAGTGGCG GCCAGAGTGC
1551 CGCCACCACT TGGCCACGTG CTCCATGATG GTGGACCACA ACATCTATGT
1601 TTGGGACGTG CGCCGGCCCT TCGTGCCAGC TGCCATGTTT GAGGAACACC
1651 GAGACGTCAC CACGGGAATT GCCTGGCGCC ACCCCACAGA CCCCTCCTTC
1701 CTGCTGTCTG GCTCCAAGGA CAGCTCGCTG TGCCAGCACC TGTTCGCGCA
1751 CGCCAGCCAG CCCGTCGAGC GCGCAACCC TGAGGGCCTC TGCTACGGCC
1801 TCTTCGGGGA CCTGGCCTTC GCCGCCAAGG AGAGCCTCGT GGCTGCCGAG
1851 TCGGGGCGGA AGCCCTACAC TGGCGACCGG CGCCACCCCA TCTTCTTTAA
1901 GCGCAAGCTG GACCTGCCG AGCCCTTCGC AGGCTTCGCC TCCAGTGCCC
1951 TCAGTGTCTT TGAGCAGGAG CCAGGTGGCG GCGGCATGCG CTGGTTTGTG
2001 GACACAGCTG AGCGTTATGC GCTGGCTGGC CGGCCACTGG CCGAGCTCTG
2051 TGACCACAAC GCAAAGGTGG CTCGAGAGCT TGGCCGCAAC CAGGTGGCGC
2101 AAACGTGGAC CATGCTGCGG ATCATCTACT GCAGCCCTGG CCTAGTGCCC
2151 ACTGCAAAAC TCACACACAG TGTGGGCAAG GGTGGCTCCT GTGGCCTCCC
2201 GCTCATGAAC AGTTTCAACC TGAAGGATAT GGCCCAAGG TTGGGCAGTG
2251 AGACGCGGCT GGACCGCAGC AAAGGAGATG CACGGAGCGA CACAGTTCTG
2301 CTCGACTCCT CGGCCACACT CATACCAAT GAGGATAACG AGGAAACCGA
2351 GGGCAGCGAC GTACCTGCCG ACTACCTGCT GGGTGACGTG GAAGGTGAGG
```

```

2401 AGGACGAGCT GTACCTGCTG GATCCGGAAC ACGCGCACCC CGAGGACCCT
2451 GAGTGCCTGC TGCCGCAGGA GGCCTTTCCG CTGCGCCACG AGATCGTGGA
2501 CACGCCCTCCC GGACCCGAGC ACCTGCAGGA CAAGGCCGAC TCCCCGCACG
2551 TGAGCGGCAG CGAGGCGGAT GTGGCCTCCC TGGCCCCCGT GGA CTCTCC
2601 TTCTCGCTCC TGTCTGTCTC ACACGCGCTC TACGACAGCC GCCTGCCGCC
2651 CGACTTCTTC GGCCTGCTGG TGC GCGACAT GCTGCACTTC TACGCTGAGC
2701 AGGGCGACGT GCAGATGGCT GTGTCTGTGC TCATCGTCCT GGGTGAACGG
2751 GTGCGCAAGG ACATCGACGA GCAGACCCAG GAGCACTGGT ACACCTCCTA
2801 CATCGACCTG CTGCAGCGCT TCCGCCTCTG GAACGTGTCC AACGAGGTGG
2851 TCAAGCTGAG CACCAGCCGC GCCGTCAGCT GCCTCAACCA GGCTCCACC
2901 ACCCTGCACG TCAACTGCAG CCACTGCAAG CGGCCATGA GCAGCCGGGG
2951 CTGGGTCTGC GACAGGTGCC ACCGCTGCGC CAGCATGTGT GCCGTCTGCC
3001 ACCACGTAGT CAAGGGTCTC TTCGTGTGGT GCCAGGGCTG CAGCCACGGC
3051 GCCACCTGC AGCACATCAT GAAGTGGCTG GAAGGCAGCT CCCACTGTCC
3101 CGCAGGCTGC GGCCACCTCT GCGAGTACTC CTGACGGGGC ATCTGTGGG
3151 CTTGCCCGGG CGGCCG

```

BLAST Results

Entry HS313D11 from database EMBL:
 Human DNA sequence from cosmid 313D11 from a contig on the short arm of
 chromosome 16. Contains ESTs, STS and CpG islands.
 Score = 6238, P = 0.0e+00, identities = 1318/1391

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 762 bp to 3131 bp; peptide length: 790
 Category: similarity to known protein

```

1 MEKMSRVTTA LGGSVLTGRT MHCHLDAPAN AISVCRDAAQ VVVAGRSIFK
51 IYAIEEEQFV EKLNLRVGRK PSLNLSADV VWHQMDENLL ATAATNGVVV
101 TWNLGRPSRN KQDQLFTEHK RTVNKVCFHP TEAHVLLSGS QDGFMKCFDL
151 RRKDSVSTFS GQSESVRDVQ FSIRDYFTFA STFENGVLQ WDIRRPDRCE
201 RMFTAHPGPV FCCDWHPEDR GWLATGGRDK MVKVWDMTH RAKEMHCVQT
251 IASVARVKWR PECRHHLATC SMMVDHNIYV WDVRRPFVPA AMFEEHRDVT
301 TGIAWRHPHD PSFLLSGSKD SSLCOHLFRD ASQPVERANP EGLCYGLFGD
351 LAFAAKESLV AAESGRKPYT GDRRHPIFFK RKLDPAPFPA GLASSALSVF
401 ETEPGGGGMR WFDVTAERYA LAGRPLAELC DHNAKVAREL GRNQVAQTWT
451 MRRIIYCSFG LVPTANLNHS VGKGGSCGLP LMNSFNLKDM APGLGSETRL
501 DRSKGDARSD TVLLDSSATL ITNEDNEETE GSDVPADYLL GDVEGEDEEL
551 YLLDPEHAHP EDPECVLPQE AFPLRHEIVD TPPGPEHLQD KADSPHVSQS
601 EADVASLAPV DSSFSLSVS HALYDSRLPP DFFGVLRDM LHFYAEQGDV
651 QNAVSVLIVL GERVRKDIDE QTQEHWYTSY IDLLQRFRLW NVSNEVVKLS
701 TSRAVSLNLQ ASTTLHVNC SCKRPMSSRG WVCDCRCHCA SMCVCHHV
751 KGLFVWCQC SHGGHLQHIM KWLEGSSHCP AGCGHLCEYS

```

BLASTP hits

Entry YDSB_SCHPO from database SWISSPROT:
 HYPOTHETICAL 93.2 KD TRP-ASP REPEATS CONTAINING PROTEIN C4F8.11 IN
 CHROMOSOME I. >TREMBL:SPAC4F8_11 gene: "SPAC4F8.11"; product:
 "beta-transducin"; S.pombe chromosome I cosmid c4F8.
 Score = 404, P = 3.0e-42, identities = 169/639, positives = 278/639

Entry PEX7_HUMAN from database SWISSPROT:
 PEROXISOMAL TARGETING SIGNAL 2 RECEPTOR (PTS2 RECEPTOR) (PEROXIN-7).
 >TREMBL:HSU76560_1 gene: "Pex7"; product: "peroxisome targeting signal
 2 receptor"; Human peroxisome targeting signal 2 receptor (Pex7) mRNA,
 complete cds. >TREMBL:HSU88871_1 gene: "HsPEX7"; product: "HsPex7p";
 Human HsPex7p (HsPEX7) mRNA, complete cds.
 Score = 220, P = 1.1e-15, identities = 62/244, positives = 107/244

Entry PEX7_MOUSE from database SWISSPROT:
 PEROXISOMAL TARGETING SIGNAL 2 RECEPTOR (PTS2 RECEPTOR) (PEROXIN-7).
 >TREMBL:MMU69171_1 product: "peroxisomal PTS2 receptor"; Mus musculus
 peroxisomal PTS2 receptor mRNA, complete cds.
 Score = 214, P = 5.3e-15, identities = 60/240, positives = 106/240

Entry ATAC2294_7 from database TREMBL:
 gene: "F11P17.7"; Arabidopsis thaliana chromosome I BAC F11P17 genomic
 sequence, complete sequence.
 Score = 232, P = 3.4e-14, identities = 68/260, positives = 120/260

Entry S66835 from database PIR:
 probable membrane protein YOL138c - yeast (*Saccharomyces cerevisiae*)
 >TREMBL:SCYOL138C_1 *S.cerevisiae* chromosome XV reading frame ORF
 YOL138c
 Score = 136, P = 2.5e-13, identities = 24/77, positives = 44/77

Alert BLASTP hits for DKFZphtes3_4f5, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_4f5, frame 3

Report for DKFZphtes3_4f5.3

```
[LENGTH]      790
[MW]           88207.10
[pI]           6.05
[HOMOL]        SWISSPROT:YDSB_SCHPO HYPOTHETICAL 93.2 KD TRP-ASP REPEATS CONTAINING PROTEIN
C4F8.11 IN CHROMOSOME I. 9e-44
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YOL138c] 5e-16
[FUNCAT]       10.04.09 regulation of g-protein activity [S. cerevisiae, YBR195c] 3e-11
[FUNCAT]       06.10 assembly of protein complexes [S. cerevisiae, YBR195c] 3e-11
[FUNCAT]       03.16 dna synthesis and replication [S. cerevisiae, YBR195c] 3e-11
[FUNCAT]       09.13 biogenesis of chromosome structure [S. cerevisiae, YBR195c] 3e-11
[FUNCAT]       04.05.01.07 chromatin modification [S. cerevisiae, YBR195c] 3e-11
[FUNCAT]       30.10 nuclear organization [S. cerevisiae, YCR072c beta-transducin family]
3e-10
[FUNCAT]       04.05.01.01 general transcription activities [S. cerevisiae, YBR198c
TAF90 - TFIID subunit] 9e-09
[FUNCAT]       04.01.04 rrna processing [S. cerevisiae, YLL011w] 1e-07
[FUNCAT]       30.09 organization of intracellular transport vesicles [S. cerevisiae,
YDL195w] 2e-07
[FUNCAT]       08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL195w]
2e-07
[FUNCAT]       30.19 peroxisomal organization [S. cerevisiae, YDR142c] 4e-07
[FUNCAT]       06.04 protein targeting, sorting and translocation [S. cerevisiae, YDR142c]
4e-07
[FUNCAT]       08.10 peroxisomal transport [S. cerevisiae, YDR142c] 4e-07
[FUNCAT]       08.01 nuclear transport [S. cerevisiae, YER107c] 4e-07
[FUNCAT]       04.07 rna transport [S. cerevisiae, YER107c] 4e-07
[FUNCAT]       30.03 organization of cytoplasm [S. cerevisiae, YER107c] 4e-07
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YGL003c] 5e-07
[FUNCAT]       06.13 proteolysis [S. cerevisiae, YGL003c] 5e-07
[FUNCAT]       04.05.01.04 transcriptional control [S. cerevisiae, YCR084c] 8e-07
[FUNCAT]       04.05.03 mrna processing (splicing) [S. cerevisiae, YPR178w] 1e-06
[FUNCAT]       03.13 meiosis [S. cerevisiae, YLR129w] 3e-06
[FUNCAT]       03.25 cytokinesis [S. cerevisiae, YCR057c] 1e-05
[FUNCAT]       03.04 budding, cell polarity and filament formation [S. cerevisiae, YCR057c]
1e-05
[FUNCAT]       06.07 protein modification (glycosylation, acylation, myristylation,
palmitoylation, farnesylation and processing) [S. cerevisiae, YEL056w] 2e-04
[FUNCAT]       30.04 organization of cytoskeleton [S. cerevisiae, YOR272w] 6e-04
[SCOP]         dlgotb_2.46.3.1.1 betal-subunit of the signal-transducing 5e-06
[PIRKW]        duplication 7e-10
[PIRKW]        signal transduction 7e-08
[PIRKW]        peroxisome 9e-06
[PIRKW]        heterotrimer 7e-08
[PIRKW]        GTP binding 7e-08
[PIRKW]        peroxisome biogenesis 9e-06
[PIRKW]        transmembrane protein 1e-14
[SUPFAM]       MS11 protein 7e-10
[SUPFAM]       WD repeat homology 1e-14
[SUPFAM]       GTP-binding regulatory protein beta chain 7e-08
[SUPFAM]       PRL1 protein 3e-08
[SUPFAM]       coatamer complex beta' chain 1e-06
[PROSITE]      CYTOCHROME_C 1
[PROSITE]      WD_REPEATS 3
[PROSITE]      MYRISTYL 10
[PROSITE]      AMIDATION 2
[PROSITE]      CAMP_PHOSPHO_SITE 2
[PROSITE]      CK2_PHOSPHO_SITE 11
```

```

[PROSITE]      TYR_PHOSPHO_SITE      1
[PROSITE]      PKC_PHOSPHO_SITE      7
[PROSITE]      ASN_GLYCOSYLATION     4
[PFAM]         WD_domain, G-beta repeats
[KW]           All_Beta
[KW]           3D
[KW]           LOW_COMPLEXITY        2.28 %

```

```

SEQ      MEKMSRVTTALGGSVLTGRTMHCHLDAPANAI SVCRDAAQVVVAGRSIFKIYAIEEEQFV
SEG      .....
lgotB    .....

SEQ      EKLNLRVGRKPSLNLSCADVWHQMDENLLATAATNGVVVTWNLGRPSRNKQDQLFTEHK
SEG      .....
lgotB    .....TTCEEEEEETTTEEEET- TTTCEEE--EEECCE

SEQ      RTVNKVCFCFPTAEHVLLSGSQDGFMKCFDLRRKDSVSTFSGQSESVRDVQFSIRDYFTFA
SEG      .....
lgotB    CCEEEEEETT-TCEEEEEETTTEEEETTTTEEEECBTTCEEEEEETTTTTEEE

SEQ      STFENGNVQLWDIRRPDCERMFTAHNQPVFCCDWHPEDRGWLATGGRDKMVKVWDMTTH
SEG      .....
lgotB    E-ETTTEEEETTTEEE-EEECCEEEEE- TTTTCEEEEEETTTEEEEC....

SEQ      RAKEMHCVQTIASVARVKWRPECRHHLATCSMMVDHNIYVDVRRFPVPAAMFEEHRDVT
SEG      .....
lgotB    .....

SEQ      TGIAWRHHPDPSFLLSGSKDSSLQHLFRDASQPVERANPEGLCYGLFGDLAFAAKESLV
SEG      .....
lgotB    .....

SEQ      AAESGRKPYTGDRRHPIFFKRKLDPAEPPAGLASSALSVFETEPGGGGMRWFVDTAERYA
SEG      .....
lgotB    .....

SEQ      LAGRPLAELCDHNAKVARELGRNQVAQTWMLRIIYCSPGLVPTANLNHSVGKGGSCGLP
SEG      .....
lgotB    .....

SEQ      LMNSFNLKDMAPGLGSETRLDRSKGDARSDTVLLDSSATLITNEDNEETEGSDVPADYLL
SEG      .....xxxx
lgotB    .....

SEQ      GDVEGEDELYLLDPEHAHPEDPECVLPQEAFLRHEIVDTPPGPEHLQDKADSPHVSQS
SEG      xxxxxxxxxxxxxxxx.....
lgotB    .....

SEQ      EADVASLAPVDSSFLLSVSHALYDSRLPPDFFGVLVRDMLHFYAEQGDVQMAVSVLIVL
SEG      .....
lgotB    .....

SEQ      GERVRKDIDEQTQEHWYTSYIDLLQRFRLWNVSNEVVKLSTSRVSCLNQASTTLHVNCS
SEG      .....
lgotB    .....

SEQ      HCKRPMSSRGWVCDRCHRCASMCVCHHVVKGLFVWCQGC SHGHLQHIMKWLEGSSHCP
SEG      .....
lgotB    .....

SEQ      AGCGHLCEYS
SEG      .....
lgotB    .....

```

Prosites for DKFZphtes3_4f5.3

PS00001	74->78	ASN_GLYCOSYLATION	PDOC00001
PS00001	468->472	ASN_GLYCOSYLATION	PDOC00001
PS00001	691->695	ASN_GLYCOSYLATION	PDOC00001
PS00001	718->722	ASN_GLYCOSYLATION	PDOC00001
PS00004	69->73	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	152->156	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	17->20	PKC_PHOSPHO_SITE	PDOC00005
PS00005	165->168	PKC_PHOSPHO_SITE	PDOC00005
PS00005	172->175	PKC_PHOSPHO_SITE	PDOC00005
PS00005	239->242	PKC_PHOSPHO_SITE	PDOC00005
PS00005	364->367	PKC_PHOSPHO_SITE	PDOC00005
PS00005	701->704	PKC_PHOSPHO_SITE	PDOC00005

PS00005	727->730	PKC_PHOSPHO_SITE	PDOC00005
PS00006	76->80	CK2_PHOSPHO_SITE	PDOC00006
PS00006	165->169	CK2_PHOSPHO_SITE	PDOC00006
PS00006	172->176	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00006	398->402	CK2_PHOSPHO_SITE	PDOC00006
PS00006	498->502	CK2_PHOSPHO_SITE	PDOC00006
PS00006	503->507	CK2_PHOSPHO_SITE	PDOC00006
PS00006	522->526	CK2_PHOSPHO_SITE	PDOC00006
PS00006	598->602	CK2_PHOSPHO_SITE	PDOC00006
PS00006	600->604	CK2_PHOSPHO_SITE	PDOC00006
PS00006	679->683	CK2_PHOSPHO_SITE	PDOC00006
PS00007	337->346	TYR_PHOSPHO_SITE	PDOC00007
PS00008	13->19	MYRISTYL	PDOC00008
PS00008	97->103	MYRISTYL	PDOC00008
PS00008	139->145	MYRISTYL	PDOC00008
PS00008	161->167	MYRISTYL	PDOC00008
PS00008	317->323	MYRISTYL	PDOC00008
PS00008	342->348	MYRISTYL	PDOC00008
PS00008	391->397	MYRISTYL	PDOC00008
PS00008	460->466	MYRISTYL	PDOC00008
PS00008	474->480	MYRISTYL	PDOC00008
PS00008	759->765	MYRISTYL	PDOC00008
PS00009	67->71	AMIDATION	PDOC00009
PS00009	364->368	AMIDATION	PDOC00009
PS00190	743->749	CYTOCHROME_C	PDOC00169
PS00678	90->105	WD_REPEATS	PDOC00574
PS00678	223->238	WD_REPEATS	PDOC00574
PS00678	269->284	WD_REPEATS	PDOC00574

Pfam for DKFZphtes3_4f5.3

HMM_NAME	WD domain, G-beta repeats		
HMM	*MrGHnnWVWCVaFSPDGrWFivSGSWDgTCRLWD*		
	++ HN++V C+ ++P+ R +++G++D+ +++WD		
Query	203	FTAHNGPVFCCDWHPEDRGWLATGGRDKMKVWVD	236

DKFZphtes3_4h6

group: intracellular transport/trafficking

DKFZphtes3_4h6 encodes a novel 622 amino acid protein with strong similarity to the kinesin light chain.

Kinesin is a microtubule-based motor protein that pulls vesicles or organelles towards the plus end of microtubules. Structural changes in the protein that drive motility are coupled to ATP binding and hydrolysis. The novel protein is similar to kinesin light chain, which is part of the functional holoenzyme tetrameric protein. The light chain has been proposed to function in coupling of cargo to the heavy chain or in the modulation of the ATPase activity of the heavy chain. The novel protein contains two kinesin light chain repeats and one RGD cell-attachment site.

The novel kinesin protein can find application in modulating the function of kinesin and modulating intracellular transport via/on microtubules.

strong similarity to Kinesin light chain

complete cDNA, complete cds, start at 150, EST hits (few)

Sequenced by AGOWA

Locus: unknown

Insert length: 2992 bp

Poly A stretch at pos. 2914, polyadenylation signal at pos. 2893

```
1  GCGGGGATGG AGCGGCGGG ACCGGCTCGC GGGTGC GG GT CCGGGTGAAG
51  CCGGAGGCAG CCAGAGTCGG AGCCGGGCCC GAGCACCAGG CGCAGGCCCC
101 GCGCCCCGCT GCCCGCACCC TCGTCCTCAC AGACGCCACA GCCATGGCCA
151 TGATGGTGT TCCGCGGGAG GAGAAGCTGA GCCAGGATGA GATCGTGCTG
201 GGCACCAAGG CTGTCTATCCA GGGACTGGAG ACTCTGCGTG GGGAGCATCG
251 TGCCCTGCTG GCTCCTCTGG TTGCACCTGA GGCCGGCGAA GCCGAGCCTG
301 GCTCGCAGGA GCGCTGCATC CTCCTGCGTC GCTCCCTGGA AGCCATTGAG
351 CTTGGGCTGG GGGAGGCCCA GGTGATCTTG GCATTGTCTG GCCACCTGGG
401 GGCTGTAGAA TCAGAGAAGC AGAAGCTGCG GGCGCAGGTG CGGCGTCTGG
451 TGCAGGAGAA CCAGTGGCTG CGTGAGGAGC TGGCGGGGAC ACAGCAGAAG
501 CTGCAGCGCA GTGAGCAGGC CGTGGCCAG CTCGAGGAGG AGAAGCAGCA
551 CTTGCTGTTC ATGAGCCAGA TCCGCAAGTT GGATGAAGAC GCCTCCCTTA
601 ACGAGGAGAA GGGGGACGTC CCCAAAGACA CACTGGATGA CCTCTTCCCC
651 AATGAGGATG AGCAGAGCCC AGCCCTAGC CCAGGAGGAG GGGATGTGTC
701 TGGTCAGCAT GGGGGCTACG AGATCCCGGC CCGGCTCCGC ACCCTGCACA
751 ACCTGGTGAT CCAATACGCC TCACAGGGCC GCTACGAGGT AGCTGTGCCA
801 CTCTGCAAGC AGGCACTCGA AGACCTGGAG AAGACGTCAG GCCACGACCA
851 CCCTGACGTT GCCACCATGC TGAACATCCT GGCACCTGGT TATCGGGATC
901 AGAACAAAGT CAAGGAGGCT GCGCACCTGC TCAATGATGC TCTGGCCATC
951 CGGGAGAAAA CACTGGGCAA GGACCACCCA GCGGTGGCTG CGACACTAAA
1001 CAACCTGGCA GTCCTGTATG GCAAGAGGGG CAAGTACAAG GAGGCTGAGC
1051 CATTGTGCAA GCGGGCACTG GAGATCCGGG AGAAGGTCTT GGGCAAGTTT
1101 CACCCAGATG TGGCCAAGCA GCTCAGCAAC CTGGCCCTGC TGTGCCAGAA
1151 CCAGGGGAAA GCTGAGGAGG TGGAATATTA CTATCGGCGG GCACTGGAGA
1201 TCTATGCTAC ACGCCTCGGG CCCGATGACC CCAATGTGGC CAAGACCAAG
1251 AACCAACCTG CTTCTGTGTA CCTGAAGCAG GGCAAGTACC AGGATGCGGA
1301 GACCTTGATC AAGGAGATCC TCACCCGCGC TCATGAGAAA GAGTTTGGCT
1351 CTGTCAATGG GGACAACAAG CCCATCTGGA TGCACGAGA GGAGCGGCAG
1401 GAAAGCAAGG ATAAGCGCCG GGACAGCGCC CCTATGGGG AATACGGCAG
1451 CTGGTACAAG GCCTGTAAAG TAGACAGCCC CACAGTCAAC ACCACCTGCG
1501 GCAGCTTGGG GGCCCTATAC CGGCGCCAGG GCAAGCTGGA AGCCGCGCAC
1551 AACTAGAGG ACTGTGCCAG CCGTAACCGC AAGCAGGGTT TGGACCCGCG
1601 AAGCCAGACC AAGGTGGTAG AACTGTGAA AGATGGCAGT GGCAGGCGGG
1651 GAGACCGCCG CAGCAGCCGA GACATGGCTG GGGGTGCCGG GCCTCGGTCT
1701 GAGTCTGACC TCGAGGACGT GGGACCTACA GCTGAGTGGA ATGGGGATGG
1751 CAGTGGCTCC TTGAGGCGCA GCGGTTCTCT TGGGAACTC CGGGATGCCC
1801 TGAGGCGCAG CAGTGAGATG CTGGTAAAGA AGCTGCAGGG GGGCACCCCC
1851 CAGGAGCCCC CTAACCCAG GATGAAGCGG GCCAGTTCCC TCAACTTCCT
1901 CAACAAGAGC GTGGAAGAGC CGACCCAGCC TGGAGGCACA GGTCTCTCTG
1951 ACAGCCGCAC TCTCAGCTCC AGCTCCATGG ACCTCTCCCG ACGAAGCTCC
2001 CTGGTGGGCT AATGCTGAAG GGGCAGCCAG TCACCAGAGC GCCCACCTGG
2051 CACACCCCCC TCACCCAGC CCTGCGCATG GGCTTGCTGC TTGTCCCGCC
2101 TGTCTCTCCC ACAGCCCTG TCTTTTCTGT TCAATCTCAG GGTAACCTTC
2151 TCCCTTGTC TCTCAGCCTG AGCCCTGGAG GCTGGGCTG CCCACTCCAG
2201 CTCCATCCCT TATTTATTC TTCCAGCAGG GCCCTCTTCC CTAGGTTCGG
2251 GCCAGCAGGA GATGCGGCT GGAGTCTCCA CCATAGACTC AGTGGCCTGG
2301 CCTCCCCAGA CCCCAGAGCC AAGAACAATA AGCACTCGCC GGCCCTTCGG
2351 CACCTCGCC CTCCTCCCC ACTCAACCCG GCGGTTGCTT CTGTATATAG
2401 AGAAATAAGT TATTGGCCGC GCGCCTCCCT TCAGTCCACG GTACTACCCG
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2451 GGCCTCCCCT CGTCCCTCTT CTAGTGGTAC CGCCCAGGCC TTAATCACCC
2501 CCATTCCGTG CGGTGGTATC TCCCAGGCTC TACATTCTCG GGAGCGGCGC
2551 CTCCCAAGGG GGTCTGGGA CCTTCTCGCG CTCCTCCTGG CCTCTGAGGG
2601 ATGCGTCTTA CCCGCGCCAT CGCCCCGTGG CCCAGGACGG GGACCTCCCC
2651 TTAGTCCGTC CTCCCACCGC CGGGCCCTGC CCCGCATCCC GGCTTATGC
2701 ACTGCCCCTC CCACCGGCC CCGCCAGGC ACGGCCGACC CCGCCCCGGG
2751 CACCGCCAC CGAGCCATCC TGCCTCGCCT CCCCCACGC CTGCAGCTTC
2801 TCGCGAGGGG CGGCGACGGT CCCCTGGTGG CAGGAGGGGC TCCCCCTGTT
2851 GCGGGTGAGG CGGCTGCTCT CTATTTTCAG ATGTTGCTGT AGAAATAAAG
2901 ACGGTTTAAA TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2951 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

```

BLAST Results

No BLAST result

Medline entries

98288268:

Two kinesin light chain genes in mice. Identification and characterization of the encoded proteins.

Peptide information for frame 3

ORF from 144 bp to 2009 bp; peptide length: 622

Category: strong similarity to known protein

Prosites motifs: RGD (502-505)

KINESIN_LIGHT (223-265)

KINESIN_LIGHT (265-307)

```

1 MAMMVFPRER KLSQDEIVLG TKAVIQGLET LRGEHRALLA PLVAPEAGEA
51 EPGSQERCIL LRRSLEAIEL GLGEAQVILA LSSHLGAVES EKQKLRAQVR
101 RLVOENQWLR EELAGTQOKL QRSEQAVACL EEEKQHLLFM SQIRKLDEDA
151 SPNEEKGDVP KDTLDDLFPN EDEQSPAPSP GGGDVSGQHG GYEIPARLRT
201 LHNLVIOYAS OGRYEVAVPL CKQALDLEK TSGHDHPDVA TMLNILALVY
251 RDQNKYKEAA HLLNDALAIR EKTGKDHFA VAATLNNLAV LYGKRKYKE
301 AEPLCKRALE IREKVLGKFH PDVAKQLSNL ALLCQNGKA EEVEYYRRA
351 LEIYATRLGP DDPNVAKTKN NLASCYLKQG KYQDAETLYK EILTRAHEKE
401 FGSVNGDNKP IWMHAEEREE SKDKRRDSAP YGEYGSWYKA CKVDSPTVNT
451 TLRSLGALYR RQKLEAAHT LEDCASRNK QGLDPASQTK VVELLDGSG
501 RRGDRSSRD MAGGAGPRSE SDLEDVGPTA EWNGDGSGL RRSFGKLR
551 DALRRSSEML VKKLQGGTPO EPPNPRMKRA SSLNFLNKS SV EPTQPGGTG
601 LSDSRTLSSS SMDLSRRSSL VG

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_4h6, frame 3

TREMBL:AF055666_1 gene: "Klc2"; product: "kinesin light chain 2"; Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds., N = 1, Score = 2824, P = 4e-294

PIR:I53013 kinesin light chain - human, N = 1, Score = 1927, P = 4.5e-199

PIR:C41539 kinesin light chain C - rat, N = 1, Score = 1919, P = 3.2e-198

SWISSPROT:KNLC_RAT KINESIN LIGHT CHAIN (KLC)., N = 1, Score = 1919, P = 3.2e-198

>TREMBL:AF055666_1 gene: "Klc2"; product: "kinesin light chain 2"; Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.
Length = 599

HSPs:

Score = 2824 (423.7 bits), Expect = 4.0e-294, P = 4.0e-294
Identities = 558/598 (93%), Positives = 572/598 (95%)

```

Query:      1 MAMMVFPREKLSQDEIVLGTKAVIQGLETLRGEHRALLAPLVAPEAGEAEFGSQERCIL 60
            MA MV PREKLSQDEIVLGTKAVIQGLETLRGEHRALLAPL + EAGEAEFGSQERC+L
Sbjct:      1 MATMVLPREKLSQDEIVLGTKAVIQGLETLRGEHRALLAPLASHEAGEAEFGSQERCLL 60

Query:     61 LRRSLEAIELGLGEAQVILALSSHLGAVESEKQKLRAQVRRVLQENQWLREELAGTQOKL 120
            LRRSLEAIELGLGEAQVILALSSHLGAVESEKQKLRAQVRRVLQENQWLREELAGTQOKL
Sbjct:     61 LRRSLEAIELGLGEAQVILALSSHLGAVESEKQKLRAQVRRVLQENQWLREELAGTQOKL 120

Query:    121 QRSEQAVAQLEEEKQHLLFMSQIRKLDE DASPNEEKGDVDPKDTLDDLPNEDEQSPAPSP 180
            QRSEQAVAQLEEEKQHLLFMSQIRKLDE P EEKGDVDPKD+LDDLPNEDEQSPAPSP
Sbjct:    121 QRSEQAVAQLEEEKQHLLFMSQIRKLDE-MLPQEEKGDVDPKDSLDDLPNEDEQSPAPSP 179

Query:    181 GGGDVSGQHGGYEIPARLRTLHNLVIQYASQGRYEVAVPLCKQALEDEKTSBGHDHPDVA 240
            GGGDV+ QHGGYEIPARLRTLHNLVIQYASQGRYEVAVPLCKQALEDEKTSBGHDHPDVA
Sbjct:    180 GGGDVAAQHGGYEIPARLRTLHNLVIQYASQGRYEVAVPLCKQALEDEKTSBGHDHPDVA 239

Query:    241 TMLNILALVYRDQNKYKEAAHLLNDALAIREKTLGKDHPAVAATLNNLAVLYGKRKYKE 300
            TMLNILALVYRDQNKYK+AAHLLNDALAIREKTLGKDHPAVAATLNNLAVLYGKRKYKE
Sbjct:    240 TMLNILALVYRDQNKYKDAHLLNDALAIREKTLGKDHPAVAATLNNLAVLYGKRKYKE 299

Query:    301 AEPLCKRALEIREKVLGKFHPDVAQKLSNLALLCQNGKAEVEYYYRRALEIYATRLGP 360
            AEPLCKRALEIREKVLGKFHPDVAQKLSNLALLCQNGKAEVEYYYRRALEIYATRLGP
Sbjct:    300 AEPLCKRALEIREKVLGKFHPDVAQKLSNLALLCQNGKAEVEYYYRRALEIYATRLGP 359

Query:    361 DDPNVAKTKNNLASCYLKQGGYQDAETLYKEILTRAHEKEFGSVNGDNKPIWMHAEEREE 420
            DDPNVAKTKNNLASCYLKQGGYQDAETLYKEILTRAHEKEFGSVNG+NKPIWMHAEEREE
Sbjct:    360 DDPNVAKTKNNLASCYLKQGGYQDAETLYKEILTRAHEKEFGSVNGENKPIWMHAEEREE 419

Query:    421 SKDKRRDSAPYGEYGSWKACKVDSPTVNTTLRSLGALYRRQKLEAAHTLED CASRNRK 480
            SKDKRRD P EYGSWKACKVDSPTVNTTLR+LGALYR +GKLEAAHTLED CASR+RK
Sbjct:    420 SKDKRRDRPM-EYGSWKACKVDSPTVNTTLRLGALYRPEGKLEAAHTLED CASRSRK 478

Query:    481 QGLDPASQTKVVVELLKDGSGRRGDRSSSRDMAGGAGPRSESDLEDVGP TAEWNGDGSGSGL 540
            QGLDPASQTKVVVELLKDGSGR G RR SRD+AG P+SESDLE+ GP AEW+GDGSGSGL
Sbjct:    479 QGLDPASQTKVVVELLKDGSGR-GHRRGSRDVAG---PQSESDLEESGPAAEWSDGSGSGL 534

Query:    541 RRSFSFGKLRDALRRSSEMLVKKLQGGTPQEPNPRMKRASSLNFLNKSVEEPTQPGG 598
            RRSFSFGKLRDALRRSSEMLV+KLQGG PQEP N RMKRASSLNFLNKSVEEP QPGG
Sbjct:    535 RRSFSFGKLRDALRRSSEMLVRKLQGGGPQEP-NSRMKRASSLNFLNKSVEEPTQPGG 591

```

Pedant information for DKFzphes3_4h6, frame 3

Report for DKFzphes3_4h6.3

```

[LENGTH]      622
[MW]           68934.82
[pI]           6.72
[HOMOL]        TREMBL:AF055666_1 gene: "Klc2"; product: "kinesin light chain 2"; Mus musculus
kinesin light chain 2 (Klc2) mRNA, complete cds. 0.0
[BLOCKS]       BL00927C Trehalase proteins
[BLOCKS]       BL01160I Kinesin light chain repeat proteins
[BLOCKS]       BL01160H Kinesin light chain repeat proteins
[BLOCKS]       BL01160G Kinesin light chain repeat proteins
[BLOCKS]       BL01160F Kinesin light chain repeat proteins
[BLOCKS]       BL01160E Kinesin light chain repeat proteins
[BLOCKS]       BL01160D Kinesin light chain repeat proteins
[BLOCKS]       BL01160C Kinesin light chain repeat proteins
[BLOCKS]       BL01160B Kinesin light chain repeat proteins
[BLOCKS]       BL01160A Kinesin light chain repeat proteins
[SUPFAM]       tetraatricopeptide repeat homology 1e-07
[PROSITE]      RGD 1
[PROSITE]      MYRISTYL 8
[PROSITE]      KINESIN_LIGHT 2
[PROSITE]      AMIDATION 2
[PROSITE]      CAMP_PHOSPHO_SITE 5
[PROSITE]      CK2_PHOSPHO_SITE 11
[PROSITE]      TYR_PHOSPHO_SITE 3
[PROSITE]      PKC_PHOSPHO_SITE 7
[PROSITE]      ASN_GLYCOSYLATION 2
[PFAM]         Kinesin light chain repeat
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY 12.54 %
[KW]           COILED_COIL 4.98 %

```

Prosite for DKFZphtes3 4h6.3

888

PS00006	568->572	CK2_PHOSPHO_SITE	PDOC00006
PS00006	589->593	CK2_PHOSPHO_SITE	PDOC00006
PS00006	610->614	CK2_PHOSPHO_SITE	PDOC00006
PS00007	339->346	TYR_PHOSPHO_SITE	PDOC00007
PS00007	339->347	TYR_PHOSPHO_SITE	PDOC00007
PS00007	424->432	TYR_PHOSPHO_SITE	PDOC00007
PS00008	71->77	MYRISTYL	PDOC00008
PS00008	86->92	MYRISTYL	PDOC00008
PS00008	182->188	MYRISTYL	PDOC00008
PS00008	187->193	MYRISTYL	PDOC00008
PS00008	402->408	MYRISTYL	PDOC00008
PS00008	482->488	MYRISTYL	PDOC00008
PS00008	598->604	MYRISTYL	PDOC00008
PS00008	600->606	MYRISTYL	PDOC00008
PS00009	292->296	AMIDATION	PDOC00009
PS00009	499->503	AMIDATION	PDOC00009
PS00016	502->505	RGD	PDOC00016
PS01160	223->265	KINESIN_LIGHT	PDOC00893
PS01160	265->307	KINESIN_LIGHT	PDOC00893

Pfam for DKFZphtes3_4h6.3

HMM_NAME Kinesin light chain repeat

HMM *RALEDREKtLGHDHPDVatMLNNLALvCRNQNKyeEvenYYN*

+ALED+EKT+GHDHPDVATMLN+LALV+R+QNKY+E++ ++N

Query 223 QALEDLEKTSBGHDHPDVATMLNIALVYRDQNKYKEAAHLLN 264

50.46 265 306 1 42 dkfzphes3_4h6.3 strong similarity to Kinesin light chain

Alignment to HMM consensus:

Query *RALEDREKtLGHDHPDVatMLNNLALvCRNQNKyeEvenYYN*

AL +REKTLG DHP VA LNNLA+++ ++KY+E+E + +

dkfzphes3 265 DALAIREKTLGKDHPAVAATLNNLAVLYGKRGKYKEAEPLCK 306

Query 348 1 42 dkfzphes3_4h6.3 strong similarity to Kinesin light chain

Alignment to HMM consensus:

HMM *RALEDREKtLGHDHPDVatMLNNLALvCRNQNKyeEvenYYN*

RALE+REK+LG HPDVA++L+NLAL+C+NQ+K EEVE YY+

Query 307 RALEIREKVLGKFHPDVAKQLSNLALLCQNGKAEVEYYR 348

39.10 349 390 1 42 dkfzphes3_4h6.3 strong similarity to Kinesin light chain

Alignment to HMM consensus:

Query *RALEDREKtLGHDHPDVatMLNNLALvCRNQNKyeEvenYYN*

RALE+ LG D P+VA+ NNLA + Q+KY+++E +Y+

dkfzphes3 349 RALEIYATRLGPDDPNVAKTKNNLASCYLKQGYQDAETLYK 390

DKFZphtes3_4ol9

group: testes derived

DKFZphtes3_4ol9 encodes a novel 1180 amino acid protein with weak similarity to human megakaryocyte stimulating factor and human mucin.

The novel protein contains a cytochrome c family heme-binding site signature.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to megakaryocyte stimulating factor and mucin

complete cDNA, complete cds, EST hits (few)

Sequenced by AGOWA

Locus: unknown

Insert length: 3767 bp

Poly A stretch at pos. 3757, polyadenylation signal at pos. 3737

```
1 GGCTAGGTTT AGCTTCAGGG GCAGCCCAGG GCAGTGTTCG TGCATATTGC
51 ATGGATGAAA GGCTGAAGGC TGCTCCTCT TGCAGGCTGG CTTCTGAGAT
101 TGCACCTTCT TCTCCTGCTA CTCCTCCAAA TCTATGACCC TTCAAGGCAG
151 AGCTGACCTG TCCGGTAATC AAGGCAATGC AGCCGGCCGC CTAGCTACAG
201 TTCACGAGCC AGTTGTCACC CAGTGGGCGG TGCATCCTCC AGCCCCCGCT
251 CACCCAGATC TCCTGGACAA AATGGAGAAA GCGCTCCAC AGCCCCAGCA
301 CGAGGGCCTC AAGTCCAAGG AGCATCTTCC GCAACAGCCT GCCGAAGGCA
351 AGACGGCGTC CCGCGCGTCC CCACGCTCC GGGCTGTGGT CGAGAGCCAG
401 GCCTTCAAGA ACATCCTGGT AGACGAGATG GACATGATGC ACGCCCGTGC
451 AGCCACGCTC ATCCAAGCCA ACTGGAGGGG CTATTGGCTC CGGCAGAAGC
501 TGATTCCCA GATGATGGCG GCCAAGGCCA TCCAGGAGGC CTGGCGGCGC
551 TTCAACAAGA GACACATCCT TCACTCCAGC AAGTCGTTGG TAAAGAAAAC
601 GAGGGCGGAG GAGGGGGACA TACCTTATCA CGCCCCACAG CAGGTGCGCT
651 TCCAGCATCC GGAAGAGAAC CGCCTTCTGT CCCCGCCCAT CATGGTGAAC
701 AAGGAGACCC AGTTCCCTTC CTGTGACAAT CTGGTCCTCT GCAGACCCCA
751 GTCGTCCCCC CTCCTGCAGC CCCCAGCAGC TCAGGGTACC CCAGAGCCCT
801 GTGTGCAGGG TCCTCATGCT GCCAGAGTCC GGGGGCTGGC CTTCTGCCA
851 CACCAGACGG TCACCATCAG ATTTCCCTGC CCAGTGAGTT TGGACGCAAA
901 ATGCCAGCCA TGCTGTCTGA CCAGAACCAT CAGAAGCACC TGCTCGTCC
951 ACATAGAGGG TGACTCAGTG AAGACCAAAC GTGTAAGTGC CCGGACCAAC
1001 AAAGCCAGGG CTCGGGAGAC ACCATTGTCC AGAAGGTATG ACCAGGCAGT
1051 TACGAGACCA TCCAGAGCCC AAACCCAGGG CCCTGTGAAA GCAGAGACCC
1101 CCAAGCCCCC CTTCCAGATA TGTCCAGGGC CCATGATCAC CAAGACTCTA
1151 CTCCAGACAT ATCCAGTGGT CTCCGTGACC CTGCCACAGA CATATCCAGC
1201 GTCCACGATG ACCACCACCC CACCAAGAC TAGCCAGTT CCCAAAGTAA
1251 CAATAATCAA GACCCACGCC CAGATGTATC CGGGGCCAC AGTGACCAAA
1301 ACTGCACCTC ACATATGCCC CATGCCACCA ATGACCAAGA TCCAGGTACA
1351 CCCCACAGCC TCCAGAACTG GCACCCACG GCAGACATGC CCTGCGACCA
1401 TCACGGCAAA GAACCGACCT CAGGTTTCCC TTCTGGCTTC CATCATGAAG
1451 AGCCTGCCCC AGGTATGCCC GGGGCTGCG ATGGCAAAGA CCCCACCCCA
1501 GATGCACCCG TCCACCACCC CAGCCAAAAA CCCATTGCAA ACATGTCTGT
1551 CAGCCACAAT GTCCAAGACT TCATCCCAGA GGAGCCAGT TGGGCTCACC
1601 AAGCCCTCAC CCCAGACCCG CCTGCCAGCC ATGATAACCA AGACCCAGC
1651 CCAGTTACGG TCGGTGGCCA CCATCCTCAA GACTCTGTGT CTGGCTCTC
1701 CAACAGTGGC AAATGTCAAG GCTCCACCCC AAGTGGCGGT AGCAGCCGGA
1751 ACTCCCAACA CCTCAGGCTC CATCCATGAG AAGCCACCCA AGGCCAAGGC
1801 CACCGTGAAT GTGAAGCAGG CTGCAAAGGT GGTGAAAGCC TCATCCCCCT
1851 CCTATTGGC TGAGGGGAAG ATCAGGTGCC TGGCTCAACC ACATCCGGGA
1901 ACTGGGGTCC CCAGGGCTGC AGCTGAGCTT CCTTTGGAAG CCGAGAAAAT
1951 CAAGACTGGC ACCCAGAAAC AGCGGAAAAC AGACATGGCA TTTAAGACCA
2001 GTGTGGCAGT GGAATGGCT GGGGCTCCAT CCTGGACAAA AGTTGCTGAG
2051 GAAGGGGACA AGCCACCTCA CGTGTATGTG CCTGTAGACA TGGCTGTCAC
2101 CCTGCCCCGG GGACAGCTGG CTGCCCACT GACCAATGCC TCATCCAGA
2151 GACATCCACC CTGCTGTCC CAGAGACCAC TGGCCGCCCC GCTGACCAAG
2201 GCCTCATCTC AGGGACATCT GCCCCTGAG CTGACCAAGA CCCCATCCCT
2251 GGCCCATCTG GACACCTGTC TGAGCAAGAT GCATCCCAAG ACACATCTGG
2301 CCACAGGTGC CGTGAAGGTC CAGTCCCAAG CGCCTCTAGC CACCTGTCTG
2351 ACCAAGACGC AGTCCCGGGG GCAGCCGATC ACAGACATAA CCACGTGCCT
2401 CATCCACAGC AGCCAGGCTG CTGATCTCAG CAGCAACACC CACTCCAGG
2451 TGCTCCTAAC AGGTCCAAG GTGTCCAACC ACGCCTGCCA GCGCTCGGT
2501 GGCCTCAGCG CCCCACCTG GGCCAAGCCA GAGGACAGAC AGACCCAGCC
2551 ACAGCCCAAC GGCACAGTGC CGGGGAAGAC CACTCAGGGG GGACCATGCC
2601 CGGCAGCCTG TGAGGTCCAG GGTATGCTGG TGCCGCCGAT GGCACCCACC
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2651 GGCCATTCCA CATGCAACGT TGAGTCCTGG GGAGACAACG GAGCCACACG
2701 TGCCCAGCCA TCAATGCCCG GCCAGGCGGT GCCCTGCCAG GAGGACACGG
2751 GCCCCGCGGA CGCTGGTGTG GTTGGTGGCC AATCGTGGAA CCGCGCATGG
2801 GAGCCAGCCA GGGGTGCTGC GTCCTGGGAC ACCTGGCGCA ACAAGGCGGT
2851 GGTGCCTCCC AGGCGGTCCG GGGAGCCAAT GGTGTCCATG CAGGCTGCAG
2901 AGGAGATCCG CATCCTCGCA GTGATCACTA TCCAGGCGGG CGTCCGTGGC
2951 TACCTGGCGC GTCGCAGGAT CCGGCTGTGG CACCGGGGGG CCATGGTCAT
3001 CCAAGCTACT TGGCGCGGCT ACCGTGTGCG GCGGAACCTG GCACACCTCT
3051 GCAGAGCCAC CACGACCATC CAGTCTGCCT GGCGCGGCTA CAGCACCCGC
3101 CCGGACCAAG CCCGGCACTG GCAGATGCTC CACCCCGTCA CGTGGGTGGA
3151 GCTGGGCAGC CGGGCCGGGG TCATGTCTGA CCGAAGCTGG TTCCAGGATG
3201 GCAGAGCCAG GACAGTATCT GACCATCGCT GCTTCCAGTC CTGCCAGGCA
3251 CACGCTTGCA GCGTCTGCCA CTCCTGAGC TCCAGGATCG GGAGCCCCGCC
3301 CAGCGTGGTG ATGCTAGTGG GCTCCAGCCC TCGCACCTGT CATACTGTG
3351 GACGCACACA GCCCACCCTG GTGGTGCAGG GCATGGGCCA GGGCACTGAG
3401 GGGCCCGGGG CAGTGTCTTG GGCCTCCGCC TACCAGCTGG CTGCCCTGAG
3451 TCCCAGGAGC CCGCATCGCC AGGACAAAGC GGCCACAGCC ATCCAGTCCG
3501 CCTGGAGGGG CTTTAAGATC CGCCAGCAGA TGAGGCAGCA GCAAATGGCA
3551 GCGAAGATAG TTCAAGCCAC CTGGCGAGGC CACCATACCC GGAGCTGTCT
3601 GAAGAACACA GAGGCCCTCT TGGGACCAGC AGACCCCTCG GCCAGCTCAC
3651 GGCACATGCA TTGGCCTGGC ATCTAGGACC CTGGCTCCCT GCAGTGGGGA
3701 CTTCGTGGGA GGCACCTATG GCTCTCTGGG TCTAATGAAT AAAGTCCTCC
3751 ACAGCCTAAA AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 134 bp to 3673 bp; peptide length: 1180
Category: similarity to known protein

```
1  MTLQGRADLS GNQGNAAGRL ATVHEPVVTQ WAVHPPAPAH PSLLDKMEKA
51  PPQPQHEGLK SKEHLPQQPA EGKTASRRVP RLRAVVESQA FKNILVDEMD
101 MMHARAATLI QANWRGYWLR OKLISQMAA KAIQEAWRRF NKRHILHSSK
151 SLVKKTRAEE GDIPYHAPQO VRFQHPENR LLSPPIMVKN ETQFPSCDNL
201 VLCRPQSSPL LQPPAAQGTG EPCVQGPAAA RVRGLAFLPH QTVTIRFPCP
251 VSLDAKCPQC LLTRTIRSTC LVHIEGDSVK TKRVSARTNK ARAPETPLSR
301 RYDQAVTRPS RAQTQGPVKA ETPKAPFQIC PGPMITKTL QTYPVVSVTL
351 PQTPASTMT TTPPKTSPVP KVTIIKTPAQ MYPGPTVTK APHTCPMPTM
401 TKIQVHPTAS RTGTPRQTC ATITAKNRPO VSLLASIMKS LPQVCPGPAM
451 AKTPPQMHPV TTPAKNPLQT CLSATMSKTS SQRSPGVTK PSPQTRLPAM
501 ITKTPAQLRS VATILKTLCL ASPTVANVKA PPQVAVAAGT PNTSGSIHEN
551 PPKAKATVNV KOAAKVVKAS SPSYLAEGKI RCLAQPHPGT GVPRAAAELP
601 LEAEKIKTGT KQAKTDMAF KTSVAVEMAG APSWTKVAEE GDKPPHVYVP
651 VDMAVTLPRG QLAAPLTNAS SQRHPPCLSQ RPLAAPLTKA SSQCHLPTL
701 TKTPSLAHL DCLSKMHSQT HLATGAVKVQ SQAPLATCLT KTQSRGQIPIT
751 DITTCCLIPAH QAADLSSNTH SQVLLTGSKV SNHACQRLGG LSAPPWAKPE
801 DRQTQPQPHG HVPGKTTQGG PCPAACEVQG MLVPPMAPTG HSTCNVESWG
851 DNGATRAQPS MPQOAVPCQE DTGPADAGVV GGOSWNRAWE PARGAASWDT
901 WRNKAVVPPR RSGEPMVSMQ AAEEIRILAV ITIQAGVRGY LARRRIRLWH
951 RGMAMVIQATW RGYRVRRLA HLCRATTTIQ SAWRGYSTRR DQARHWQMLH
1001 PVTWVELGSR AGVMSDRSWF QDGRARTVSD HRCFQSCQAH ACSVCHSLSS
1051 RIGSPPSVVM LVGSSPRTCH TCGRTQPTRV VQGMGQGTG PGAVSWASAY
1101 QLAALSPROP HRQDKAATAI QSAWRGFKIR QQMRQQQMAA KIVQATWRGH
1151 HTRSKLNTE ALLGPADPSA SSRHMHWPGI
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_4o19, frame 2

TREMBL:HSU70136_1 product: "megakaryocyte stimulating factor"; Human
megakaryocyte stimulating factor mRNA, complete cds., N = 2, Score =
242, P = 9.6e-16

Sbjct: 873 PDESTPELSAEPTPKALENSPKEPGVP--TTKTPAATKPEMTTAKDKTTERDLRTTPET 930

Query: 627 EMAGAPSWTK-VAEEGDKPPHVYPVDMAVTLPRGQLAAPLTNASSQRHPPCLSQRLPAA 685
 A AP TK A +K + +T Q+ + T ++ L LA

Sbjct: 931 TTA-APKMTKETATTTTEKT-----TESKITATTTQVTSTTTQDTPFKITTLKTTTLAP 983

Query: 686 PLTKASSQGHLPTELTKTPSLAHLDTCLSKMHSQTHLATGAVKVQS-----QAPLATCLT 740
 +T + + TE+ P +T K + AT K Q + P +T

Sbjct: 984 KVT-TTKKTITTTTEIMNKPE----ETAKPKDRATNSKAT-TPKPKQPTKAPKKPTSTKKP 1037

Query: 741 KTQSR-GQPITDIT----TCLIPAHQAADLSSNTHSQVLLTGSKVSNHACQRLGGLSAPP 795
 KT R +P T T T +P + Q ++ N + S

Sbjct: 1038 KTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEMLQTTTRPNQTPNSKLVEVNPKSEDA 1097

Query: 796 W-AKPEDRQTQPPQPHGVPGKTTQGGPCPAACEVQGMVLVPPMAPTGHSTCN 845
 A+ E +PH +P T P QG+++ PM + CN

Sbjct: 1098 GGAEGETPHMLLRPHVFMPEVTPDMDYLPRVFN-QGIIINPMLSDETNIEN 1147

Score = 198 (29.7 bits), Expect = 2.3e-11, Sum P(2) = 2.3e-11
 Identities = 142/513 (27%), Positives = 200/513 (38%)

Query: 204 RPQSSPLLQPPAAQGTPEPCVQGPAAARVGLAFLPHQTVTIRFPCPVSLDAKQPCLLT 263
 R + P +PP G + H V+ + +P L

Sbjct: 207 RTKKKPTPKPPVDEAGSLDNGDFKVTTPTDSTTQHNVSTSPKITTAKPINPRPSLPP 266

Query: 264 R--TIRSTCLVHIEGDSVKTKRVSARTNKARAP---ETPLSRRYDQAVTRPSR---AQQT 315
 T + T L + +V+TK + TNK + E S + Q++ + S A T

Sbjct: 267 NSDTSKETSLSLVNKETTVETKETT-TNKQSTSDGKEKTSKAKETQSIKTSKADLAPTS 325

Query: 316 GPKAETPKAPFQICPGPMITKTLQTYPVVSVTLPTQTYPASTMTTTPPKTSPVPKVTII 375
 + TPKA GP +T T + P T P+ PAST TP + +P +

Sbjct: 326 KVLAKPTPKAE-TTTKGPALE-TPKEPTP---TTPKE-PAST---TPKEPTPTTKSAP 375

Query: 376 KTPAQMYPGPTVTKTAPHTC--PMPTMTKIQVHPTASRTGTPTQTC-PATITAKNRQVVS 432
 TP + P PT TK+AP T P PT TK + PT + P T PA T K+ P

Sbjct: 376 TTPKE--PAPTTTKSAPTTTPKEPAPTTTK-EPAPTTTPKEPAPTTTKAPTTTKSAPTT 432

Query: 433 ---LLASIMKSLPQVCPGPAMAKTTPQMHVTTPAKNPLQTCLSATMSKTSSQSPVGV 489
 + K P PA TP + P TTP K P T + T + +P

Sbjct: 433 KEPAPTTPKKAPTTTPKEPAPT-TPKEPTP-TTP-KEPAPTTKEPAPT-TPKEPAPTAPK 488

Query: 490 KPSPQT-RLPAMIT-KTPAQLRVA---TILK---TLCLASPTVANVKAPPQVAVAGT 540
 KP+P T + PA T K PA + T K T ++PT AP A T

Sbjct: 489 KPAPTTKEPAPTTTPKEPAPTTTKESPTTPKEPAPTTTKSAPTTTKAPTTTKSAPTT 548

Query: 541 PNT-SGSIHENP----PKAKATVNVKQAAKV-KASSPSYLAEGKIRCLAQPHPGTGVP 594
 P S + + P PK A K+ A K +P+ E +P P P+

Sbjct: 549 PKEPSPTTTKEPAPTTTPKEPAPTTPKKAPTTTPKEPAPTTTPKEPAPTTTKKPAPTA--PK 606

Query: 595 AAAELPLEAEKIKGTQKQAKTDMAFKTSVAVEMAGAPSWTK-VAEEGDKPPHVYPVDM 653
 A P ++ T K+ K + AP+ + +A + P P +

Sbjct: 607 EPA--PTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEP 664

Query: 654 AVTLPRGQLAAPLTNASSQRHP-PCLSQRLAAPLTAKASSQGHLPTELTKTPSLAHLDT 712
 A T P+ AAP T + P P + P AP T P E T T

Sbjct: 665 APTTPKA--AAPNT---PKAPPTTPKEP--APTTPKEPAPTTPKETAPTTPKGTAPTT 716

Query: 713 LSK 715
 L +

Sbjct: 717 LKE 719

Score = 108 (16.2 bits), Expect = 4.3e-02, Sum P(2) = 4.3e-02
 Identities = 60/214 (28%), Positives = 85/214 (39%)

Query: 265 TIRSTCLVHIEGDSVKTKRVSAR-TNKA--RAPETP-LSRRYDQAVTRPSRAQTQGPVKA 320
 T + +H D T +SA T KA +P+ P + A T+P T

Sbjct: 862 TTKEPTTIHKSDE-STPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTAKDKTT 920

Query: 321 ETP--KAPFQICPGPMITK-TLLQTYPVVSVTLPTQTYPASTMTTTPPKTSPVPKVTIIKT 377
 E P P +TK T T + T TTT T+P K+T +KT

Sbjct: 921 ERDLRTTPETTTAAPKMTKETATTTTEKTIESKITATTTQVTSTTTQD-TTPF-KITTLKT 978

Query: 378 PAQMYPGPTVTK---TAPHTCPMPTMT-KIQVHPTASRTGTPTQTCPATITAKNRQVSL 433
 + P TTK T P T K + T S+ TP+ P A +P +

Sbjct: 979 TT-LAPKVTTTKTITTTTEIMNKPEETAKPKDRATNSKATTPKPKQPTK--APKKPTSTK 1035

Query: 434 LASIMKSL--PQVCPGPA-MAKTPPMHPTTPAKNPLQ 470
 M + P+ P P M T P+++P + A+ LQT

Sbjct: 1036 KPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEMLQ 1075

Score = 56 (8.4 bits), Expect = 3.1e-12, Sum P(2) = 3.1e-12

895

Prosites for DKFZphtes3_4o19.2

PS00001	542->546	ASN_GLYCOSYLATION	PDOC00001
PS00001	668->672	ASN_GLYCOSYLATION	PDOC00001
PS00004	282->286	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	76->79	PKC_PHOSPHO_SITE	PDOC00005
PS00005	148->151	PKC_PHOSPHO_SITE	PDOC00005
PS00005	244->247	PKC_PHOSPHO_SITE	PDOC00005
PS00005	265->268	PKC_PHOSPHO_SITE	PDOC00005
PS00005	278->281	PKC_PHOSPHO_SITE	PDOC00005
PS00005	281->284	PKC_PHOSPHO_SITE	PDOC00005
PS00005	285->288	PKC_PHOSPHO_SITE	PDOC00005
PS00005	288->291	PKC_PHOSPHO_SITE	PDOC00005
PS00005	299->302	PKC_PHOSPHO_SITE	PDOC00005
PS00005	322->325	PKC_PHOSPHO_SITE	PDOC00005
PS00005	414->417	PKC_PHOSPHO_SITE	PDOC00005
PS00005	424->427	PKC_PHOSPHO_SITE	PDOC00005
PS00005	481->484	PKC_PHOSPHO_SITE	PDOC00005
PS00005	610->613	PKC_PHOSPHO_SITE	PDOC00005
PS00005	671->674	PKC_PHOSPHO_SITE	PDOC00005
PS00005	679->682	PKC_PHOSPHO_SITE	PDOC00005
PS00005	900->903	PKC_PHOSPHO_SITE	PDOC00005
PS00005	959->962	PKC_PHOSPHO_SITE	PDOC00005
PS00005	987->990	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1015->1018	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1049->1052	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1065->1068	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1106->1109	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1146->1149	PKC_PHOSPHO_SITE	PDOC00005
PS00005	1171->1174	PKC_PHOSPHO_SITE	PDOC00005
PS00006	22->26	CK2_PHOSPHO_SITE	PDOC00006
PS00006	42->46	CK2_PHOSPHO_SITE	PDOC00006
PS00006	156->160	CK2_PHOSPHO_SITE	PDOC00006
PS00006	546->550	CK2_PHOSPHO_SITE	PDOC00006
PS00006	848->852	CK2_PHOSPHO_SITE	PDOC00006
PS00006	988->992	CK2_PHOSPHO_SITE	PDOC00006
PS00006	1003->1007	CK2_PHOSPHO_SITE	PDOC00006
PS00006	1027->1031	CK2_PHOSPHO_SITE	PDOC00006
PS00008	11->17	MYRISTYL	PDOC00008
PS00008	14->20	MYRISTYL	PDOC00008
PS00008	539->545	MYRISTYL	PDOC00008
PS00008	591->597	MYRISTYL	PDOC00008
PS00008	746->752	MYRISTYL	PDOC00008
PS00008	777->783	MYRISTYL	PDOC00008
PS00008	853->859	MYRISTYL	PDOC00008
PS00008	878->884	MYRISTYL	PDOC00008
PS00008	882->888	MYRISTYL	PDOC00008
PS00008	1008->1014	MYRISTYL	PDOC00008
PS00008	1053->1059	MYRISTYL	PDOC00008
PS00008	1083->1089	MYRISTYL	PDOC00008
PS00190	1042->1048	CYTOCHROME_C	PDOC00169

(No Pfam data available for DKFZphtes3_4o19.2)

DKFZphtes3_50j4

group: testes derived

DKFZphtes3_50j4 encodes a novel 187 amino acid protein proline rich protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown, prolin rich protein

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 1186 bp

Poly A stretch at pos. 1176, polyadenylation signal at pos. 1126

```
1  CACTGGGCGT CTGAAGCTCA GAGCTCACCC CTGAGATGGG CTCTCCTAGG
51 CCTCCTGGGA TGAGGGAGCC ACCAGGACCC AGTGCTGTGA TGCCTGCTCT
101 TCCCTCTACC AGCACCTGCC CGCCCAGAGA CCAGGGCACC CCTGAAGTCC
151 AGCCCACCCC TGCAAAGGAC ACATGGAAGG GCAAGCGGCC TCGATCCCAG
201 CAGGAGAACC CAGAGAGCCA GCCTCAGAAG AGGCCACGCC CCTCAGCCAA
251 GCCCTCCGTC GTAGCTGAGG TCAAGGGCAG CGTCTCGGCC AGCGAACAGG
301 GCACCTTGAA TCCCACGGCT CAAGACCCCT TCCAGCTCTC CGCTCCTGGC
351 GTCTCCTTGA AGGAGGCTGC AAATGTTGTG GTCAAGTGCC TCACCCCTTT
401 CTACAAGGAG GGCAAGTTTG CTTCCAAGGA GTTGTTTAAA GGCTTTGCCC
451 GCCACCTCTC ACACTTGCTG ACTCAGAAGA CCTCTCCTGG AAGGAGCGTG
501 AAAGAAGAGG CCCAGAACCT CATCAGGCAC TTCTTCCATG GCCGGGCCCC
551 GTGCGAGAGC GAAGCTGACT GGCATGGCCT GTGTGGCCCC CAGAGATGAC
601 CAACTGCTGG CTGGGCAGGG CCCGCGTCCT CCCCAGATT CTAGCATGGG
651 TCATCCTGGG CCTCACCTGC TGATGCCAGG GCCATCGTCT TTTCTCAGTC
701 CTTCTCCTTT CCAACCATA TGGGCTTTGG GGATGACCCC AGACACCCCC
751 TGAATCCAGG TCAGAGGTCA GCCCACCTTT CTTTCTGCTT GCAAAGCCTA
801 TAGACCCTTC TCAGAGCGGT CCTCATGGCT GGGTTTCTTG GGACACATGT
851 CGAGGACAGA AGGTGGAGGG TGGTGGAGCT GCTGCTGGAA GAAGGGGAAG
901 GAAGAGTGGC CCCTCCCCGA GTTCTAAGTC AGGATGAGGC CCACCTGTCC
951 AAGGTATCGG AACCTACCCA GGGGACCCTC AGATCCTCCA CCCACTCCCC
1001 CATCCATTAC GATGCCAGCT TCCAGCCTTG CCCAGTCAAG AGCTGTGGCA
1051 GAGGAGAGGC AGCCAGGCCC TGTTCTTGCT CAGCTCTGTC TCAGGAAGGC
1101 CAGGCTGAC AGATGTTTGG GAGAGGAATA AAGTTGTGTT GTTGTGGGGC
1151 ATGACGGCGT GCACACAGCC CTTTTCAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3
-----ORF from 36 bp to 596 bp; peptide length: 187
Category: putative protein

```
1  MGSPRPPGMR EPPGPSAVMP ALPSTSTCPP RDQGTPEVQP TPAKDTWKKG
51  RPRSQQENPE SQPQKRPRPS AKPSVVAEVK GSVSASEQGT LNPTAQDPFQ
101 LSAPGVSLKE AANVVVKCLT PFYKEGKFAS KELFKGFARH LSHLLTQKTS
151 PCRSVKEEAQ NLIRHFFHGR ARCESEADWH GLCGPQR
```

BLASTP hits

Entry MMU92455_1 from database TREMBL:

product: "WW domain binding protein 7"; Mus musculus WW domain binding
protein 7 mRNA, partial cds.
Score = 134, P = 6.9e-08, identities = 45/125, positives = 56/125

Alert BLASTP hits for DKFZphtes3_50j4, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3_50j4, frame 3

Report for DKFZphtes3_50j4.3

[LENGTH] 187
[MW] 20353.06
[pI] 9.76
[PROSITE] MYRISTYL 1
[PROSITE] AMIDATION 1
[PROSITE] CK2_PHOSPHO_SITE 6
[PROSITE] PKC_PHOSPHO_SITE 6
[KW] All_Alpha
[KW] LOW_COMPLEXITY 8.56 %

SEQ MGSFRPPGMRPEPPGSAVMPALPSTSTCPPRDQGTPEVQPTPAKDTWKGRPRSQQENPE
SEG xxx
PRD ccc

SEQ SQPQKRPRPSAKPSVVAEVKGSVSASEQGTLNPTAQDPFQLSAPGVSLKEAANVVVKCLT
SEG
PRD cccccccccccccchhhhhccccccccccccccccccccccccccccccccchhhhhheeecc

SEQ PFYKEGKFASKELFKGFARHLSHLLTQKTSPPGRSVKEEAQNLI RHFFHGRARCESEADWH
SEG
PRD cccccccchhhhhhhhhhhhhhhhhheeeccccchhhhhhhhhhhhhhhccchhhhhhhhh

SEQ GLCGPQR
SEG
PRD ccccccc

Prosites for DKFZphtes3_50j4.3

PS00005	3->6	PKC_PHOSPHO_SITE	PDOC00005
PS00005	46->49	PKC_PHOSPHO_SITE	PDOC00005
PS00005	70->73	PKC_PHOSPHO_SITE	PDOC00005
PS00005	107->110	PKC_PHOSPHO_SITE	PDOC00005
PS00005	146->149	PKC_PHOSPHO_SITE	PDOC00005
PS00005	154->157	PKC_PHOSPHO_SITE	PDOC00005
PS00006	54->58	CK2_PHOSPHO_SITE	PDOC00006
PS00006	84->88	CK2_PHOSPHO_SITE	PDOC00006
PS00006	94->98	CK2_PHOSPHO_SITE	PDOC00006
PS00006	107->111	CK2_PHOSPHO_SITE	PDOC00006
PS00006	154->158	CK2_PHOSPHO_SITE	PDOC00006
PS00006	175->179	CK2_PHOSPHO_SITE	PDOC00006
PS00008	81->87	MYRISTYL	PDOC00008
PS00009	48->52	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_50j4.3)

DKFZphtes3_50n06

group: testes derived

DKFZphtes3_50n06 encodes a novel 186 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes..

unknown

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 1095 bp

Poly A stretch at pos. 1085, polyadenylation signal at pos. 1061

```

  1 CAAGACCCTC GGAGCCAAGA AACAACTG AGTTCCAGAT TTCGGAAGGT
  51 TCACGAGTGT TGCCGACACG CCCTCCCAAC TGCAGACATC CTCCTGGAG
101 GACCTGCTGT GCTCACATGC CCCCTGTCC AGCGAGGACG ACACCTCCCC
151 GGGCTGTGCA GCCCCCTCCC AGGCACCTT CAAGGCCTTC CTCAGTCCCC
201 CAGAGCCACA TAGCCACCGA GGCACCGACA GGAAGCTGTC CCCGCTCCTG
251 AGCCCCCTTG AAGACTCACT GGTGGACAAG ACCCTGCTGG AGCCCAGGGA
301 GATGGTCCGG CCTAAGAAGG TGTGTTTCTC GGAGAGCAGC CTGCCCACCG
351 GGGACAGGAC CAGGAGGAGC TACTACCTCA ATGAGATCCA GAGCTTCGCG
401 GGCGCCGAGA AGGACGCGCG CGTGGTGGGC GAGATCGCCT TCCAGCTGGA
451 CCGCCGCATC CTGGCCTACG TGTTCCTGGG CGTGACGCGG CTCTACGGCT
501 TCACGGTGGC CAACATCCCC GAGAAGATCG AGCAGACCTC CACCAAGTCT
551 CTGGACGGCT CCGTGGACGA GAGGAAGCTG CGCGAGCTGA CGCAGCGCTA
601 CCTGGCCCTG AGCGCGCGCC TGGAGAAGCT GGGCTACAGC CGCGACGTGC
651 ACCCGCGGTT CAGCGAGTTC CTCATCAACA CCTACGGAAT CCTGAAGCAG
701 CGGCCCGACC TGC CGCGCCAA CCCCTGCA AGCAGCCCGG CCGCGCTGCG
751 CAAGCTGGTC ATCGACGTGG TGCCCCCAA GTTCCTGGGC GACTCGCTGC
801 TGCTGCTCAA CTGCCTGTGC GAGCTCTCCA AGGAGGACGG CAAGCCCCTC
851 TTCGCTGGT GAGCCGCCCC GCGCCGCGCG CTTGCTGTC AGTAAACGCG
901 TTTGTTCCAA CCCGGGGCGG CGGTGCCTCC TGCGCGTCCC CCCGGAGGGG
951 AAAGGGCCGC GTCCCCCGCG CGCGAGGCCA GAGAAGGCCG CGCTCCCACC
1001 GGTGCTGGGC CCCGACCGCA GCCCGCCGCT GCCCGACCT GCGGAGTGCT
1051 TCTCACCCTT CATTAAATC ATCCGTTTGC TTGTCAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 302 bp to 859 bp; peptide length: 186

Category: putative protein

Classification: no clue

```

  1 MVRPKKVCFS ESSLPTGDRT RRSYYLNEIQ SFAGAEKDAR VVGEIAFQLD
  51 RRILAYVFPV VTRLYGFTVA NIPEKIEQTS TKSLDGSVDE RKLRELTORY
101 LALSARLEKL GYSRDVHFAF SEFLINTYGI LKQRPDLRAN PLHSSPAALR
151 KLVIDVVPK FLGDSLLLLN CLCELSKEDG KPLFAW
```

BLASTP hits

No BLASTP hits available

No Alert BLASTP hits found

Pedant information for DKFZphtes3_50n06, frame 2

Report for DKFZphtes3_50n06.2

```
[LENGTH]      186
[MW]           21049.39
[pI]           9.28
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY      5.38 %
```

```
SEQ      MVRPKKVCFSESSLPTGDRTRRSYYLNEIQSFAGA EKDKARVVG EIA FQLD RRI LAYVFPG  
SEG  
PRD      cccccceeeccccc cccccccccccccch hhhhhh hhhhhh hhhhhh hhhhhh hhhhhh hhhhhh hhhhhh hhhhhh hccccc
```

```
SEQ      VTRLYGFTVANIPEKIEQTSTKSLDGSVDERKLRELTQRYLALSARLEKLGYSRDVHPAF
SEG
PRD      ceeeeeeeeeeccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhccccccccch
```

```
SEQ      SEFLINTYGILKQRPDLRANPLHSSPAALRKLVIDVVPKFGLGDSLLLLNCLCELSKEDG
SEG                                           .xxxxxxxxxxxxx
PRD      hhhhhhccccccccccccccccccccccchhhhhhhhhhhccccccccchhhhhhhhhhhhhcccc
```

```
SEQ      KPLFAW
SEG      . . . . .
PRD      CCCCCC
```

(No Prosite data available for DKFZphtes3_50n06.2)

(No Pfam data available for DKFZphtes3_50n06.2)

DKF2phtes3_50n23

group: testes derived

DKF2phtes3_50n23 encodes a novel 499 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

2 EST hits
(from other testis librarys) testis specific cDNA?

Sequenced by DKFZ

Locus: unknown

Insert length: 1907 bp

Poly A stretch at pos. 1897, polyadenylation signal at pos. 1872

```
1 GGGCACCAGC CACTTTCAC CATGACTGTG CGCTCGAGGG TCGCAGATGT
51 GTTCGGCAGC AAGGACACTG AGAGCCTTGA GCCTGTGCTT TTACCCTTAG
101 TAGATCGCAG GTTTCCTAAG AAATGGGAAA GACCGGTGGC AGAAAGCTTA
151 GGCCACAAAG ACAAGACCA GGAGGACTAC TTCCAGAAGG GAGGACTCCA
201 AATTAAGTTC CACTGTAGCA AGCAGCTGTC TCTAGAGAGC TCCAGGCAGG
251 TGACCTCTGA GAGCCAAGAG GAGCCCTGGG AGGAGGAATT CGGCCGGGAG
301 ATGCGGAGGC AGCTGTGGCT GGAGGAGGAG GAGATGTGGC AGCAGCGGCA
351 GAAGAAGTGG GCCCTGCTGG AGCAGGAGCA TCAGGAGAAG CTGCGGCAGT
401 GGAATCTGGA AGACCTGGCC AGGGAGCAAC AGCGGAGATG GGTCCAGCTA
451 GAAAAGGAGC AGGAGAGCCC ACGGAGAGAG CCAGAGCAGC TAGGGGAGGA
501 TGTGGAGAGG AGGATCTTCA CACCCACCAG TCGATGGAGG GACTTGGAGA
551 AGGCAGAGCT ATCATTAGTG CCTGCCCCAA GCCGGACCCA ATCTGCTCAC
601 CAAAGCAGGA GGCCACACTT GCCCATGTCT CCTAGTACCC AGCAGCCTGC
651 CCTGGGAAAG CAGAGACCTA TGAGTTCAGT GGAGTTTACC TACAGACCAC
701 GGACCCGCGC AGTTCACCAC AAGCCCAAGA AATCTGCCTC CTTTCCTGTC
751 ACTGGGACAT CCATCCGAAG GCTGACCTGG CCCTCTTTGC AGATATCCCC
801 TGCAAATATT AAGAAGAAGG TGTACCACAT GGACATGGAG GCCCAGAGGA
851 AGAACCTGCA GCTCCTGAGT GAGGAGTCTG AGTTGAGGCT GCCCCACTAC
901 CTGCGCAGCA AAGCACTGGA GCTCACCACC ACCACCATGG AGCTGGGCGC
951 GCTCAGGCTG CAGTACCTGT GCCATAAGTA CATCTTCTAT AGACGCCTCC
1001 AGAGCCTCCG GCAAGAAGCG ATCAACCATG TACAAATCAT GAAAGAAACG
1051 GAGGCTTCCT ACAAGGCCCA GAACCTCTAC ATCTTCCTGG AAAACATTGA
1101 CCGCCTGCAG AGTCTCAGGC TGCAGGCCTG GACGGACAAG CAGAAGGGGC
1151 TGGAGGAGAA GCACCGAGAG TGCCTGAGCA GCATGGTGAC CATGTTCCCC
1201 AAGCTCCAGC TGGAGTGGAA CGTTCACCTG AACATCCCTG AGGTCACCTC
1251 GCCAAAGCCA AAGAAATGCA AGTTGCCTGC AGCCTCAGCC CGGCACATCC
1301 GCCCCAGTGG CCCCACCTAC AAGCAGCCCT TTCTGTCTAG GCACCGGGCA
1351 TGTGTGCCCC TGCAGATGGC CCGCCAACAG GGGGAAGCAGA TGGAGGCTGT
1401 CTGGAAGACC GAGGTGGCCT CCTCCAGTTA CGCAATAGAA AAAAAGACCC
1451 CTGCCAGCCT TCCCCGGGAC CAGCTGAGGG GACACCCAGA TATTCCCCGG
1501 CTGTTGACAC TGGACGTGTA GTCTCCTGTC CACAAAAGCC TGAACCTCCT
1551 GAAGGCCAGC TAAGCGCCTC AGCGAACCAA AGGAAGGAAT GCCAGGAACC
1601 TACAAATGAA TCCGCTTAGC TTGTTCAAAA AAAGTCAAGC GAGTCACTCC
1651 CTGGAACCCA AATAAGCCAG AAGGATCAAG ACAGCCCGAG TCTCCACTGC
1701 ATCCCTCAGC CAGTGATTCT CAACCTTCTG AGGGACGGAA ACCACAGAG
1751 AACTTGGTCA AAATGCAGGT TCCCAGCTGG TGCTTTTAAA GAAACCTCTC
1801 GGGGGTTGCT GAGTACTCCT AGAACTTTGA GAAACTGTC TTCCCTCCTG
1851 CAGTCCCCAA ACTCTACATT TTAATAAAAT AGAGGTTGGT TTATTTTAAA
1901 AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 22 bp to 1518 bp; peptide length: 499
 Category: similarity to known protein
 Classification: no clue

```

1  MTVRSRVADV FGSKDTESLE PVLLPLVDRR FPKKWERPVA ESLGHKDKDO
51 EDYFQKGLQ IKFHCSKQLS LESSRQVTSE SQEEPWEEEF GREMRRQLWL
101 EEEEMWQQRQ KKWALLEQEH QEKLRQWNLE DLAREQQRW VQLEKEQESP
151 RREPEQLGED VERRIFTPTS RWRDLEKAE SLVPAPSRTQ SAHQSRPHL
201 PMSPTQQA LGKQRPMSV EFTYRPRTRR VPTKPKKSAS FVPTGTSIRR
251 LTWPSLQISP ANIKKKVYHM DMEAQRKNLQ LLSESELRL PHYLRSKALE
301 LTTTMMELGA LRLQYLCHKY IFYRRLQSLR QEAINHVQIM KETEASYKAQ
351 NLYIFLENID RLQSLRLQAW TDKQKGLEEK HRECLSSMVT MFPKLQLEWN
401 VHLNIPEVTS PKPKCKLPA ASPRHIRPSG PTYKQFSLR HRACVPLQMA
451 RQGGKQMEAV WKTEVASSY AIEKKTASL PRDQLRGHPD IPRLTLTDV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_50n23, frame 1

PIR:S28589 trichohyalin - rabbit, N = 1, Score = 134, P = 5.3e-05

TREMBLNEW:AF132479_1 product: "Ese2L protein"; Mus musculus Ese2L
 protein mRNA, complete cds., N = 1, Score = 130, P = 0.00017

>PIR:S28589 trichohyalin - rabbit
 Length = 1,407

HSPs:

Score = 134 (20.1 bits), Expect = 5.3e-05, P = 5.3e-05
 Identities = 88/354 (24%), Positives = 154/354 (43%)

Query: 29 RRFPPKKWERPVAESLGHKDKDQEDYFQKGLQIK-FHCSKQLSLESSRQVTSESQEEPWE 87
 R++ K +R + L + ++E ++ G + F +QL +++ E +EE +
 Sbjct: 165 RQYRDKERQLRQLEERRAEELRRRKGDAEEFIEELRRRQQLKRELREEEQQ 224

Query: 88 EEFGREMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLEDLAREQQRWVQLEKEQ 147
 RE + L+EEE RQ++W E Q++LR+ LE++ RE+++R Q E+ +
 Sbjct: 225 RRERREQHERA-LQEEELLRQRRRE-EPREQQLRR-ELEEI-REREQRLQEEERRE 280

Query: 148 ESPRREPEQLGEDVERRIFTPTSRWRDLEKAELSLVPAPSRTQSAHQSRPHLPMSPSTQ 207
 + RRE ++L E ERR ++ + E L R Q Q R + +
 Sbjct: 281 QQLRRE-QRL-EQEERREQRLRELEEIREREQRLQEEERREQRLQEEERREQQLKRELE 338

Query: 208 QPALGKQRPMSVVEFTYRPRTRRVPTKPKKSASFVPTGTSIRRLTWPSLQISPAIKK-K 266
 + +QR +E R R + + + ++ A G S+ R W S A ++ K
 Sbjct: 339 EIREREQR---LEQEEK-REQLLAEVREQAR--ERGESLTR-RWQRQLESEAGARQSK 390

Query: 267 VYHMDMEAQRKNLQLLSESELRLPHYLRSKALELTTTMM-----ELGALRLQYLCHKY 320
 VY +R+ Q L ++ E R R + LE E R Q L +
 Sbjct: 391 VYS---RPRRQEEQSLRQDQERR-QRQERERELEEQARRQQWQAEESERRRQLSARP 446

Query: 321 IFYRRLQSLRQEAINHVQIMKETEASYKAONLYI-FLENIDRLQSL-RLQAWTDKQKGLE 378
 R Q +E Q +E E + + + FLE ++LQ R Q ++ E
 Sbjct: 447 SLRER-QLRAEERQEQRFREEEQRRERQELQFLEEEELQRRERAAQQLQEEEDSFQE 505

Query: 379 EKHR 382
 ++ R
 Sbjct: 506 DRER 509

Score = 119 (17.9 bits), Expect = 2.2e-03, P = 2.2e-03
 Identities = 79/357 (22%), Positives = 150/357 (42%)

Query: 33 KWERPVAESLGHKDKDQEDYFQKGLQIKFHCSKQLSLESSRQVTSESQEEPWEEEFGR 92
 ++ E+ + + K +++E Q+ + + +Q R+ + + + EE+F +
 Sbjct: 990 RREEQLRQERDRKFRREEQLQE---REEERLRRQERDRKFRREEERQLRRQLEEQFRQ 1046

Query: 93 EMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLEDLAREQQRWVQLEKEQESPRR 152
 E R+ LEE+ + Q+++K L QE K R+ E+ R +Q R QL +E++ R
 Sbjct: 1047 ERDRKFRLEE-QRQEEK-QLRRQERDRKFR---EEQRRRQEREQQLRRERDRKFR 1101

Query: 153 EPEQLGEDVERRIFTPTSRWRDLEKAELSLVPAPSRTQSAHQSR--RPHLPMSPSTQQA 210

Sbjct: 1102 E EQL ++ E R R L + E L + + + R R + +++
 EEEQLQEREEERLRQERARKLREEE-QLLRREEQLLRQERDRKFREEEQLLQESEER 1160

Query: 211 LGKQ---RPMSSVEFTYRPRTRRVPTKPKKSASFVVTGTSIRRLTWPSLQISPANIKKKV 267
 L + Q R + E + R + +++ +R+ Q ++++

Sbjct: 1161 LRRQERERKLREEEQLLQEREEERLRQERARKLREEEQLLRQEEQLRQERARKLREEE 1220

Query: 268 YHMDMEAQ-----RKNLQLLS-EESELRLPHYLRSKALELTTTMMELGALRLOYL 316
 + E Q R+ QLL EE ELR + + E E LR Q

Sbjct: 1221 QLLRQEEQLRQERDRKFREEEQLLRREEQLLRERDRKFREEEQLLQEREEERLRQER 1280

Query: 317 CHKYIFYRRLQSLRQEAINHVMQIMKETEASYKAQNLYIFLENIDRLQ-SLRLQAWTDKQK 375
 K + L E ++ +E + Y+A+ + E RL+ LR + +++

Sbjct: 1281 ARK--LREEEQLLFEEQEEQRLRQERDRRYRAEEQFAREEKSRRLERELRQEEEQRRR 1338

Query: 376 GLEEKHRE 383
 E K RE

Sbjct: 1339 ERERKFRE 1346

Score = 109 (16.4 bits), Expect = 1.9e-01, P = 1.7e-01
 Identities = 37/113 (32%), Positives = 60/113 (53%)

Query: 67 KOLSLESSRQVTSESO--EEPWEEFGRMRRQLWLEEEEMWQORQKKWALLEQEHQEK 124
 +QL E R+ E Q +E EE R+ R + EEE++ Q+R+++ L QE + KL

Sbjct: 764 QQLRRERDRKFREEEQLLQEREEERLRQERERKLREEEQLLQEREE-RLRRQERERKL 822

Query: 125 ROWNLEDLAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEKAE 179
 R+ E L +E++ ++ +E+E RE EQL E+ + R R L + E

Sbjct: 823 REE--EQLLQEREEERLR-RQERERKLREEEQLLRQEEQEL--RQERARKLREEE 872

Score = 107 (16.1 bits), Expect = 3.0e-01, P = 2.6e-01
 Identities = 35/109 (32%), Positives = 61/109 (55%)

Query: 71 LESSRQVTSESQEEPWE-EEFGRMRRQL---WLEEEEMWQORQKKWALLEQEHQEKLRQ 126
 L Q+ ES+EE +E +++RR+ + EEE++ Q+R+++ L QE + KLR+

Sbjct: 742 LREEEQLLQESSEERLRQEREQQLRRERDRKFREEEQLLQEREE-RLRRQERERKLRE 800

Query: 127 WNLEDLAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEKAE 179
 E L +E++ ++ +E+E RE EQL ++ E R R L + E

Sbjct: 801 E--EQLLQEREEERLR-RQERERKLREEEQLLQEREEERLRQERERKLREEE 850

Score = 104 (15.6 bits), Expect = 9.4e-02, P = 9.0e-02
 Identities = 84/339 (24%), Positives = 149/339 (43%)

Query: 67 KOLSLESSRQVTSESQEEPWEEFGRMRRQL-WLEEEEMWQORQKKWALLEQE--HQEK 123
 +QL E ++ +EE EE R+L +LEEE Q+R++ L E++ ++

Sbjct: 451 RQLRAERQEQEQRFREE---EEQRRERRQELQFLEEEELQRRERAQQLQEEDSFQEDR 507

Query: 124 LRQWNLEDLAREQQRRWVQLEKEQESPRR---EP---EQLGEDVE-RRIFTPTSRWRDL 175
 R+ ++ Q RW QL++E + R +P EQL E+ E +R R R+

Sbjct: 508 ERRRRQEQORPGQTWRW-QLQEEAQRRTLYAKPGQEQQLREEEELQREKRRQEREREY 566

Query: 176 EKAELSLVPAPSRQTSAHQSRPHLPMSPSTQQPALGKQRPMSSEFTYRPT---RRV 231
 + E L + + R + + Q+ L + R + E + R RR

Sbjct: 567 REEE-KLQREDEKRRRQERERQYRELEELRQEEQL-RDRKLREEEQLLQEREEERLRQ 624

Query: 232 PTKPK---KSASFVVTGTSIRRLTWPSLQISPANIKKKVYHMDMEAQRK---NLQLLSEE 285
 + K + +R+ L+ +++ + E +RK QLL E

Sbjct: 625 ERERKLREEEQLLRQEEQLRQERERKLREEEQLLRREEQLRQERERKLREEEQLLQER 684

Query: 286 SELRLPHYLRSKALE-----LTTTMMELGALRLQYLCHKYIFYRRL-QSLRQEAINHVM-- 337
 E RL R++ L L EL R + L + RR Q LRQE +

Sbjct: 685 EEERLRQERARKLREEEQLLRQEEQLRQERERKLREEEQLLRREEQLLRQERDRKLRE 744

Query: 338 --QIMKETEASYKAQNLYIFLENIDRLQSLRLQAWTDKQKGLEEKHRECL 385
 Q+++E+E + E +L+ R + + +++ L+E+ E L

Sbjct: 745 EEQLLQESSEERLRQ-----EREQQLRRERDRKFREEEQLLQEREEERL 789

Score = 103 (15.5 bits), Expect = 1.2e-01, P = 1.1e-01
 Identities = 42/152 (27%), Positives = 74/152 (48%)

Query: 36 ERPVAESLGHKDKDQEDYFQKGGQLIKFHCSKOLSLESSRQVTSESQEEPWEEFGR-REM 94
 ER + K +++E ++ +++ ++L E + + E QE E + RE

Sbjct: 835 ERLRRQERERKLREEEQLLRQEEQLRQERARKLR-EEEQLLRQEEQLRQERDRKLREE 893

Query: 95 RRQLWLEEEEMWQORQKWA---LLEQEHQEKLRQWNLEDLAREQQ---RRWVQ-LEKE 146
 + L EE+E+ Q+R +K LL++ +E+LR+ E RE++ RR Q L +E

Sbjct: 894 EQLLRQEEQLRQERDRKLREEEQLLQESSEERLRQERERKLREEEQLLRREEQLRRE 953

Query: 147 QESPRREPEQLGEDVERRIFTPTSRWRDLEKAE 179
 + RE EQL ++ E R R L + E

Sbjct: 954 RARKLREEEQLLQEREEERLRRQERARKLREEE 986

Score = 103 (15.5 bits), Expect = 7.8e-01, P = 5.4e-01
Identities = 31/91 (34%), Positives = 52/91 (57%)

Query: 67 KQLSLESSRQVTSSESQEEFPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQ 126
++L E R++ E Q EE+ R+ R+ EEE++ Q+R+++ L QE KLR+

Sbjct: 642 QELRQERERKLREEEQLLRREEQELRQERERKLREEEQLLQEREEE-RLRRQERARKLRE 700

Query: 127 WNLEDLAREQQRRWVQLEKEQESPRREPEQL 157
E L R++++ +L +E+E RE EQL

Sbjct: 701 E--EQLLRQEEQ---ELRQERERKLREEEQ 726

Score = 101 (15.2 bits), Expect = 2.0e-01, P = 1.8e-01
Identities = 38/111 (34%), Positives = 57/111 (51%)

Query: 72 ESSRQVTSSESQEEFPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLE 130
E R++ E Q EE E RE R+L EEE++ Q+R+++ L QE KLR+ +

Sbjct: 931 ERERKLREEEQLLRREEQELRRERARKL-REEEQLLQEREEE-RLRRQERARKLREEE-Q 987

Query: 131 DLAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEKAELSL 182
L RE+Q +L +E++ RE EQL ++ E R R + E L

Sbjct: 988 LLRREEQ---ELRQERDRKFREEEQLLQEREEERLRRQERDRKFREEERQL 1035

Score = 101 (15.2 bits), Expect = 1.3e+00, P = 7.2e-01
Identities = 33/108 (30%), Positives = 56/108 (51%)

Query: 72 ESSRQVTSSESQEEFPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLE 131
E R++ E Q EE+ R+ R+ EEE++ +Q +++ L QE KLR+ E

Sbjct: 841 ERERKLREEEQLLRQEEQELRQERARKLREEEQLLRQEEQ---LRQERDRKLREE--EQ 895

Query: 132 LAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEKAE 179
L R++++ +L +E++ RE EQL ++ E R R L + E

Sbjct: 896 LLRQEEQ---ELRQERDRKLREEEQLLQEESEERLRRQERERKLREEE 940

Score = 99 (14.9 bits), Expect = 2.0e+00, P = 8.7e-01
Identities = 32/97 (32%), Positives = 50/97 (51%)

Query: 72 ESSRQVTSSESQEEFPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLE 131
E R+ E Q EE E R L EEE Q +++ L QE + KLR+ E

Sbjct: 578 EKRRRQERERQYREELRQEEQLRDRKLREEEQLLQEREEERLRRQERERKLREE--EQ 635

Query: 132 LAREQ-----QRRWVQLEKEQESPRREPEQLGEDVERRI 165
L R++ Q R +L +E++ RRE ++L ++ ER++

Sbjct: 636 LLRQEEQELRQERERKLREEEQLLRREEQELRQERERKL 674

Score = 99 (14.9 bits), Expect = 2.0e+00, P = 8.7e-01
Identities = 34/111 (30%), Positives = 58/111 (52%)

Query: 67 KQLSLESSRQVTSSESQ--EEPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEK 124
++L E R++ E Q +E EE R+ R+ EEE++ +O +++ L QE + KL

Sbjct: 664 QELRQERERKLREEEQLLQEREEERLRRQERARKLREEEQLLRQEEQ---LRQERERKL 720

Query: 125 RQWNLEDLAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEK 177
R+ + L RE+Q L +E++ RE EQL ++ E R + L +

Sbjct: 721 REEE-QLLRREEQ---LRQERDRKLREEEQLLQEESEERLRRQEREQQLR 768

Score = 98 (14.7 bits), Expect = 2.6e+00, P = 9.2e-01
Identities = 37/146 (25%), Positives = 77/146 (52%)

Query: 20 EPVLLPLVDRRFPKKWERPVAESLGHKDKQEDYFQKGGQIKFHCSKQLSLESSRQVTS 79
E LL ++ ++ ER + E + +E+ ++ K +QL + +++

Sbjct: 655 EEQLLRREEQELRQERERKLREEEQLLQEREEERLRRQERARKLREEEQLLRQEEQELRQ 714

Query: 80 ESQEEFPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLE-LAREQQR 138
E + + EEE + +RR+ L +E ++ +++ LL++ +E+LR+ E L RE+ R

Sbjct: 715 ERERKLREEE--QLLRREEQLLRQERDRKLREEEQLLQEESEERLRRQEREQQLRREDR 772

Query: 139 RWVQLEKEQESPRREPEQLG-EDVERRI 165
++ E+EQ RE E+L ++ ER++

Sbjct: 773 KF--REEEQLLQEREEERLRRQERERKL 798

Score = 97 (14.6 bits), Expect = 3.3e+00, P = 9.6e-01
Identities = 38/129 (29%), Positives = 63/129 (48%)

Query: 72 ESSRQVTSSESQ--EEPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWN 129
E R++ E Q +E EE R+ R+ EEE++ +Q +++ L QE KLR+

Sbjct: 817 ERERKLREEEQLLQEREEERLRRQERERKLREEEQLLRQEEQ---LRQERARKLREE-- 871

Query: 130 EDLAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEKAELSLVPAPSRT 189
E L R++++ +L +E++ RE EQL E+ + R R L + E L+

Sbjct: 872 EQLLRQEEQ---ELRQERDRKLRREEEQLLRQEEQEL--RQERDRKLRREE-QLLQESEEE 925

Query: 190 QSAHQSRPHL 200
+ Q R L

Sbjct: 926 RLRRQERERKL 936

Score = 96 (14.4 bits), Expect = 4.1e+00, P = 9.8e-01
Identities = 41/132 (31%), Positives = 69/132 (52%)

Query: 46 KDKDQEDYFQKGGLOI-KFHCSKQLSLESSRQVTSESQEEFPWEEFGRMRRQLWLEEEE 104
+++ QE F + Q+ + ++QL E S Q E + E+ G+ R QL +EE

Sbjct: 473 RERRQELQFLEEEQLQRRERAAQLQEEDSFQEDRERRRRQEQRPQTWRWQL---QEE 529

Query: 105 MWQQRQKKWALLEQEHQEKLRQWNLEDLAREQRRWVQLEKEQESPRPEQLGEDVERR 164
++R +A Q QE+LR+ E+L RE++R+ E+E+E E Q ED +RR

Sbjct: 530 AQRRRHTLYAKPGQ--QEQLREE--EELQREKRRQ---EREREYREEEKLQREDEKRR 581

Query: 165 IFTPTSRWRDLEK 177
++R+LE+

Sbjct: 582 RQERERQYRELEE 594

Score = 96 (14.4 bits), Expect = 4.1e+00, P = 9.8e-01
Identities = 35/138 (25%), Positives = 76/138 (55%)

Query: 28 DRRFPKKWERPVAESL-GHKDKDQEDYFQKGGLOIKFHCSKQLSLESSRQVTSESQEEPW 86
+R++ + E E L K ++E Q+ + ++ L Q+ + ++E

Sbjct: 586 ERQYRELEELRQEEQLRDRKLRREEEQLLQEREERLRRQERERKLREEEQLLRQEEQE-L 644

Query: 87 EEEFGRMRRQLWL---EEEMWQQRQKKWALLEQEHQEKLRQWNLEDLAREQRRWVQL 143
+E R++R + L EE+E+ Q+R++K L +E Q L++ E L R+++ R +L

Sbjct: 645 RQERERKLREEEQLLRREEQELRQERERK---LREEEQ-LLQEREERLRRQERAR--KL 698

Query: 144 EKEQESPRPEQLGEDVERRI 165
+E++ R+E ++L ++ ER++

Sbjct: 699 REEEQLLRQEEQELRQERERKL 720

Score = 95 (14.3 bits), Expect = 5.2e+00, P = 9.9e-01
Identities = 59/282 (20%), Positives = 121/282 (42%)

Query: 20 EPVLLPLVDRFPKKWERPVAESLGHKDKDQEDYFQKGGLOIKFHCSKQLSLESSRQVTS 79
E LL ++ ++ ER + E + +E+ ++ K +QL + ++

Sbjct: 655 EEQLLRREEQELRQERERKLREEEQLLQEREERLRRQERARKLRREEEQLLRQEEQELRQ 714

Query: 80 ESQEEPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEKLRQWNLED-LAREQQR 138
E + + EEE + +RR+ L +E ++ +++ LL++ +E+LR+ E L RE+ R

Sbjct: 715 ERERKLREEE--QLLRREEQLLRQERDRKLRREEQLLQESEEERLRRQEREQQLRREDR 772

Query: 139 RWVQLEKEQESPRPEQLG-EDVERRIFTPTSRWRDLEKAELSLVPAPSRTQSAHQ--S 195
++ E+EQ RE E+L ++ ER++ ++ E+ L + + Q

Sbjct: 773 KF--REEEQLLQEREERLRRQERERKLREEEQLLQEREERLRRQERERKLREEEQLLQ 830

Query: 196 RPHLPMSPSTQOPALGKQPMSSVEFTYRPRTRRVPTKPKKSASFVGTGTSIRRLTWPS 255
R + ++ L ++ + E R R ++ +R+

Sbjct: 831 EREEERLRRQERERKLREEEQLLRQE-EQELRQERARKLRREEEQLLRQEEQELRQERDRK 889

Query: 256 LQISPANIKKKVYHMDMEAQRK---NLQLLSESELRLPHYLRSKAL 299
L+ +++++ + E RK QLL E E RL R + L

Sbjct: 890 LREEEQLLRQEEQELRQERDRKLRREEEQLLQESEEERLRRQERERKL 936

Score = 94 (14.1 bits), Expect = 1.1e+00, P = 6.8e-01
Identities = 35/116 (30%), Positives = 59/116 (50%)

Query: 72 ESSRQVTSESQEEFPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEK-----L 124
E +R++ E Q EE+ R+ R + + EEE++ Q+R+++ L QE K L

Sbjct: 977 ERARKLRREEEQLLRREEQELRQERDRKFREEEQLLQEREERLRRQERDRKFREERQL 1035

Query: 125 RQWNLEDLAREQRRWVQLEKEQESPRPEQLGEDVERRIFTPTSRWRDLEKAELSL 182
R+ LE+ R+++ R +LE EQ +E +QL R F + R ++ E L

Sbjct: 1036 RRQEELEQFRQERDRKFRLE-EQIRQEKEEKQLRRQERDRKFREEEQRRRQEREQQL 1092

Score = 94 (14.1 bits), Expect = 1.1e+00, P = 6.8e-01
Identities = 51/166 (30%), Positives = 76/166 (45%)

Query: 67 QLSLESSRQVTSESQ--EEPWEEFGRMRRQLWLEEEEMWQQRQKKWALLEQEHQEK 123
++L E R+ E Q +E EE R+ R R+L EEE++ + Q++ L QE+

Sbjct: 1250 QELRRERDRKFREEEQLLQEREERLRRQERARKLRREEEQLLFEEQEEQRL---RQER 1305

Query: 124 LRQWNLED-LAREQRRWVQLEKEQESPRPEQLGEDVERRIFTPTSRWRDLEKAELSL 182
R++ E+ ARE++ R +LE+E R+E EQ R F R E+ E

Sbjct: 1306 DRRYRAEEQFAREEKSR--RLEREL---RQEEQRRRRERERKFREEQLRRQEE-EQRR 1359

Query: 183 VPAPSRQTSAHQSRPHLPMSPTQPPALGKQRPMSSEVFTYRPRTRVP 232
 R QSR L P T+Q A R E+ R++ P
 Sbjct: 1360 RQLRERQFREDQSRQVL--EPGTRQFARVPVRSSPLYEYIQEQRSYRP 1407

Score = 93 (14.0 bits), Expect = 8.3e+00, P = 1.0e+00
 Identities = 41/145 (28%), Positives = 72/145 (49%)

Query: 28 DRRFPKKWERPVAESLGHKDKQEDYFQKGLQIKFHCSKQLSLESSROVTSSESQEEPW- 86
 +RR ++ ER + E + + Q + + Q + L R + QE+ +
 Sbjct: 408 ERRQRQERERELEEQARRQQWQAEESERRRQ-RLSARPSLRERQLRAEERQEQRFR 466

Query: 87 -EEEFGREMRRLQ-LWEEEMWQQRQKKWALLEQE--HQEKLROWNLEDLAREQQRRWVQ 142
 EEE RE R++L +LEEE Q+R++ L E++ +++ R+ ++ Q RW Q
 Sbjct: 467 EEEQRERRRQELQFLEEEELQRRRRAQQLQEEDSFQEDRERRRRRQEQRPGQTWRW-Q 525

Query: 143 LEKEQESPRR----EP---EQLGEDVE 162
 L++E + R +P EQL E+ E
 Sbjct: 526 LQEEAQRRRHTLYAKPGQEQELREEE 552

Score = 91 (13.7 bits), Expect = 2.4e+00, P = 9.1e-01
 Identities = 38/110 (34%), Positives = 57/110 (51%)

Query: 72 ESSROVTSSESQEEPWEE-EFGREMRRLWLWEEEMWQQRQKKWALLEQEHQEKLROWN- 129
 E R++ E Q EE E RE R+L EEE++ Q+R+++ L QE KLR+
 Sbjct: 931 ERERKLREEQLLRREEQLRRERARKL-REEEQLLQEREEE-RLRRQERARKLREEEQ 988

Query: 130 -----EDLAREQQRRWVQLEKEQESPRREPEQLGEDVERRIFTPTSRWRDLEKAE 180
 ++L +E+ R++ E+EQ RE E+L R F R L + EL
 Sbjct: 989 LRREEQLRQERDRKF--REEEQLLQEREEERLRRQERDRKFREEER--QLRRQEL 1040

Score = 89 (13.4 bits), Expect = 2.2e+00, P = 8.9e-01
 Identities = 35/138 (25%), Positives = 65/138 (47%)

Query: 82 QEEPWEEFEGREMRRLWLWEEEM--WQQRQKKWALLEQEHQEKLROWNLEDLAREQQRR 139
 Q E++ E+R + + +E E WQ++++ L E+E Q K R+ + +R+ + +
 Sbjct: 111 QNRQEDQRRFELDRQFEDEPERRRWQKQEQERELAEFEEQKKRERFEQHYSRQYRD 170

Query: 140 WVQLEKEQ-ESPRREPEQL---GEDVERRIFTPTSRWRDLEKAE LSLVPAPSRQTSAHQ 194
 +L+++ E R E EQL G D E F + R E+ EL Q +
 Sbjct: 171 EQRLQROELEERRAEELRRRGRDAEE--FIEEEQLRRREQQELKR-ELREEEQORRE 227

Query: 195 SRRPHLPMSPTQPPALGKQR 215
 R H ++ L ++R
 Sbjct: 228 RREQHERALQEEELRRQR 248

Score = 50 (7.5 bits), Expect = 2.2e+00, P = 8.9e-01
 Identities = 34/160 (21%), Positives = 67/160 (41%)

Query: 325 RLQSLRQEAINHVOIMKETEASYKAONLYIFLENIDRL-QSLRLQAWTDKOKGLEEKHRE 383
 R+ R+E Q+ +E E + + LE +R Q LR + +++ E++ R+
 Sbjct: 245 RQRWRREEPREQQQLRRELEIREERQ--LEQEERREQQLRREQRLEQEERREQQLRR 301

Query: 384 CLSSMTMFPKLQLEWNVHLNIP-EVTSPPKPKCKLPAASPRHIRPSGPTYKQPFSLRHR 442
 L + +L+ E + E + K +L R R ++ L+
 Sbjct: 302 ELEEIREREQRLEQEERREQRLEQEERREQQLKRELEEIREREQRLEQEERREQQLAEV 361

Query: 443 ACVPLQMARQQGKQMEAVWKTEVASSSYAIEKKTASLPRDQ 484
 + AR++G+ + W+ ++ S + A + K S PR Q
 Sbjct: 362 R---EQARERGESLTRRWQRQLESEAGARQSKV-YSRPRRQ 398

Score = 40 (6.0 bits), Expect = 1.9e-01, P = 1.7e-01
 Identities = 32/115 (27%), Positives = 47/115 (40%)

Query: 276 RKNLQLLSESELRLPHYLRSKAL--ELTTTMEGLALRLQYLCHKYIFYRRL-QSLRQE 332
 R+ QLL E E RL R++ L E E LR Q K+ +L Q +E
 Sbjct: 959 REEEQLQEREEERLRRQERARKLREEEQLLRREEQELR-QERDRKFREEEQLLQEREE 1017

Query: 333 AINHVI---MKETEASYKAONLYI-FLENIDRLQSLRLQAWTDKQ-KGLEEKHRE 383
 + + +E E + Q L F + DR L Q +K+ K L + R+
 Sbjct: 1018 RLRRQERDRKFREEERQLRRQELLEEQFRQERDRKFRLEEIQIRQEKEEQQLRRQERD 1073

Score = 37 (5.6 bits), Expect = 1.6e+00, P = 7.9e-01
 Identities = 27/108 (25%), Positives = 43/108 (39%)

Query: 276 RKNLQLLSESELRLPHYLRSKAL--ELTTTMEGLALRLQYLCHKYIFYRRLQSLRQE 332
 R+ QLL E E RL R+ L E E LR Q K R + L QE
 Sbjct: 775 REEEQLQEREEERLRRQERERKLREEEQLLQEREEERLRRQERERKL---REEEQLLQE 831

Query: 333 AINHVOIMKETEASYKAONLYIFLENIDRLQSLRLQAWTDKQKGLEEKHRE 383
 +E E + + + E L+ R+ +++ L ++ +E
 Sbjct: 832 REERLRRQERERKLREEEQLLRQEE-QELRQERARKLREEEQLLRQEEQE 881

Pedant information for DKFZphtes3_50n23, frame 1

Report for DKFZphtes3_50n23.1

[LENGTH] 499
[MW] 58885.69
[pI] 9.67
[KW] All Alpha
[KW] LOW_COMPLEXITY 10.42 %

SEQ MTVRSRVADVFGSKDTESELPVLLPLVDRRFPPKKWERPVAESLGHKDKDQEDYFQKGGLO
SEG
PRD cccccceeeccccccccceeeccccccccccccchhhhhhccccccccccccccccce

SEQ IKFHCSKQLSLESSRQVTSESQEEPWEEEFGREMRRLWLEEEEMWQQRQKKWALLEQEH
SEG
PRD eeeecchhhhhccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ QEKLQWNLEDLAREQRRWVQLEKEQESPREPEQLGEDVERRIFTPTSRWRDLEKAEL
SEG
PRD hhh

SEQ SLVPAPSRQTSAHQSRRLPMPSPSTQQPALGKQRPMSSEFTYRPRTRRVPTKPKKSAS
SEG
PRD hccccccchhhhhccccccccccccccccccccccccccccceeeccccccccccccceee

SEQ FPVTGTSIRRLTWPSLQISPANIKKKVYHMDMEARKNLQLLSESELRLPHYLRSKALE
SEG
PRD eccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ LTTTMMELGALRLQYLCHKYIFYRRLQSLRQEAINHVOIMKETEASYKAQNLVIFLENID
SEG
PRD hhh

SEQ RLQSLRLQAWTDKQKGLEEKHRECLSSMVTMFPKLQLEWNVHLNIPEVTSPKPKKCKLPA
SEG
PRD hhhhhhhhhhhhhcchhh

SEQ ASPRHIRPSGPTYKQPFSLRHRACVPLQMARQOGKQMEAVWKEVASSSYAIEKKTASL
SEG
PRD cccccccccccccchhhhhhhccchhhhhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ PRDQLRGHPDIPRLTLTDV
SEG
PRD ccccccccccccccccccc

(No Prosite data available for DKFZphtes3_50n23.1)

(No Pfam data available for DKFZphtes3_50n23.1)

DKFZphtes3_6b21

group: testes derived

DKFZphtes3_6b21 encodes a novel 781 amino acid protein without similarity to human KIAA0256 gene product.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to KIAA0256

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: /map="356.3 cR from top of Chr9 linkage group"

Insert length: 3360 bp

Poly A stretch at pos. 3314, polyadenylation signal at pos. 3300

```
1 GGCAAGCCGA CGGCCCGCTG CTGGCCTCCG TGACGCGGCC TCCTCCGCGC
51 CTCGCGGCAT GCGTCGGAG GGGCCGCGGG AGCCCGAAAG CGAGGGCATC
101 AAGTTATCAG CAGATGTCAA ACCATT'TGTC CCCAGATT'TG CCGGGCTCAA
151 TGTGGCATGG TTAGAGTCCT CAGAAGCATG TGTCTTCCCC AGCTCTGCAG
201 CCACATACTA TCGTTTGTG CAGGAACCAC CAGTGACAGA AATGTTTACT
251 CAGTGCCTGG CTCCCAGTAT CTTTATAACC AACCCAGTTG TTACCGAGGT
301 TTTCAAAACAG TGAAGCATCG AAATGAGAAC ACATGCCCTC TCCACACAAG
351 AATGAAAGCT CTGTTTAAGA AGAAAACCTA TGATGAGAAA AAAACGTATG
401 ATCAGCAAAA GTTTGACAGT GAAAGGGCTG ATGGAACAT ATCATCTGAG
451 ATAAAATCAG CTAGAGGTTT ACATCATT'TG TCCATT'TACG CTGAGAATAG
501 TTTGAAATCA GATGGTTACC ATAAGCGAAC AGACAGGAAA TCCAGAATCA
551 TTGCAAAAAA TGTATCTACC TCCAAACCTG AGTTTGAATT TACCACACTG
601 GACTTTCCTG AACTGCAAGG TGCAGAGAAC AATATGTCAG AGATACAGAA
651 GCAACCCCAAG TGGGGACCTG TCCACTCTGT CTCTACCGAC ATTTCTCTTC
701 TAAGAGAAGT AGTAAAACCA GCTGCAGTGT TATCAAAGGG TGAAATAGTG
751 GTGAAAAATA ACCCAAATGA ATCTGTAACT GCTAATGCCG CTACCAATTC
801 TCCTTCATGT ACAAGAGAGT TATCTTGGAC ACCAATGGGT TATGTTGTTC
851 ACAGACACTT ATCTACAGAA CTGTCAGCAG CCCCTAAAAA TGTACTTCT
901 ATGATAAACT TAAAGACCAT TGCTTCATCA GCAGATCCTA AAAATGTTAG
951 TATACCATCT TCTGAAGCTT TATCTTCGGA TCCTTCCTAC AACAAAGAAA
1001 AACACATTAT TCATCCTACC CAAAAGTCTA AAGCATCACA AGGTAGTGAC
1051 CTTGAACAAA ATGAAGCCTC AAGAAAGAA TGAAGAAAGA AAGAAATATC
1101 TACATCAAAA TATGAAGTCC TGACAGTTCA AGAGCCTCCA AGGATTGAAG
1151 ATGCCGAGGA ATTTCCCAAC CTGGCAGTTG CATCTGAAAG AAGAGACAGA
1201 ATAGAGACAC CGAAATTTC AATCTAAGCAG CAGCCACAGG ATAATTTTAA
1251 AAATAATGTA AAGAAGAGCC AGCTTCCAGT GCAGTTGGAC TTGGGGGGCA
1301 TGCTGACAGC CTGGGAGAAG AAGCAGCACT CTCAGCATGC AAAGCAGTCC
1351 TCCAAACCAG TGGTAGTCTC AGTTGGAGCA GTGCCAGTCC TTTCCAAAGA
1401 ATGTGCATCA GGGGAGAGAG GCCGCCGCAT GAGTCAAATG AAGACCCGCG
1451 ACAATCCCTT GGACTCCAGC GCCCCTACTG TGAAGAAAGG GAAGCAGAGG
1501 GAGATCCCCA AGGCCAAGAA GCCAACCTCA CTGAAGAAGA TTATTTTGAA
1551 AGAACGGCAA GAGAGAAAGC AGCGTCTCCA AGAAAATGCT GTGAGTCCAG
1601 CTTTTACCAG TGATGACACA CAAGATGGAG AGAGTGGTGG TGATGACCAG
1651 TTTCCCGAGC AGGCAGAGCT GTCAGGGCCA GAGGGGATGG ACGAAGTATG
1701 CTCCACTCCT TCGGTTGAGG ACAAAGTCTG AGAGCCACCA GGCACAGAGC
1751 TCCAGAGGGA CACAGAGGCC TCCCACCTTG CTCCCAATCA CACCACCTTC
1801 CCTAAGATCC ACAGCCGAGC ATTCAGGGAT TACTGCAGCC AGATGCTTAG
1851 TAAAGAAGTG GATGCTTGTG TTACCGACCT ACTCAAAGAA CTGGTCCGTT
1901 TCCAAGACCG TATGTACCAG AAAGATCCAG TCAAGGCCAA GACTAAACGT
1951 CGACTTGTGT TGGGGTTGAG GGAGGTTCTC AAACACCTGA AGCTCAAAAA
2001 ACTGAAATGT GTCAATTATTT CTCCCAACTG TGAGAAGATA CAGTCAAAAG
2051 GTGGGCTGGA TGACACTTTG CACACAATTA TTGATTATGC CTGTGAGCAG
2101 AACATTCCCT TTGTGTTTGC TCTCAACCGC AAAGCTCTGG GGCAGAGTTT
2151 GAATAAGGCA GTTCCTGTCA GTGTGGTGGG GATCTTCAGC TATGATGGGG
2201 CCCAGGATCA GTTCCACAAG ATGGTTGAGC TGACAGTGGC GGCCCGACAG
2251 GCGTACAAGA CCATGCTGGA GAATGTGCAG CAGGAGCTGG TGGGAGAGCC
2301 CAGGCTCAGC GCACCTCCCA GCCTACCCAC ACAGGGCCCC AGCTGCCCTG
2351 CAGAAGATGG CCCCCAGCC CTGAAAGAAA AAGAAGAGCC AACTACATT
2401 GAAATCTGCA AAAAACATCT GGAAGCATAC AGTGGATGTA CCCTGGAGCT
2451 AGAAGAAATC TTGGAGGCTT CAACCTCTCA AATGATGAAT TTGAATTTAT
2501 GAGAGTTCCT GCCTGTGTGT CTGTATTTTG GGTAAGGAGG GGAGGTCTGA
2551 AAAAGACTTT GGGGCTTTT CTCTGTGTTT TCATGACAA GTAAATTTGTG
2601 TAACTGTTGA ATCTGAAAT TGATCAGCAT TAAAGGGCAC ATGAAGCAGT
2651 GTCTGCAGGC GTTCAGTGCT GCGGAGCCTG TTAAAGGTCA CTCAGATGTG
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2701 CAGGTGTTAA TCTTCTCTAA AAGCCTGGTT ATACAGCTCT GGCTTTCTGA
2751 GCACACTACG GATCTGGAAA ATACTGGAAA ATGTGATACT TAGAATACTT
2801 TGGCTGCTAA GGAAACTTCC TCTCCATTGC AGAATAGCTG AGCCAAGTGA
2851 GTGAGTTTGC AGAAAGCAGG TGGTGAGCTC CTGCCTGCTG CAGGTTGCCA
2901 TGGAGGGCCA TTCCTGCCCG GCAACAGCAC CGTCCTGCAG GGAGCCACTT
2951 GGCAGAGGG TGCAGGGCTG CTGGTGTGAG AGCAAGAGGG CTACAGGGAA
3001 AGGGCCCTTT CTCAGGGGAT GTAGCTTTTT TAAAAGATT TGGGAACACTT
3051 GGAGGATTTG CTAAATGAG CCTCAGAAGG AAAATTGGTT TTCTAACCTG
3101 TGACTTTTTT AAATGAATTA TTCCTTTCAG TCTTTATTTT TCAAAGAAAC
3151 AATGTGTATT GAAGTACCTA GATTGTGTTG ATAATCAACA AATCTTTCCT
3201 TTTTCAATGA ACATATTCTG AATGTGGTTT CTGTCTTAGA CCAGGAGGAC
3251 AGAGTTTGCT TTCATATTTT CCCTGTAAGT AAGAGGGCTT ATTTATTTTA
3301 AATAAGAGT AATTATTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3351 AAAAAAAAAA

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BLAST Results

Entry HS773347 from database EMBL:
human STS WI-18160.
Score = 813, P = 2.9e-30, identities = 167/171

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 157 bp to 2499 bp; peptide length: 781
Category: similarity to known protein

```

1 MVRVLRSMCL PQLCSHILSV CSGTTSDRNV YSVPGSQYLY NQPSCYRGFQ
51 TVKHRNENTC PLPQEMKALF KKKTYDEKKT YDQKFDSER ADGTISSEIK
101 SARGSHHLSI YAENSLKSDG YHKRTDRKSR IIAKNVSTSK PEFEFTTLDF
151 PELQGAENNM SEIQKQPKWG PVHSVSTDIS LLREVVKPAA VLSKGEIVVK
201 NNPNESVTAN AATNSPSCTR ELSWTPMGYV VRQTLSTELS AAPKNVTSMI
251 NLKTIASSAD PKNVSISSSE ALSSDPSYNK EKHIHPTQK SKASQGSdle
301 QNEASRNKK KKEKSTSKYE VLTQEPPIRI EDAEEFPNLA VASERRDRIE
351 TPKFQSKQPP QDNFKNNVKK SQLPVQLDLG GMLTALEKKQ HSQHAKQSSK
401 PVVSVGAVP VLSKECASGE RGRRMSQMKT PHNPLDSSAP LMKKGKQREI
451 PKAKKPTSLK KIILKERQER KQRLQENAVS PAFTSDDTDQ GESGGDDQFP
501 EQAELSGPEG MDELSTPSV EDKSEEPGPT ELQDTEASH LAPNHTTFPK
551 IHSRRFRDYC SQMLSKEVDA CVDLLKELV RFQDRMYQKD PVKAKTKRRL
601 VLGLREV LKH LKLLKLCVI ISPNCEKIQS KGGLDLTLHT IIDYACEQNI
651 PFVFALNRKA LGRSLNKAVP VSVVGIFSYD GAQDQFHKM ELTVAAARQAY
701 KTMLENVQOE LVGEPRPQAP PSLPTQGPSC PAEDGPPALK EKEEPHYIEI
751 WKKHLEAYSG CTLELESLE ASTSQMMNLN L

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_6b21, frame 1

SWISSPROT:Y256_HUMAN HYPOTHETICAL PROTEIN KIAA0256., N = 1, Score = 786, P = 3.6e-78

TREMBL:PFMAL3P3_15 gene: "MAL3P3.15"; Plasmodium falciparum MAL3P3, N = 2, Score = 161, P = 5.1e-10

TREMBL:RNNFLH_1 Rat heavy neurofilament subunit (NF-H) mRNA, 3' end., N = 1, Score = 150, P = 9.1e-07

>SWISSPROT:Y256_HUMAN HYPOTHETICAL PROTEIN KIAA0256.
Length = 635

HSPs:

Score = 786 (117.9 bits), Expect = 3.6e-78, P = 3.6e-78
Identities = 190/424 (44%), Positives = 263/424 (62%)

Query: 369 KKSQLPVQLDLGGMLTALEKKQHSQHAQ--SSKPVVSVGAVPVLSKECASGERGRMS 426
 KK++ PVQLDLG ML ALEK+Q + A+Q +++P+ +V + ++ + S
 Sbjct: 16 KKNKTPVQLDLGDLAALAEKQQAMKARQITNTRPLSYTVVTAASFHTKDNKPLTKS 75

Query: 427 Q-MKTPHNPLDSSAPLMKKKGKQREIPKAKKPTSLKKIILKERQERKQRLQENAVSPAFTS 485
 Q T N +D ++ KKGK++EI K K+PT+LKK+ILKER+E+K RL + S
 Sbjct: 76 QPCLTSFNSVDIASSKAKKGKEKEIAKLKRPTALKKVILKEREKKGRLTVD--HNLLGS 133

Query: 486 DDTQDGESGGDDQFPEQAELSGPEGMDLISTPSVEDKSEEPG--TELQRDTEASHL-- 541
 ++ + D P++ G+ + S S+ S+ P T + + + AS
 Sbjct: 134 EEPTMHLDFIDDLPEIVSQEDTGLS-MPSDTSLSPASQNSPYCMTFVVSQGSFSSGIG 192

Query: 542 APN-HTTFPKIHSRRFRDYCSQMLSKEVDACVTDLLKELVRFQDRMYQKDPVKAKTKRRL 600
 +P +T KIHS+RFR+YC+Q+L KE+D CVT LL+ELV FQ+R+YQKDPV+AK +RRL
 Sbjct: 193 SPMASSTITKIHSKRFRFYCNQVLCKEIDECVTLLQLVVSFQERIYQKDPVRAKARRRL 252

Query: 601 VLGLREVLKHLKLLKLCVVIISPNCCKIQSKGGLD+ L+ +I A EQ IPFVFALNRKA 660
 V+GLREV KH+KL K+KCVIISPNCCKIQSKGGLD+ L+ +I A EQ IPFVFALNRKA
 Sbjct: 253 VMGLREVTKHMKLNKIKCVIISPNCCKIQSKGGLDEALYNVIAMAREQEIIPFVFALGRKA 312

Query: 661 LGRSLNKAVPVSVVGIFSYDGAQDQFHKMVELTVAARQAYKTMLENVQQLVGEPRP--- 717
 LGR +NK VPVSVVGIF+Y GA+ F+K+VELT AR+AYK M+ ++QE E
 Sbjct: 313 LGRCVNKLVPVSVVGIFNYFGAESLFNKLVELTEEARKAYKDMVAAMEQEQAEEALKNVK 372

Query: 718 QAPPSLP-TQGPS-----CPAEDGPPALKEKEEPHYIEIWKHLEAYSGCTL---ELE 766
 + P + ++ PS C P + E E Y W+ +E G E E
 Sbjct: 373 KVPHHMHSRNPASASAIISFCVISEP--ISEVNEKEYETNWRNMVETSDGLEASENEKE 430

Query: 767 ESLEASTSQ 775
 S + STS+
 Sbjct: 431 VSCKHSTSE 439

Pedant information for DKFZphtes3_6b21, frame 1

Report for DKFZphtes3_6b21.1

{LENGTH} 781
 {MW} 87393.44
 {pI} 8.94
 {HOMOL} SWISSPROT:Y256_HUMAN HYPOTHETICAL PROTEIN KIAA0256. 4e-75
 {PROSITE} MYRISTYL 4
 {PROSITE} AMIDATION 1
 {PROSITE} CAMP_PHOSPHO_SITE 3
 {PROSITE} CK2_PHOSPHO_SITE 16
 {PROSITE} TYR_PHOSPHO_SITE 4
 {PROSITE} PKC_PHOSPHO_SITE 16
 {PROSITE} ASN_GLYCOSYLATION 6
 {KW} Alpha_Beta
 {KW} LOW_COMPLEXITY 8.45 %

SEQ MVRVLRSMCLPQLCSHILSVCSGTTSDRNVSVPGSQYLYNQPSQYRGFTVKHRNENTC
 SEG
 PRD ccc

SEQ PLPQEMKALFKKKTYDEKTYDQKFDSEADGTISSEIKSARGSHHLSIYAENSLKSDG
 SEG
 PRD cccchhhhhhhhhccchhhhhhhhhhhccccccccchhhhhhhcccccccccccccccc

SEQ YHKRTDRKSRIIAKNVSTSKPEFEFTTLDPELQGAENNMSEIQKQPKWGPVHSVSTDIS
 SEG
 PRD cccccchhhhhheccccccccccccccccccccccccccccchhhhhccccccccccccch

SEQ LLREVVKPAAVLSKGEIVVKNNPNESVTANAATNSPSCRELSTWTFMGYVVRQTLSTELS
 SEG
 PRD hhhhhhhhecc

SEQ AAPKNVTSMINLKTIASSADPKNVSIIPSEALSSDPSYNKEKHIIHPTQKSKASQGSdle
 SEG
 PRD cccccccccchhhhhhhccccccccccccccccccccccccccccccccccccchhhhhhhccccch

SEQ QNEASRNKKKKKSTSKYEVLTVQEPPIEDAEFPNLAVASERRDRIETPKFQSKQOP
 SEG
 PRD hhhhhccccccccccccccccccccccccccccchhhhhhhccccchhhhhhhhhhhcccccccc

SEQ QDNFKNNVKKSQLPVQLDLGGMLTALEKKQHSQHAQSSKPVVSVGAVPVLSKECASGE
 SEG
 PRD cccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccc

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SEQ      RGRMSQMKTPHNPLDSSAPLMKKGKQREIPKAKKPTSLKKIILKERQERKQRLQENAVS
SEG      .....
PRD      chhhhhhhccccccccccccchhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhcc

SEQ      PAFTSDDTDQGESGGDDQFPEQAELSGPEGMDLISTPSVEDKSEEPGTELQRDTEASH
SEG      .....
PRD      cccccccccccccccccchhhhhhhccccceeecccccccccccccccccccccccccc

SEQ      LAPNHTTFFPKIHSRRFRDYCSQMLSKEVDACVTDLLKELVRFQDRMYQKDPVKAKTKRRL
SEG      .....
PRD      cccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhh

SEQ      VLGLREVLKHLKLLKLCVVISPNCEKIQSKGGLDDTLHTIIDYACEQNIPIFVFALNRKA
SEG      .....xxxxxxxxxxxx.....
PRD      hhhhhhhhhhhhhhhheeeccccccccccccchhhhhhhhhhhhhccccceeecccccc

SEQ      LGRSLNKAVPVSVVGIFSYDGAQDQFHKMVELTVAARQAYKTMLENVQQELVGEPRPQAP
SEG      .....
PRD      cccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc

SEQ      PSPLTQGPSPCAEDGPPALKEKEEPHYIEIWKKHLEAYSGCTLELESLEASTSQMMNLN
SEG      .....xxxxxxxxxxxx.....
PRD      cccccccccccccchhhhhhhccccceeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc

SEQ      L
SEG      .
PRD      C

```

Prosites for DKFZphtes3_6b21.1

PS00001	135->139	ASN_GLYCOSYLATION	PDOC00001
PS00001	159->163	ASN_GLYCOSYLATION	PDOC00001
PS00001	204->208	ASN_GLYCOSYLATION	PDOC00001
PS00001	245->249	ASN_GLYCOSYLATION	PDOC00001
PS00001	263->267	ASN_GLYCOSYLATION	PDOC00001
PS00001	544->548	ASN_GLYCOSYLATION	PDOC00001
PS00004	71->75	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	423->427	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	454->458	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	51->54	PKC_PHOSPHO_SITE	PDOC00005
PS00005	88->91	PKC_PHOSPHO_SITE	PDOC00005
PS00005	101->104	PKC_PHOSPHO_SITE	PDOC00005
PS00005	115->118	PKC_PHOSPHO_SITE	PDOC00005
PS00005	125->128	PKC_PHOSPHO_SITE	PDOC00005
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00005	288->291	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005
PS00005	316->319	PKC_PHOSPHO_SITE	PDOC00005
PS00005	343->346	PKC_PHOSPHO_SITE	PDOC00005
PS00005	351->354	PKC_PHOSPHO_SITE	PDOC00005
PS00005	398->401	PKC_PHOSPHO_SITE	PDOC00005
PS00005	458->461	PKC_PHOSPHO_SITE	PDOC00005
PS00005	553->556	PKC_PHOSPHO_SITE	PDOC00005
PS00005	596->599	PKC_PHOSPHO_SITE	PDOC00005
PS00006	24->28	CK2_PHOSPHO_SITE	PDOC00006
PS00006	74->78	CK2_PHOSPHO_SITE	PDOC00006
PS00006	139->143	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	193->197	CK2_PHOSPHO_SITE	PDOC00006
PS00006	257->261	CK2_PHOSPHO_SITE	PDOC00006
PS00006	297->301	CK2_PHOSPHO_SITE	PDOC00006
PS00006	317->321	CK2_PHOSPHO_SITE	PDOC00006
PS00006	323->327	CK2_PHOSPHO_SITE	PDOC00006
PS00006	384->388	CK2_PHOSPHO_SITE	PDOC00006
PS00006	484->488	CK2_PHOSPHO_SITE	PDOC00006
PS00006	493->497	CK2_PHOSPHO_SITE	PDOC00006
PS00006	506->510	CK2_PHOSPHO_SITE	PDOC00006
PS00006	519->523	CK2_PHOSPHO_SITE	PDOC00006
PS00006	640->644	CK2_PHOSPHO_SITE	PDOC00006
PS00006	702->706	CK2_PHOSPHO_SITE	PDOC00006
PS00007	581->588	TYR_PHOSPHO_SITE	PDOC00007
PS00007	740->748	TYR_PHOSPHO_SITE	PDOC00007
PS00007	740->748	TYR_PHOSPHO_SITE	PDOC00007
PS00007	73->82	TYR_PHOSPHO_SITE	PDOC00007
PS00008	93->99	MYRISTYL	PDOC00008
PS00008	155->161	MYRISTYL	PDOC00008
PS00008	380->386	MYRISTYL	PDOC00008

WO 01/12659

PCT/IB00/01496

PS00008	633->639	MYRISTYL	PDOC00008
PS00009	421->425	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_6b21.1)

DKFZphtes3_6c11

group: signal transduction

DKFZphtes3_6c11 encodes a novel 1025 amino acid protein with similarity to *A. ambisexualis* antheridiol steroid receptor.

The novel protein is a putative steroid receptor. It shares similarity with yeast YNL132w and contains the ATP/GTP-binding site motif A (P-loop) and RGD site, similar to the *A. ambisexualis* antheridiol steroid receptor.

The new protein can find application in modulating/blocking the expression of genes controlled by this receptor.

strong similarity to YNL132w

strong similarity to *S.pombe*/YDK9_SCHPO, *S.cerevisiae*/YNL132w, *C.elegans*/F55A12.8

Sequenced by BMFZ

Locus: unknown

Insert length: 3966 bp

Poly A stretch at pos. 3890, polyadenylation signal at pos. 3873

```

1  GCTGTGCCTT CTCTTTCGGA GTTGTTCCGT GCTCCACGT GCTTCCCCTT
51  CTCCACTGGC TGGGATCCCC CGGGCTCGGG GCGCAGTAAT AATTTTTCAC
101 CATGCATCGG AAAAAGGTGG ATAACCGAAT CCGGATTCTC ATTGAGAAATG
151 GACTAGCTGA GCGGCAAAGA TCTCTCTTTG TTGTAGTTGG GGATCGAGGA
201 AAAGATCAGG TGGTAATACT TCATCACATG TTATCCAAAG CAACTGTGAA
251 GGCTCGGCCT TCAGTGTCTG GGTGTTATAA GAAAGAGCTG GGGTTTAGCA
301 GTCACCGGAA GAAAAGAATG CGACAGCTGC AGAAGAAAAT AAAGAATGGA
351 ACACTGAACA TAAAGCAGGA CGACCCCTTT GAACTCTTCA TAGCAGCCAC
401 AAACATTGCG TACTGCTACT ACAACGAGAC CCACAAGATC CTGGGCAATA
451 CCTTCGGCAT GTGTGTGCTG CAGGATTTTG AAGCCTTAAC TCCAAACTTG
501 CTGGCCAGGA CTGTAGAAAC AGTGGAAGGT GGTGGGCTAG TGGTCATCCT
551 CCTACGGACC ATGAACCTAC TCAAGCAATT GTACACAGTG ACTATGGATG
601 TGCATTCCAG TTACAGAACT GAGGCCCATC AGGATGTGGT GGGGAAGATT
651 AATGAAAGGT TTATTCTGTC TCTGGCCTCT TGTAAGAAGT GTCTCGTCAT
701 TGATGACCAG CTCAACATCC TGCCCATCTC CTCCACGTT GCCACCATGG
751 AGGCCCTGCC TCCCCAGACT CCGGATGAGA GTCTTGCTCC TTCTGATCTG
801 GAGCTGAGGG AATTGAAGGA GAGCTTGACG GACACCCAGC CTGTGGGTGT
851 GTTGGTGGAG TGCTGTAAGA CTCTAGACCA GGCCAAAGCT GTCTTGAAAT
901 TTATCGAGGG CATCTCTGAA AAGACCCTGA GGAGTACTGT TGCATCACA
951 GCTGCTCGAG GACGGGGAAA ATCTGCAGCC CTGGGATTGG CGATTGCTGG
1001 GGCGGTGGGA TTTGGGTACT CCAATATCTT TGTTACCTCC CCAAGCCCTG
1051 ATAACCTCCA TACTCTGTTT GAATTTGTAT TTAAAGGATT TGATGCTCTG
1101 CAATATCAGG AACATCTGGA TTATGAGATT ATCCAGTCTC TAAATCCTGA
1151 ATTTAAACAA GCAGTGATCA GAGTGAATGT ATTTCGAGAA CACAGGCAGA
1201 CTATTCAATA TATACATCCT GCAGATGCTG TGAAGCTGGG CCAGGCTGAA
1251 CTAGTTGTGA TTGATGAAGC TGCCGCCATC CCCCTCCCCT TGGTGAAGAG
1301 CCTACTTGCG CCTACCTTG TTTTCATGGC ATCCACCATC AATGGCTATG
1351 AGGGCACTGG CCGGTCACTG TCCCTCAAGC TAATTCAGCA GCTCCGTCAA
1401 CAGAGCGCCC AGAGCCAGGT CAGCACCCT GCTGAGAATA AGACCACGAC
1451 GACAGCCAGA TTGGCATCAG CGCGGACACT GCATGAGGTG TCCCTCCAGG
1501 AGTCAATCCG ATACGCCCTT GGGGATGCAG TGGAGAAGTG GCTGAATGAC
1551 TTGCTGTGCC TGGATTGCCT CAACATCACT CGGATAGTCT CAGGCTGCCC
1601 CTTGCCTGAA GCTTGTGAAC TGTAATATGT TAATAGAGAT ACCCTCTTTT
1651 GCTACCACAA GGCTCTGAA GTTTTCCTCC AACGGCTTAT GGCCCTCTAC
1701 GTGGCTTCTC ACTACAAGAA CTCTCCCAAT GATCTCCAGA TGCTCTCCGA
1751 TGCACCTGCT CACCATCTCT TCTGCCTTCT GCCTCCTGTG CCCCCACCC
1801 AGAATGCCCT TCCAGAAGTG CTTGCTGTTA TCCAGGTGTG CTTGAAGGG
1851 GAGATTTCTC GCCAGTCCAT CTTGAACAGT CTGTCTCGAG GCAAGAAGGC
1901 TTCAGGGGAC CTGATTCCAT GGACAGTGTG AGAACAGTTC CAAGATCCAG
1951 ACTTTGGTGG TCTGTCTGGT GGAAGGGTCG TTCGATGTC GTTTCACCA
2001 GATTATCAAG GGATGGGCTA TGCGAGCCGT GCTCTGCAGC TGCTGCAGAT
2051 GTACTATGAA GGCAGGTTTC CTTGTCTGGA GGAAAAGGTC CTTGAGACAC
2101 CACAGGAAAT TCACACCGTA AGCAGCGAGG CTGTCACTT GTTGAAGAG
2151 GTCATCACTC CCGGAAGGA CCTGCCTCCT TTAATCTCA AATTGAATGA
2201 GAGGCCTGCT GAACGCCTGG ATTACCTGGG TGTTCTCTAT GGCTTGACCC
2251 CCAGGCTCCT CAAGTTCTGG AAACGAGCTG GATTTGTTCC GTTATCTG
2301 AGACAGACCC CGAATGACCT GACCGGAGAG CACTCGTGCA TCATGCTGAA
2351 GACGCTCACT GATGAGGATG AGGCTGACCA GGGAGGCTGG CTTGCAGCCT
2401 TCTGGAAGA TTTCCGACGG CGGTTCTTAG CCTTGCTCTC CTACCAAGTC
2451 AGTACCTTCT CTCTTCCCT GGCTCTGAAC ATCATTGAGA ACAGGAACAT
2501 GGGGAAGCCA GCCCAGCCTG CCCTGAGCCG GGAGGAGCTG GAAGCACTCT

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2551 TCCTCCCTTA TGACCTGAAG CGGCTGGAGA TGTATTCACG GAATATGGTG
2601 GACTATCACC TCATCATGGA CATGATCCCG GCCATCTCTC GCATCTATTT
2651 CCTGAACCAG CTGGGGGACC TGGCCCTGTC TCGGGCTCAG TCGGCTCTTC
2701 TCTTGGGGAT TGGCCTGCAG CATAAGTCTG TGGACCAGCT GGAAAAGGAG
2751 ATTGAGCTGC CCTCGGGCCA GTTGATGGGA CTTTTCAACC GGATCATCCG
2801 CAAAGTTGTG AAGCTATTTA ATGAAGTTCA GGAAAAGGCC ATTGAGGAGC
2851 AGATGGTGGC AGCGAAGGAT GTGGTCATGG AGCCCACGAT GAAGACCCTC
2901 AGTGACGACC TAGATGAAGC AGCAAAGGAA TTTCAGGAGA AACACAAGAA
2951 GGAAGTAGGG AAGCTGAAGA GCATGGACCT CTCTGAATAC ATAATCCGTG
3001 GGGACGATGA AGAGTGGAAAT GAAGTTTGA ACAAAGCTGG GCCGAACGCC
3051 TCGATCATCA GCCTGAAAAG TGACAAGAAA AGGAAGTTAG AGGCCAAACA
3101 AGAACCACAA CAGAGCAAGA AGTTGAAGAA CAGAGAGACA AAGAACAAAA
3151 AAGATATGAA ACTGAAGCGG AAGAAATAGT GAAGAGAAAC TCGGGCATCT
3201 GTGTTTGATC ATGGGAAGAT ACTCTCACTA ACTGAACCTT CTCTGGCTGG
3251 ACTGTTAAAA GCAACGAGAG GCCCCGGCAC ACCTGGAAGC TGGCCGCGAA
3301 TTCGGCTCTT GGGCCTGTGT GTCTGTGAGC TCAACCTGGC TAAAGGCAGA
3351 GTCACCTCCA AATGGGTCTC TTAGAACTT GATGGCTGGG CACTGCCATC
3401 TCTAGAATTG CCACGAGTCT CTCTCTTCCT GCCCAGTCCA GGGCCCTCCT
3451 TTCCTATAAG TTCATATTTT GCTTTGAGCC AGCTTTTGTG TCTCATTTCC
3501 ACACATGTGG AAGCCACGTT GCCTCTCGAC CGCCTGAGGC CCTTAAGTAC
3551 ATCGCTTTCT GGTGGTGGCC AGGAGGCTGC TGCTGGGCGC CTGGGTCTCT
3601 CTTTGTGGAC TTGTACCTGG AGCAGGAGGA ACTCCAGTCC GTCCCGGCAT
3651 CCATGGCAGC CCGCGGTTAG GTGCGCCAGG GTTTGCTGAT GTTGTCTTGT
3701 GCTGTTCCAC TCTTGGCTCC AGCAGACCCA CTGTCCCGA AAAGCCTGAT
3751 CCTGTAGTTT ATGTAGAATG CCACATCTGC GTCCTCAAGA CCTGTTTCAT
3801 CCATTTGGGA AAAGATGTTG GGAAGGCCA CTTTGCTCGC AGGGGTGAGG
3851 GGAAGGATAG AGAATCTATT TTTAATAAAT AACATTCTAG AATGAAAAAA
3901 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3951 AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 102 bp to 3176 bp; peptide length: 1025
Category: similarity to unknown protein
Classification: unclassified
Prosite motifs: RGD (966-969)
ATP_GTP_A (284-292)

```
1 MHRKKVDNRI RILIENGVAE RQRSLFVVVG DRGKDQVVIL HHMLSKATVK
51 ARPSVLWCYK KELGFSSHRK KRMRLQKKI KNGTLNIKQD DPPELFIAAT
101 NIRYCYNET HKILGNTFGM CVLQDFEALT PNLLARTVET VEGGGLVVIL
151 LRTMNSLKQL YVTMTDVHSR YRTEAHQDVV GRFNERFILS LASCKKCLVI
201 DDQLNILPIS SHVATMEALP PQTPDES LGP SDLELRELKE SLQDTPQVGV
251 LVDCCKTLDQ AKAVLKFI EG ISEKTLRSTV ALTAARGRGK SAALGLAIAG
301 AVAFGYSNIF VTSPSPDN LH TLFEFVFKGF DALQYQEHLD YEIIQSLNPE
351 FNKAVIRVNV FREHRQTIQY IHPADAVKLG QAEVLVIDEA AAIPPLPVKS
401 LGGPYLVFMA STINGYEGTG RSLSLKLIQQ LRQSAQSQV STTAENKTTT
451 TARLASARTL HEVSLQESIR YAPGDAVEKW LNDLLCLDCL NITRIVSGCP
501 LPEACELYYV NRDTLFCYHK ASEVFLQRLM ALYVASHYKN SPNDLQMLSD
551 APAHHLFCLL PVPPTQNAL PEVLAVIQVC LEGEISROSI LNSLSRGKKA
601 SGDLIPWTVS EQFQDPDFGG LSGGRVVRIA VHPDYQGMGY GSRALQLLQM
651 YYEGRFPCL EKVLETPEI HTVSSEAVSL LEEVITPRKD LPPLLLKLNE
701 RPAERLDYLG VSYGLTPRLL KFWKRAGFVP VYLRQTPNDL TGEHSCIMLK
751 TLTDEDEADQ GGWLAAFWKD FRRRFLALLS YQFSTFSPSL ALNIIQNRNM
801 GKPAQPALSR EELEALFLPY DLKRLEMYSR NMVDYHLIMD MIPAIISRIYF
851 LNQLGDLALS AAQSALLGI GLQHKSDVDL EKEIELPSGQ LMGLFNRIIR
901 KVVKLFNEVQ EKAIEEQMVA AKDVMMEPTM KTLSDDLDEA AKEFQEKHKK
951 EVGKLKMDL SEYIIRGDDE EWNEVLNKG PNASIISLKS DKKRKLEAKQ
1001 EPKQSKKLKN RETKNKKDMK LKRKK
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKF2phtes3_6c11, frame 3

TREMBL:CEAF3130_4 gene: "F55A12.8"; *Caenorhabditis elegans* cosmid F55A12., N = 1, Score = 2782, P = 1.1e-289

PIR:S55151 probable membrane protein YNL132w - yeast (*Saccharomyces cerevisiae*), N = 2, Score = 2549, P = 3.5e-273

SWISSPROT:YXX1_ACHAM HYPOTHETICAL PROTEIN (FRAGMENT)., N = 1, Score = 1013, P = 3.2e-102

SWISSPROT:YDK9_SCHPO HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I., N = 1, Score = 2843, P = 3.8e-296

>SWISSPROT:YDK9_SCHPO HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.

Length = 1,033

HSPs:

Score = 2843 (426.6 bits), Expect = 3.8e-296, P = 3.8e-296
Identities = 576/1033 (55%), Positives = 750/1033 (72%)

```

Query:      1 MHRKKVDNRIRILIENGVAERQSRSLFVVVGDRGKDQVVILHHMLSKATVKARPSVLWCYK 60
             M +K +D+RI LI+NG +E+QRS FVVVGDR +DQVV LH +LS++ V ARP+VLW YK
Sbjct:      1 MPFKALDSRIPTLIKNGCQEKQRSFFVVVGDRARDQVVNLHWLLSQSKVAARNVLMWYK 60

Query:     61 KEL-GFSSHRKKRMRQLQKKIKNGTLNLIKQDDPFELFIAATNIRYCYYNETHKILGNTFG 119
             K+L GF+SHRKKR +++K+IK G + +DPFELF + TNIRYCY Y E+ KILG T+G
Sbjct:     61 KDLLGFTSHRKKRENKIKKEIKRGIRDPNSEDPFELFCSITNIRYCYKSEKILGQTYG 120

Query:    120 MCVLQDFEALTPNLLARTVETVEGGGLVVILLRTMNSLKQLYTVMQVHSRYRTEAHQDV 179
             M VLQDFEALTPNLLART+ETVEGGG+VV+LL +NSLKQLYT++MD+HSRYRTEAH DV
Sbjct:    121 MLVLQDFEALTPNLLARTIETVEGGGIVVLLHKLNSLKQLYTMSMDIHSRYRTEAHSDV 180

Query:    180 VGRFNERFILSLASCKKCLVIDDQNLNIPISSHVATMEALPPQTPDES LGPSDLELRELK 239
             RFNERFILSL +C+ CLVIDD+LN+LPIS ++ALPP +++ + ++EL+
Sbjct:    181 TARFNERFILSLGNCENCLVIDDELNVLPISGG-KNVKALPPTLEEDN--STQNSIKELQ 237

Query:    240 ESLQDTPQVGVLVDCCKTLDQAKAVLKFIIEGISEKTLRSTVALTAARGRGKSAALGLAIA 299
             ESL + P G LV KTLQQA+AVL F+E I EK+L+ TV+LTA RGRGKSAALGLAIA
Sbjct:    238 ESLGEDHPAGALVGVTKTLDQARAVLTFVESIVEKSLKGTVSLTAGRGRGKSAALGLAIA 297

Query:    300 GAVAFGYSNIFVTSPSPDNLHTLFEFVFKGFDALQYQEHLDYEEIIQSLNPEFNKAVIRVN 359
             A+A GYSNIF+TSPSP+NL TLFEF+FKGFDAL Y+EH+DY+IIQS NP ++ A++RVN
Sbjct:    298 AAIAGYSNIFITSPSPENLKTLEFEI FKGFDALNYEEHVVDYDIIQSTNPAYHNAIVRVN 357

Query:    360 VFREHRQTIQYIHPADAVKLGQAEVLVVIDEAAAIPPLVKSLLGPYLVFMASTINGYEGT 419
             +FR+HRQTIQYI P D+ LGQAEVLVVIDEAAAIPPLV+ L+GPYLVFMASTINGYEGT
Sbjct:    358 IFRDHRQTIQYISPEDSNVLGQAEVLVVIDEAAAIPPLVRLKIGPYLVFMASTINGYEGT 417

Query:    420 GRSLSLKLIQQLRQSAQSQVSTTAENKTTTARLASARTLHEVSLQESIRYAPGDAVEK 479
             GRSLSLKL+QQLR+QS S + NK+ + + + S RTL E+SL E IRYA GD +E
Sbjct:    418 GRSLSLKLLQQLREQSRI--YSGSGNNKSDSQSHI-SGRTLKEISLDEPIRYAMGDRIEL 474

Query:    480 WLNLLCLDCLN-ITRIVS-GCPLPEACELYVNDRDTLFCYHKASEVFLQRLMALYVASH 537
             WLN LLCLD + ++R+ + G P P C LY V+RDTLF YH SE FLQR+M+LYVASH
Sbjct:    475 WLNKLLCLDAASYVSRMATQGFPHIPSECSLYRVSRDTLFSYHPISEAFQRMMSLYVASH 534

Query:    538 YKNSPNDLQMLSDAPAHHLFCLLPVPVPTQNALPEVLAVIQVCLEGEISRQSIILNSLSRG 597
             YKNSPNDLQ++SDAPAH LF LLPPV LP+ + VIQ+ LEG ISR+SI+NSLSRG
Sbjct:    535 YKNSPNDLQMLSDAPAHQLFVLLPPVDLKNPKLPDPICVQLALEGSISRESIMNSLSRG 594

Query:    598 KKASGDLIPWTVSEQFQDPDFGGLSGGRVVRIVHPDYQGMGYGSRALQLLQMYEGRFP 657
             ++A GDLPW +S+QFQD +F L G R+VRIAV P++ MGYG+RA+QLL Y+EG+F
Sbjct:    595 QRAGGDLIPWLISQQFQDENFAALGGARIVRIAVSPEHVKMGYGTAMQLLHEYFEGKFI 654

Query:    658 CLEEKVLETPQEIHVSSEAV---SLLEEVIPTPR--KDLPLLLKLNERPAERLDYLGVS 712
             E+ + + E + +L E I R K +PPLLLKL+E E L Y+GVS
Sbjct:    655 SASEEFKAVKHSKLRIGDEEIENTALQTEKIHVRDAKTMPPLLLKLSELQPEPLHYVGVS 714

Query:    713 YGLTPRLLKFWKRAGFVPVYLROTPNDLTGEHSCIMLKTLTDEDEADQGGWLAAFWKDFR 772
             YGLTP L KFWKR G+ P+YLROTPNDLTGEH+C+ML+ L D WL AF ++F
Sbjct:    715 YGLTPSLQKFWKREGYCPLYLROTPNDLTGEHTCVMLRLVLEGRDSE---WLGAFAQNFY 770

Query:    773 RRFLALLSYQFSTFSPSLALNIIQNRNMGKP----AQPALSREELEALFLPYDLKRLEMY 828
             RRFL+LL YQF F+ AL+++ N G + L+ EE+ +F YDLKRLE Y
Sbjct:    771 RRFLSLLGYQREFAAITALSLVDACNNGTKYVVNSTSKLTNEEINNVSFESYDLKRLESY 830

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Query: 829 SRNMVDYHLIMDMIPASIRYFLNQLGD-LALSAAQSALLLGIGLQHKSVDOLEKEIELP 887
 S N++DYH+I+D++P ++ +YF + D + LS Q ++LL +GLQ+K++D LEKE LP
 Sbjct: 831 SNNLLDYHVIVDLLPKLAHLYFSGKFPDSVKLSPVQQSVLLALGLQYKTIDTLEKEFNLP 890

Query: 888 SGQLMGLFNRIIRKVVKLFNEVQEKAIEEQMVAAKDVVME-----PTMKTLSDDLDE 939
 S QL+ + ++ +K++K +E++ K IEE++ + K P ++L ++L E
 Sbjct: 891 SNQLLAMLVKLSKKIMKCIDETKDIEELGSNKKTESSNSKLPEFTPLQQSLEELQE 950

Query: 940 AAKEFQ-EKHKKEVGKLSMDLSEYIIRGDDEEWNEVLNKGAPNASIISLKSDDKKRLEA 998
 A E +K+ + ++DL +Y IRG++E+W KA N I R +
 Sbjct: 951 GADEAMLALREKQRELINADLEKYAIRGNEEDW-----KAAEN-QIQKTNGKGARVVISI 1004

Query: 999 KQEPKQSKKL--KNRETKNKKDMKLKRKK 1025
 K E +++ L +++TK K K K +K
 Sbjct: 1005 KGEKRKNSLDASDKKTKEKPSSKKKFRK 1033

Pedant information for DKFZphtes3_6c11, frame 3

Report for DKFZphtes3_6c11.3

[LENGTH] 1025
 [MW] 115704.57
 [pI] 8.50
 [HOMOL] PIR:S55151 probable membrane protein YNL132w - yeast (*Saccharomyces cerevisiae*)
 0.0
 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YNL132w] 0.0
 {FUNCAT} r general function prediction [H. influenzae, H11254] 2e-05
 {PROSITE} ATP_GTP_A 1
 {PROSITE} RGD 1
 [KW] Alpha_Beta
 [KW] LOW_COMPLEXITY 11.80 %

SEQ MHRKKVDNRIRILIENGVAERQKSLFVVVGDRGKDQVVLHMHLSKATVKARPSVLWCYK
 SEG
 PRD cccccccchhhhhccccccccceeeeeccccceeeehhhhhhhhhccccceehhhh

SEQ KELGFSSHRKKRMRQLQKKIKNGTLNLIKQDDPFELFIAATNIRYCYNETHKILGNTFGM
 SEG
 PRD hhhccccchhhhhhhhhhhhhccccccccceeeeeccccceeeccccceccccce

SEQ CVLQDFEALTPNLLARTVETVEGGGLVVILLRTMNSLKQLYTVMVHSRYRTEAHQDVV
 SEGxxxxxxxxxxxxxxxx.....
 PRD eehhhhhccccchhhhhhhhhccccceeeeeccccchhhhhhhhhhhhhhhhhhhhhhh

SEQ GRFNERFILSLASCKKCLVIDDQNLNLPISSHVATMEALPPQTPDESGLGPSDLRELKE
 SEG
 PRD hhhhhhhhhhhccccceeeeeccccceccccccccccccccccccccccccchhhhhhhhh

SEQ SLQDTQPVGVLDCCCKTLDQAKAVLKFIEGISEKTLRSTVALTAARGRGKSAALGLAIAG
 SEGxxxxxxxx.....
 PRD hhccccceeeehhhhhhhhhhhhhhhhhhhhhhhhhheeeccccccchhhhhhhhh

SEQ AVAFGYSNIFVTSPPDNLHTLFEFVFKGFDALQYQEHLDYEIIQSLNPEFNKAVIRVNV
 SEG xxx.....
 PRD hhhccccceeeccccccchhhhhhhhhhhhhhhhhhhhhhhheeeccccccceeeeh

SEQ FREHRQTIQYIHPADAVKLGQAEVLVVIDEAAIPLPLVKSLGPLYVFMASINGYEGTG
 SEG
 PRD hhhhhhheeeccccccccceeeehhhhhccchhhhhhhccccceeecccccccc

SEQ RSLSLKLIQQLRQQAQSQVSTTAENKTTTARLASARTLHEVSLQESIRYAPGDAVEKW
 SEGxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....
 PRD cchhhhhhhhhhhhhhhhhhhccccccccccchhhhhhhhhhhhhheeeccccchhh

SEQ LNDLLCLDCLNITRIVSGCPLPEACELYVNRTLFCYHKASEVFLQRLMALYVASHYKN
 SEG xxxxxxxxxxx.....
 PRD hhhhhccccceeeccccccccceeeccccccccchhhhhhhhhhhhhhhhhhhhhcc

SEQ SPNDLQMLSDAPAHHLFCLLPVPPTQNALPEVLAVIQVCLEGEISRQSIILNSLSRGKKA
 SEG
 PRD cccccccccccccceeeccccccccccchhhhhhhhhhhccccchhhhhhhcccccc

SEQ SGDLIPWTVSEQFQDPDFGGLSGGRVVRIVVHPDYQCMGYSRALQLLQMYEGRFPCL
 SEG
 PRD cccchhhhhhhhhhhccccccccceeeccccccccccchhhhhhhhhhhccccchhh

SEQ EKVLETPQEIHTVSSEAVSLLEEIVTPRKDLPLLLKLNERPAERLDYLGVSYGTLPRLL

```

SEG      .....xxxxxxxxx.....
PRD      hhhhhccccccchhhhhhhhhhhhhhhccccccccccccccccccccccccccccccccchhh

SEG      KFWKRAGFVPVYLRQTPNDLTGEHSCIMLKTLTDEDEADQGGWLAAFWKDFRRRFLALLS
SEG      .....
PRD      hhhhhccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhh

SEG      YQFSTFSPSLALNIIQNRNMGKPAQPALSREELEALFLPYDLKRLEMYSRNMVDYHLIMD
SEG      .....
PRD      hhhhhcchhhhhhhhhhhccccccccchhhhhhhhhhhhhccchhhhhhhhhccchhhhhhhhh

SEG      MIPAIISRIYFLNQLGDLALSAAQSALLLGIGLQHKSVQLEKEIELPSGQLMGLFNRIIR
SEG      .....xxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      hhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEG      KVVKLFNEVQEKAIEEQMVAADVVMEPTMKTLSDDLDEAAKEFQEKHKKEVGKLSMDL
SEG      .....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcc

SEG      SEYIIRGDDEEWNEVLNKGPNASIISLKSDDKRRKLEAKQEPKQSKKLKNRETKNKKDMK
SEG      .....xxxxxxxxxxxxxxxxxxxx
PRD      cccccccccchhhhhhhhhccccccccccccccccccccccccccccccccccccchhh

SEG      LKRKK
SEG      xxxxx
PRD      hhccc
    
```

Prosite for DKFZphtes3_6c11.3

PS00016	966->969	RGD	PDOC00016
PS00017	284->292	ATP_GTP_A	PDOC00017

(No Pfam data available for DKFZphtes3_6c11.3)

DKFZphtes3_6dl6

group: testes derived

DKFZphtes3_6dl6 encodes a novel 695 amino acid protein nearly identical to a sequence from human PAC clone WUGSC:H_DJ1185I07.2.

The cDNA is different to the proposed gene model: it contains additional exons.
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

WUGSC:H_DJ1185I07.2, differences to genmodel

differences to genmodel of WUGSC:H_DJ1185I07.2 two exons skippt,

Sequenced by BMFZ

Locus: /map="7q11.23-q21"

Insert length: 4572 bp

Poly A stretch at pos. 4540, polyadenylation signal at pos. 4520

```
1  GCGCGCGCTA  GCTTCGGAGT  CTCCGCGCGG  CACCTCAGCC  GCCTCCTAGC
51  GCGCGCGCGC  TCGCTCCTAC  GCCTAAAATG  ACCAATGTGT  GATTTCAGTG
101 GAATAAATGG  CGTCCAAAGT  CACAGATGCT  ATAGTCTGGT  ATCAAAAGAA
151 GATTGGAGCA  TATGATCAAC  AAATATGGGA  AAAATCTGTT  GAACAGAGAG
201 AAATCAAGGG  GCTAAGGAAT  AAACCAAAGA  AAACAGCACA  TGTGAAACCA
251 GACCTCATAG  ATGTTGATCT  TGTAAGAGGG  TCTGCATTTG  CAAAGGCCAA
301 GCCTGAAAGT  CCTTGGACTT  CTCTGACCAG  AAAGGGAATT  GTTCGAGTTG
351 TATTTTTCCC  CTTTTCTTTC  CGGTGGTGGT  TACAAGTAAC  ATCAAAGGTC
401 ATCTTTTTCT  GGCTTCTTGT  CCTTTATCTT  CTTCAAGTTG  CTGCAATAGT
451 ATTATTCTGC  TCCACTTCTA  GCCCACACAG  CATACCTCTG  ACAGAGGTGA
501 TTGGGCGGAT  ATGGCTGATG  CTGCTCCTGG  GAACTGTGCA  TTGCCAGATT
551 GTTTCACACA  GAACACCCAA  ACCTCCTCTA  AGTACAGGGG  GTAAAAGAAG
601 AAGGAAATTA  AGAAAAGCAG  CCCATTTGGA  AGTACATAGG  GAAGGAGATG
651 GTTCTAGTAC  CACAGATAAC  ACACAAGAGG  GAGCAGTTCA  GAACCACGGT
701 ACAAGCACCT  CTCACAGCGT  TGGCACTGTC  TTCAGAGATC  TCTGGCATGC
751 TGCTTTCTTT  TTATCAGGAT  CAAAGAAAGC  AAAGAATTCA  ATTGATAAAT
801 CAACTGAAAC  TGACAATGGC  TATGTATCCC  TTGATGGGAA  GAAGACTGTT
851 AAAAGCGGTG  AAGATGGAAT  ACAAACCATT  GAACCTCAGT  GTGAAACTAT
901 TCGACCAGAA  GAGACAGCCT  GGAACACAGG  AACACTGAGG  AATGGTCCTA
951 GCAAAGATAC  CCAAAGGACA  ATAACAAATG  TCTCTGATGA  AGTCTCCAGT
1001 GAGGAAGGTC  CTGAAACAGG  ATACTCATTG  CGTCGTCATG  TGGACAGGAC
1051 TTCTGAAGGT  GTTCTTCGGA  ATAGAAAGTC  ACACCATTAT  AAGAAACATT
1101 ACCCTAATGA  GGACGCCCCC  AAATCGGGTA  CTAGTTGCAG  CTCTCGCTGT
1151 TCAAGTTCCA  GACAGGATTC  TGAGAGTGCA  AGGCCAGAAT  CTGAAACAGA
1201 AGATGTGTTA  TGGGAAGACT  TGTTACATTG  TGCAGAATGC  CATTATCTTT
1251 GTACCAGTGA  GACAGATGTG  GAAAATCATC  AGATTAATCC  ATGTGTGAAA
1301 AAAGAATATA  GAGATGACCC  TTTTCATCAG  AGTCATTTGC  CCTGGCTCCA
1351 TAGTTCCCA  CCAGGATTAG  AAAAAATAAG  TGCTATAGTA  TGGGAAGGTA
1401 ATGATTGTAA  GAAAGCAGAC  ATGTCTGTAC  TTGAAATCAG  TGGAATGATA
1451 ATGAACAGAG  TGAACAGCCA  TATACCAGGA  ATAGGATACC  AGATTTTGG
1501 AAATGCAGTC  TCTCTCATA  TGGGTTTAAC  TCCATTGTGT  TTCGACTTTT
1551 CTCAAGCTAC  AGACTTGGAA  CAATCACAG  CACATTCTGC  TTCAGAACTT
1601 TATGTGATTG  CATTTGGTTC  TAATGAAGAT  GTCATAGTTC  TTTCTATGGT
1651 TATAATAAGT  TTTGTGGTTC  GCGTGTCTCT  TGTGTGGATT  TTTCTTTTTT
1701 TGCTCTGTGT  AGCAGAAAGA  ACTTATAAAC  AGCGATTACT  TTTTGCAAAA
1751 CTCTTTGGAC  ATTTAACATC  TGCAAGGAGG  GCTCGAAAAT  CTGAGGTTCC
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1901 TCATCTGCTT  TCTTATTGAC  TATCTCAGTT  GTATTTATCT  GTTGTGCCCC
1951 GATAAACCTC  TACTTGAAAA  TGGAGAAAAA  ACCTAACAAA  AAGGAGGAAC
2001 TGACACTAGT  GAATTAATGTT  TTAAACTGG  CTAATAAAT  GCTAAAGGAG
2051 TTGGACAGTC  CTTTATGATT  ATATGGGCTT  ACAATGAATC  CGCTGCTTTA
2101 TAACATCACC  CAGGTTGTTA  TCCTGTCAGC  TGTCTCTGGT  GTTATCAGTG
2151 ACTTGCTTGG  ATTTAATTTA  AAGCTATGGA  AGATTAAGTC  ATGACAATTC
2201 AAAGAAAAGA  AGATGTAGCC  TCTTTTCCAG  AATAAGAGTA  CTGACTAAGC
2251 TGCTTGAAAG  ATTGTCACTG  ATTCTTTGCT  TCAGGAGTCT  CAGCTAGGGA
2301 GTTGAGTGT  TTACATCAGA  CTGTCTGTG  CAATTCCTAT  ATTTATTTTA
2351 CTGGTTCACT  TTTTATTACA  TTTATTTTAG  TCTTTATATT  TTTATTTTAA
2401 AGCATTTAGT  TACTTAGTTG  TTGAAAGGGT  GATGAAACTG  ATATCCAGAT
2451 ACTTGAGATC  CTGGTAATTG  GTCATAAATA  ATTGGCAAAA  TAACAAATTG
2501 TGAAATAGA  AGCCATTGCT  CAGCACCCTT  TCTCCATCAA  TGCCGTGAAC
2551 TTGCCTTACT  TGAGGAAAAA  TTCTTAACT  TTGGAATATT  GCATTGAAC
2601 CAGCTATACA  CATAAACAT  TTTCTTGGT  AAATCAAGAT  CCAGTCAGGG
```

```
2651 TTTCTCTTGA ATTATTTTGG AACAAATGCCA GGATCCAAAC TGATTAAGTT
2701 ACAGTTTAAAG CACCCCTTCAG TATTAATATA TACGGTATTA TATAACAGGT
2751 CAACAAGTGC TCTTTGATGA TAAACTTGT AATAGAGCAA TAATTGTAAA
2801 TGGTTACCAT ACTGTAAGAT ATTTTGATAA AAATTAAC TAATACTTG
2851 TATTTATTTG AAACACTGGG CTGTTTGAC AGCTCCAAC GTGCATGCTC
2901 AAAATGTGCA CTTTTTAAAA TTGTTACTTT TAATGCGTAT CTTTATATGG
2951 GATCTGTTAT AGTATACTAG GGCATGATAT GGTATCCTTT TGAGTGAGGT
3001 ATATACTCAT CTCACAAGTG AAGTGCCTAC TGATATTACT AAAGTACATT
3051 ATGTTTACTC AAGTAAATAA TTTTCTCCCC ATGGTACACT CTAGTGTAGG
3101 CTATTCATAC CACACTGAAA TGAACAAC TGAAATAAGG CTAAGAACCA
3151 ATAAAATATT TCTCTAATTG CTAGTTGTAA AACTGTATCC AAATTTTCAG
3201 AAAAGACAGG TTCAGCTTGC AAATTCTATC CTCTAAACTT ATCTGGTGCA
3251 TTCTCCCCAC CCCACCCCA TTATATAAGG GCTATTTTAG ATGCTTTTAA
3301 CCTCCCCAAC AAATAATTTG CCAAGTGTCC AATGAGAACT TATCATGTTG
3351 GTGTGTTAGG TAAATCGGGC AAATATGATA GTGTCTTACA TTGGGCCTTG
3401 ATTTTAAAGT GTTATATTTG TACAATCGAG TATTTTAGAA ATTACATGAA
3451 ACATGAAACA GTTTTGTCAA TTTTCTTAA ACTGGGCATC TGGTTTCTAA
3501 AAATTTATTT GAAACAATCT AGAATTTTCT TGGTGCAAAG TGTATCATGT
3551 GGAATATCCT CATATTTTTA CCATATTTTA AGAACTTTAA GACGATTAAT
3601 TGTAATAAAT TTATTTGATT GGTGCAGTTC TAATCCCTAA ATCATAATCT
3651 TAAAATCAGG AATGTGTGGA GAACAGAGCC ATGTCATATC ACTTTGCTCT
3701 TACCATTCCT TTTGATCAGC CTCAATTCAG CCTCATTGTG TAGTATGTTT
3751 TTTCTTTCTA TGAAAAACAA CAGAAAGCAT TTCATTTTAT TTGCCTATGT
3801 TCAAAATATG TTAATAATGA CCAAAGTGCA TTCTGAGTTT TTTCAAGGAA
3851 TGTAATACTG GAGCTTTAAG AACATACTTA GTTCTCATG TGAAAACTTA
3901 GGCTTTGTCT GATGTTTTTC CTTCCTCTAT TGTCTAATGT TGAGGTTGTT
3951 TTTAGGAATT ATGTTTTATA AACTTTTCA ATATAAGGTA CATGCCTATA
4001 CAGAACTTAA CATTTTGCAC AGAATATATC AAATATATTT TGAGAAAAAA
4051 AGTACGGCAT GAGTTCGTG AGGAATAAAA GATGAACTA TTGTATCTCA
4101 CAAAAAATCT TATTTAGAAA TGGAAATATT TTTGAGAAAA GTAGCTGAGT
4151 ATACTGGTTT AAGAAAATGC TTGTTTTAGA TTGAGGTTAA CTTAGAGTTG
4201 GGAGTTGATT TATTAAGTAC AGTATACCTC TCAACAGTTT ATAAATAATA
4251 TGTGTAATTA TGTGAGTGTG GGCAGCAGTA GAATACTAAA AGGAAAATGT
4301 CATGTTAAGC AATTTTCAGAA CATTAACCTGA ACTATTTTCA AACCAGAAAA
4351 ATTGACATTG CTGCCTTTAA GAATACCATG AATGTAAGAA ATTGAAAGAA
4401 ATTGTAATAA ATCACAATAA ATAGAAATGG CAGTTCAAAG AGAATTGTGG
4451 CAGATGTTGT GTGTGAACCTG TGTGTTCTTT GCCACATGTG TTGTATTTGA
4501 AAGTTTTTACA GTAAGTTTAA AATAAACAT TCTGTGACTG AAAAAAATAA
4551 AAAAAAATAA AAAAAAATAA AA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 107 bp to 2191 bp; peptide length: 695
Category: known protein
Classification: unclassified
Prosites motifs: CYTOCHROME_C (375-381)

```
1 MASKVTDIAV WYOKKIGAYD QOIWEKSVEQ REIKGLRNKP KKTAAHVKPD
51 IDVDLVRGSA FAKAKPESPW TSLTRKGIVR VVFFPFFFRW WLQVTSKVIF
101 FWLLVLYLLQ VAAIVLFCST SSPHSIPLTE VIGPIWMLML LGTVHCQIVS
151 TRTPKPPPLST GKKRRRLKLRK AAHLEVHREG DGSSTTDNTQ EGAVQNHGTS
201 TSHSVGVTFR DLWHAFFLS GSKKAKNSID KSTETDNGYV SLDGKKT VKS
251 GEDGIQNHPE QCETIRPEET AWNTGTLRNG PSKDTQRTIT NVSDEVSSEE
301 GPETGYSLRR HVDRTSEGVL RNRKSHHYKK HYPNEDAPKS GTSCSSRCSS
351 SRQDSSEARP ESETEDVLWE DLLHCAECHS SCTSETDVEN HQINPCVKKE
401 YRDDPFHQSH LPWLHSHPG LEKISAIWVE GNDCKKADMS VLEISGMIMN
451 RVNSHIPGVI YQIFGNAVSL ILGLTPFVFR LSQATDLEQL TAHSASELYV
501 IAFGSNEDVI VLSMVIISFV VRVSLVWIFF FLLCVAERTY KQRLLEAKLF
551 CHLTSAARRAR KSEVPHERLK KVQNIKMWLS LRSYLKRRGP QRSVDVIVSS
601 AFLLTISVVF ICCAQINLYL KMEKKPNKKE ELTLVNNVLK LATKLLKELD
651 SPFRLYGLTM NPLLYNITQV VILSAVSGVI SDLLGFNLKL WKIKS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_6d16, frame 2

PIR:S38170 SRP40 protein - yeast (*Saccharomyces cerevisiae*), N = 1,
Score = 100, P = 0.08

TREMBL:AC004990_1 gene: "WUGSC:H_DJ1185I07.2"; Homo sapiens PAC clone
DJ1185I07 from 7q11.23-q21, complete sequence., N = 2, Score = 2693, P
= 0

>TREMBL:AC004990_1 gene: "WUGSC:H_DJ1185I07.2"; Homo sapiens PAC clone
DJ1185I07 from 7q11.23-q21, complete sequence.
Length = 588

HSPs:

Score = 2693 (404.1 bits), Expect = 0.0e+00, Sum P(2) = 0.0e+00
Identities = 510/515 (99%), Positives = 512/515 (99%)

```
Query:   35 GLRNKPKKTAHVKPDLDVLDVRGSAFAKAKPESPWTSLTRKGIVRVVFFPFFFRWWLQV 94
          GLRNKPKKTAHVKPDLDVLDVRGSAFAKAKPESPWTSLTRKGIVRVVFFPFFFRWWLQV
Sbjct:   1  GLRNKPKKTAHVKPDLDVLDVRGSAFAKAKPESPWTSLTRKGIVRVVFFPFFFRWWLQV 60

Query:   95 TSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVIGPIWMLLLGTVHCQIVSTRTP 154
          TSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVIGPIWMLLLGTVHCQIVSTRTP
Sbjct:   61 TSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVIGPIWMLLLGTVHCQIVSTRTP 120

Query:   155 KPPLSTGGKRRRKLKRAAHLEVHREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWH 214
          KPPLSTGGKRRRKLKRAAHLEVHREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWH
Sbjct:   121 KPPLSTGGKRRRKLKRAAHLEVHREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWH 180

Query:   215 AAFFLSGSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPQCETIRPEETAWNT 274
          AAFFLSGSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPQCETIRPEETAWNT
Sbjct:   181 AAFFLSGSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPQCETIRPEETAWNT 240

Query:   275 GTLRNGPSKDTQRTITNVSDVSSEEGPETGYSLRRHVDRTSEGLRNKRKSHHYKKHYPN 334
          GTLRNGPSKDTQRTITNVSDVSSEEGPETGYSLRRHVDRTSEGLRNKRKSHHYKKHYPN
Sbjct:   241 GTLRNGPSKDTQRTITNVSDVSSEEGPETGYSLRRHVDRTSEGLRNKRKSHHYKKHYPN 300

Query:   335 EDAPKSGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQIN 394
          EDAPKSGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQIN
Sbjct:   301 EDAPKSGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQIN 360

Query:   395 PCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMSVLEISGMIMNRVNS 454
          PCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMSVLEISGMIMNRVNS
Sbjct:   361 PCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMSVLEISGMIMNRVNS 420

Query:   455 HIPGIGYQIFGNAVSLILGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM 514
          HIPGIGYQIFGNAVSLILGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM
Sbjct:   421 HIPGIGYQIFGNAVSLILGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM 480

Query:   515 VIISFVVRVSLVWIFFFLCVAERTYKQRLLEAKL 549
          VIISFVVRVSLVWIFFFLCVAERTYKQ L+ K+
Sbjct:   481 VIISFVVRVSLVWIFFFLCVAERTYKQINLYLKM 515
```

Score = 409 (61.4 bits), Expect = 0.0e+00, Sum P(2) = 0.0e+00
Identities = 92/115 (80%), Positives = 98/115 (85%)

```
Query:   595 DVIVSS----AFLLTISVVFI-----CCA-----QINLYLKMEKKPNKKEELTLVNNVLK 640
          DVIV S   +F++ +S+v+i   C A   QINLYLKMEKKPNKKEELTLVNNVLK
Sbjct:   474 DVIVLSMVIISFVVRVSLVWIFFFLCVAERTYKQINLYLKMEKKPNKKEELTLVNNVLK 533

Query:   641 LATKLLKELDSPFRLYGLTMNPLLYNITQVVILSAVSGVISDLLGFNLKLWKIKS 695
          LATKLLKELDSPFRLYGLTMNPLLYNITQVVILSAVSGVISDLLGFNLKLWKIKS
Sbjct:   534 LATKLLKELDSPFRLYGLTMNPLLYNITQVVILSAVSGVISDLLGFNLKLWKIKS 588
```

Pedant information for DKFZphtes3_6d16, frame 2

Report for DKFZphtes3_6d16.2

[LENGTH] 695
[MW] 78466.68
[pI] 9.30
[HOMOL] TREMBL:AC004990_1 gene: "WUGSC:H_DJ1185I07.2"; Homo sapiens PAC clone DJ1185I07
from 7q11.23-q21, complete sequence. 0.0

{PROSITE} CYTOCHROME_C 1
{KW} TRANSMEMBRANE 6
{KW} LOW_COMPLEXITY 5.32 %

SEQ MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTAHVKPDLDVDLVRGSA
SEG
PRD cccccceehhhhhhhccccchhhhhhhhhhhhhhhcccccccccccccccccccccccccccc
MEM

SEQ FAKAKPESPWTSLTRGIVRVVFFPFFFRWLQVTSKVIFFWLLVLYLLQVAAIVLFCST
SEG
PRD hhhcc
MEMMM

SEQ SSPHSIPLTEVIGPIWMLMLLLGTVHCQIVSTRTPKPLSTGGKRRRKLKAAHLEVHREG
SEG
PRD cccccceehhh
MEMMM

SEQ DGSSTDTNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLSGSKAKNSIDKSTETDNGYV
SEG
PRD ccc
MEM

SEQ SLDGKKTVKSGEDGIQNHQPQCETIRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEE
SEG
PRD cccccceehhh
MEM

SEQ GPETGYSLRRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSRRQDSESARP
SEG
PRD cccccceehhh
MEM

SEQ ESETEDVLWEDLLHCAECHSSCTSETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPG
SEG
PRD cccccchhh
MEM

SEQ LEKISAIWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFR
SEG
PRD cccccceehhh
MEMMM

SEQ LSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWIFFLLCVAERTY
SEG
PRD hhh
MEMMM

SEQ KORLLFAKLFCHLTSARRARKSEVPFHRLKKVQNIKMWLSLRSYLKRRGPQRSVDIVSS
SEG
PRD hhh
MEMMM

SEQ AFLLTISVVFICCAQINLYLKMEKKPNKKEELTVNNVLKLATKLLKELDSPFRLYGLTM
SEG
PRD eeeeeeeeeehhh
MEMMM

SEQ NPLLYNITQVVILSAVSGVISDLLGFNLKLWKIKS
SEG
PRD cchhh
MEMMM

Prosites for DKFZphtes3_6d16.2

PS00190 375->381 CYTOCHROME_C PDOC00169

(No Pfam data available for DKFZphtes3_6d16.2)

DKFZphtes3_72k11

group: testes derived
DKFZphtes3_72k11 encodes a novel 233 amino acid protein with similarity to S.pombe
hypothetical repeat-containing protein.

The novel protein contains 5 leucine zippers and a microbodies C-terminal targeting signal (S-K-L) signature. This sequence is responsible for transport of proteins from free polysomes into the microbodies.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to S.pombe hypothetical repeat-containing protein

complete cDNA, complete cds, 6 EST hits (3 from testis derived
libraries)

Sequenced by DKFZ

Locus: unknown

Insert length: 1134 bp

Poly A stretch at pos. 1124, polyadenylation signal at pos. 1088

```
1 AACCTTTCAA GTGCCCCCTC CTTTCCTTAA AGTCTTTTAT AGGGGTCCCC
51 TTCTTGGCCA TCTCCATCCT GTGAGTCAGG ACTGAAAGGG CACAGACAGG
101 TCACTGCCAG CATTGTTGGG GCAAGCCTGC AAGCACGCAT CACTGGGGAT
151 CTGACATGAC AATGGCCGCC TGCCCCCTCT GAGGGCTACA GGACTTACCC
201 CAGTGGGAAG CAGCTAAGCA GGTCTGACCA GCCGACCTGG ACCTGGCCAA
251 GGGTCCCTGC ATCCCTCATG GCCACCCCGC CATTCCGGCT GATAAGGAAG
301 ATGTTTTTCT TCAAGGTGAG CAGATGGATG GGGCTTGCCT GCTTCCGGTC
351 CCTGGCGGCA TCCTCTCCCA GTATTGCGCA GAAGAACTA ATGCACAAGC
401 TGCAGGAGGA AAAGGCTTTT CGCGAAGAGA TGAAAAATTT TCGTGAAAAA
451 ATAGAGGACT TCAGGGAAGA GATGTGGACT TTCCGAGGCA AGATCCATGC
501 TTTCCGGGGC CAGATCCTGG GTTTTGGGA AGAGGAGAGA CCTTCTGGG
551 AAGAGGAGAA AACCTTCTGG AAAGAGGAAA AATCCTTCTG GGAAATGGAA
601 AAGTCTTTCA GGGAGGAAGA GAAAACCTTC TGGAAAAAGT ACCGCACTTT
651 CTGGAAGGAG GATAAGGCCT TCTGGAAGA GGACAATGCC TTATGGGAAA
701 GAGACCGGAA CCTTCTTCAG GAGGACAAGG CCCTGTGGGA GGAAGAAAAG
751 GCCCTGTGGG TAGAGGAAAG AGCCCTCCTT GAGGGGGAGA AAGCCCTGTG
801 GGAAGATAAA ACGTCCCTCT GGGAGGAAGA GAATGCCCTC TGGGAGGAAG
851 AGAGGGCCTT CTGGATGGAG AACAAATGGCC ACGTTGCCGG AGAGCAGATG
901 CTCGAAGATG GGCCCCACAA CGCCAACAGA GGGCAGCGCT TGCTGGCCTT
951 CTCCCGAGGC AGGGCGTAGC CAGCATGCAG GTGCAGGGCC CTGTGGTCCA
1001 GACTCCCTCG GGTGGGATT CAAGTCCAGG GTGAGCCCAT GTGCTGGAGA
1051 AAATACACAC TCATTGGTCT CTTGCTTTG AAAGATCCAA TAAAGTCCTG
1101 AGGCAAGGTT TGGAAAACCA ACTTAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 268 bp to 966 bp; peptide length: 233
Category: similarity to known protein
Prosite motifs: MICROBODIES_CTER (231-234)
LEUCINE_ZIPPER (142-164)
LEUCINE_ZIPPER (149-171)
LEUCINE_ZIPPER (156-178)
LEUCINE_ZIPPER (163-185)
LEUCINE_ZIPPER (170-192)
LEUCINE_ZIPPER (170-192)

```

1  MATPPFRLIR  KMFSFKVSRW  MGLACFRSLA  ASSPSIRQKK  LMHKLQEEKA
51 FREEMKIFRE  KIEDFREEMW  TFRGKIHAFR  GQILGFWEE  RPFWEEETKF
101 WKEEKSEFW  EKSFREEER  FWKKYRTFW  EDKAFWKEDN  ALWERDRNLL
151 QEDKALWEE  KALWVEERAL  LEGEKALWED  KTSLWEEENA  LWEEERAFWM
201 ENNGHVAGEO  MLEDGPHNAN  RGORLLAFSR  GRA

```

Entry SPCC330_4 from database TREMBLNEW:
gene: "SPCC330.04c"; product: "hypothetical repeat-containing protein";
S.pombe chromosome III cosmid c330.
Score = 149, P = 1.6e-08, identities = 55/187, positives = 88/187

Entry A45973 from database PIR:
trichohyalin - human
Score = 147, P = 3.0e-07, identities = 57/194, positives = 94/194

Alert BLASTP hits for DKFZphtes3 72k11, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3 72k11, frame 1

Report for DKFZphtes3_72k11.1

```
[LENGTH]          233
[MW]               28752.65
[pI]               5.70
[PROSITE]          LEUCINE_ZIPPER 5
[PROSITE]          MICROBODIES_CTER 1
[PROSITE]          MYRISTYL 1
[PROSITE]          CK2_PHOSPHO_SITE 3
[PROSITE]          PKC_PHOSPHO_SITE 4
[KW]               All_Alpha
[KW]               LOW_COMPLEXITY 15.45 %
```

```
SEQ      MATPPFRLIRKMFSEFKVSRWMLGACFRSLAASSPSIRQKKLMHKLQEKAFFREEMKIFRE
SEG      .....
PRD      cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
```

```
SEQ      KIEDFREEMWTFRGKIHAFRGQILGFWEERPFWEEEKTFWKEEKSFWENEKSFREEKT  
SEG      .....XXXXXXXXXXXXXXX.....  
PRD      hhhhhhhhhhhhhhhhhccccccccccccccchhhhhhhhhhhhhhhhhhhhhhh
```

```
SEQ      FWKKYRTFWKEDKAFWKEDNALWERDRNLLQEDKALWEEEKALWVEERALLEGEKALWD
SEG
PRD      hhhccccccccccchhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
```

SEQ KTSLWEEENALWEEERAFWMENNGHVAGEQMLEDGPHNANRGQRLLAFSRGRA
 SEG . . . xxxxxxxxxxxxxxxx . . .
 PRD cccchhhhhhhhhhhhhhhhhhhhhcccccchhhhhhhccccccccchhhhhhhhhccc

Prosites for DKFZphtes3_72k11.1

PS00005	14->17	PKC_PHOSPHO_SITE	PDOC00005
PS00005	35->38	PKC_PHOSPHO_SITE	PDOC00005
PS00005	71->74	PKC_PHOSPHO_SITE	PDOC00005
PS00005	113->116	PKC_PHOSPHO_SITE	PDOC00005
PS00006	106->110	CK2_PHOSPHO_SITE	PDOC00006
PS00006	113->117	CK2_PHOSPHO_SITE	PDOC00006
PS00006	183->187	CK2_PHOSPHO_SITE	PDOC00006
PS00008	81->87	MYRISTYL	PDOC00008
PS00342	231->234	MICROBODIES_CTER	PDOC00299
PS00029	142->164	LEUCINE_ZIPPER	PDOC00029
PS00029	149->171	LEUCINE_ZIPPER	PDOC00029
PS00029	156->178	LEUCINE_ZIPPER	PDOC00029
PS00029	163->185	LEUCINE_ZIPPER	PDOC00029
PS00029	170->192	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphres3_72k11.1)

DKF2phtes3_72k15

group: cell structure and motility

DKF2phtes3_72k15 encodes a novel 188 amino acid protein with strong similarity to *Rattus norvegicus* actin-filament binding protein Frabin.

FGD1-related F-actin-binding protein (Farbin/FGD1) is a novel F-actin-binding protein. The gene locus *fgd1* seems to be responsible for faciogenital dysplasia or Aarskog-Scott syndrome. Frabin binds F-actin and shows F-actin-cross-linking activity. Overexpression of frabin in Swiss 3T3 cells and COS7 cells induces cell shape change and c-Jun N-terminal kinase activation, as described for FGD1. Because FGD1 has been shown to serve as a GDP/GTP exchange protein for Cdc42 small G protein, it is likely that frabin is a direct linker between Cdc42 and the actin cytoskeleton. Cdc42p is an esin yeast, Cdc42p transduces signals to the actin cytoskeleton to initiate and maintain polarized growth and to mitogen-activated protein morphogenesis. In mammalian cells, Cdc42p regulates a variety of actin-dependent events and induces the JNK/SAPK protein kinase cascade, which leads to the activation of transcription factors within the nucleus. The novel protein seems to be the human orthologue of rat frabin.

The new protein can find application in modulating of cell structure and motility as well as modulation of the JNK/SAPK pathway.

strong similarity to actin-filament binding protein Frabin

2 EST hits

Sequenced by DKF2

Locus: unknown

Insert length: 1845 bp

Poly A stretch at pos. 1835, polyadenylation signal at pos. 1816

```
1 GTGATGGAGA GTGCTGTTAT GATAGATGAA TCTAGGAAAG CCTCTTTGGA
51 GATGTGATAC CTGAACAGAA CCCCGAATGA TAAGAAGAAA TACCAGTGTT
101 TTAGGAGAGA TTGTCTTAAG CAGAGAACAG CAGCTGCAAA GACCCCAAGA
151 CACATACACT TGGTTATTAA GAATGGGAGC AGCAAGGAGT ATGGCAAGAA
201 CACAGTGAGT TTTCCCTTGA GTGTGTGAGG AAGCCCTCAG AGTTTGTGAC
251 TGACTTGTAG AGGTTCTAGT GGAGGGGATC AGAGTGGAAG CAAAGAGACC
301 AGTTAAAAAG GTATGGCAGC ATGAATAAAA AAGTTTGTAG AGTATTCATT
351 ATGCCCTCCA AATAAAAAAC TCTTTGGTTC ATAATTGTGT CATAAATTAA
401 GGACTGGCTA CACTGTACTA TTTAAAAATG TTAAGAAACA TCAATAAGTA
451 AAAATGTTAG GAAGAGATGA TAAATACGTA AGTATTATAT CTAATAAGT
501 CTTTACTAAC TAGTCACATT ATTAACAGT GCAAGGATCA AGAAAAAGTTA
551 AGCGTTGAAA AATAAATAAA TAAGTTATAA ATAAATAAAA CAGCCCAAGG
601 AAATGTTCCA GTCCCCATAG GTAGACTCGG GGTCTCTTTC TTTATTTAAA
651 TCTTTATTTA AATGTGGATA GCATCCCAAG AGACTTGGGT CTACACTAAG
701 AATATTCAAA TCCATGTTTC TGAAACCATC AGAGATAGAA AAAAAAAGTA
751 GCGAATATCC CTTTTCAACT GGAATAAACT TGTCTTAATT CTAGAACTTT
801 TCCATACCAA TGTTTTCATG CTTCTTTTGT ATTTTATCTT TTAGCTCATT
851 ATCAAATTAT AGTGATTGTA AGAAAGAGTC TGCTGTGAAC CTAAATGCTC
901 CTAGAACCCC AGGAAGGCAT GGATTGACAA CCACACCTCA ACAAACCTC
951 CTCTCCACAG ACTTGCCACA GAGGCAGGGA AATGATACAG ATAAGACTCA
1001 GGGTGCACAG ACTTGTGTGG CCAACGGTGT AATGGCAGCA CAAAACCAGA
1051 TGGAATGTGA GGAGGAGAAA GCTGCCACTC TTAGCTCAGA TACTTCTATT
1101 CAAGCTTCTG AACCTTGCT TGATACGCAC ATAGTGAATG GAGAAAGAGA
1151 TGAAACTGCC AGAGCTCCTG CATCACCCAC AACAGATAGC TGTGATGGAA
1201 ATGCTTCTGA CAGTAGCTAC AGGACTCCAG GCATAGGCCC AGTGCTCCCC
1251 CTAGAAGAAA GAGGGGCAGA AACAGAAACC AAGGTACAAG AGAGGGGAAA
1301 TGGGGAAAGC CCTCTGGAAC TGGAGCAGCT GGACCAGCAC CATGAGATGA
1351 AGGTAGAGCA TGAGACTAGC TCATGAGCAG GGAAACCCCT GCCTATTCGA
1401 TTGTTGTCTT AAAACTCTTT ATTTATTGCA CCCCTGAAAT GTATGAATCA
1451 GATCACCCAC TATGGCAGTT AAACGATTTT CAAGCTCTGG CTGCTGATTA
1501 GCATTTCCTT TATGCTCTAA GCAGATATTT CACTTTTCTT TTTCATGTAG
1551 TTTCTGTATA TATCTCTGTT GTAATTTCAG GAGTCAGAAC AGTGTGGAAA
1601 CTTTAAATATA GAAATCCAC AAATGTATTG TTTTACATA GAAAGAAAAT
1651 GTTCCTTGTT GCTCTAGATG TTGGTGTCTG ATCCCTAATA CTTACGGGCC
1701 AAGCAAGAAG AAATTGTATA ATCTTTGTG TTCAGAAAGT TCTAATAGAA
1751 TAAATAGGCC TGTAAGATGA ACTTGCCACT AGTAAATGTT ACTTTTAAGG
1801 ACATGAATAT GGAAGTATTA AATTATTCAA CAGATAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

98334590:

Frabin, a novel FGD1-related actin filament-binding protein capable of changing cell shape and activating c-Jun N-terminal kinase.

Peptide information for frame 3

ORF from 810 bp to 1373 bp; peptide length: 188

Category: similarity to known protein

Classification: Cell structure/motility

```

1 MFSCFLCILS FSSLSNYS DLKKESAVNLNA PRTPGRHGLT TTPQKLLSQ
51 HLPQROGNDT DKTQGAQTCV ANGVMAAQNQ MECEEEKAAT LSSDTSIQAS
101 EPLLDTHIVN GERDETATAP ASPTTDSCDG NASDSSYRTP GIGPVLPLEE
151 RGAETETKVQ ERENGESPLE LEQLDQHHEM KVEHETSS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_72k15, frame 3

TREMBL:AF038388_1 product: "actin-filament binding protein Frabin";
Rattus norvegicus actin-filament binding protein Frabin mRNA, complete
cds., N = 1, Score = 428, P = 1.8e-39

>TREMBL:AF038388_1 product: "actin-filament binding protein Frabin"; Rattus
norvegicus actin-filament binding protein Frabin mRNA, complete cds.
Length = 766

HSPs:

Score = 428 (64.2 bits), Expect = 1.8e-39, P = 1.8e-39
Identities = 90/174 (51%), Positives = 115/174 (66%)

```

Query:      12 SSSLSNYS DLKKESAVNLNAPRTPGRHGLT TTPQKLLSQ HLPQROGNDT DKTQGAQTCVA 71
              S LS+Y+D++K+S +NLN P+TP +HGLT+T QKL S PQ+Q D+D+ QG C+A
Sbjct:      31 SVLSSYTDVQKDSTMNLNIPQTPRQHGLTSTTPQKLPSHKSPQKQEKDSDQNQQGHGCLA 90

Query:      72 NGVMAAQNQMECEEEKAATLSSDTSIQASEPLLDTHIVNGERDETATAPASPTTDSCDGN 131
              NGV AAQ+QMECE EK A LS +T Q + D H++NG R+ET T AS T+S D N
Sbjct:      91 NGVAAAQSQMECETEKEAALSPETDTQTAAASPDHVLNGVRNETTDSASSVTNSHDEN 150

Query:      132 ASDSSYRTPGIGPVLPLEERGAETETKVQERENGESPLELEQLDQHHEMKVEHE 185
              A DSS RT G LP +E E ++QERENG S L LDQHHE+K +E
Sbjct:      151 ACDSSCRTQGTDLGLPSKEGEPVIEAELQERENGLSTEGLNPLDQHHEVKETNE 204

```

Pedant information for DKFZphtes3_72k15, frame 3

Report for DKFZphtes3_72k15.3

```

[LENGTH]      188
[MW]           20388.32
[pI]           4.62
[HOMOL]        TREMBL:AF038388_1 product: "actin-filament binding protein Frabin"; Rattus
norvegicus actin-filament binding protein Frabin mRNA, complete cds. 2e-38
[KW]           All Alpha
[KW]           SIGNAL PEPTIDE 16
[KW]           LOW_COMPLEXITY 12.77 %

```

```

SEQ  MFSCFLCILSFSSLSNYS DLKKESAVNLNAPRTPGRHGLT TTPQKLLSQ HLPQROGNDT
SEG  .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD  ccchhhhhccccccccccccccccccccccccccccccccccccccccchhhhhhhcccccccccc

SEQ  DKTQGAQTCVANGVMAAQNQMECEEEKAATLSSDTSIQASEPLLDTHIVNGERDETATAP

```

```

SEG      .....xxxxx
PRD      cccccceecchhhhhhhhhhhhhhhhhhhcccccceecccccceecccccccccc

SEQ      ASPTTDSCDGNASDSSYRTPGIGPVLPLEERGAETETKVQERENGESPLELEQLDQHHEM
SEG      xxxxx.....
PRD      cccccccccccccccccccccccccccccccccchhhhhhhhhcccccchhhhhhhhhhh

SEQ      KVEHETSS
SEG      .....
PRD      hhhhcccc
    
```

(No Prosite data available for DKFZphtes3_72k15.3)

(No Pfam data available for DKFZphtes3_72k15.3)

DKFZphtes3_72p16

group: intracellular transport and trafficking

DKFZphtes3_72p16 encodes a novel 796 amino acid protein with very strong similarity to Mus musculus maternal-embryonic 3 (Mem3) gene.

Mem3 was isolated from a partial subtraction library of mouse unfertilized eggs and preimplantation embryos. Its transcript is abundant in the unfertilized egg and also actively transcribed from the newly formed zygotic genome. As Mem3, the novel protein is similar to yeast VPS (vacuolar protein sorting) 35. The null allele of VPS35 results in yeast in a differential defect in the sorting of vacuolar carboxypeptidase Y (CPY), proteinase A (PrA), proteinase B (PrB), and alkaline phosphatase (ALP).

The new protein can find application in modulation the sorting of proteins into different compartments.

strong similarity to mouse MEM3 and yeast VPS35

Sequenced by DKFZ

Locus: /map="16p13.3"

Insert length: 2707 bp

Poly A stretch at pos. 2697, no polyadenylation signal found

```

1 CTACGCGCGG GCGGGGTGCT GCTTGCTGCA GGCTCTGGGG AGTCGCCATG
51 CCTACAACAC AGCAGTCCCC TCAGGATGAG CAGGAAAAGC TCTTGGATGA
101 AGCCATACAG GCTGTGAAGG TCCAGTCATT CCAAATGAAG AGATGCCTGG
151 ACAAACACAA GCTTATGGAT TCTCTAAAAC ATGCTTCTAA TATGCTTGGT
201 GAACTCCGGA CTTCTATGTT ATCACCAGAG AGTTACTATG AACTTTATAT
251 GGCCATTTCT GATGAAGTGC ACTACTTGGA GGTCTACCTG ACAGATGAGT
301 TTGCTAAAGG AAGGAAAGTG GCAGATCTCT ACGAAGTTGT ACAGTATGCT
351 GGAAACATTA TCCCAAGGCT TTACCTTTTG ATCAGAGTTG GAGTTGTATA
401 TGTCAGTCA TTTCTCAGT CCAGGAAGGA TATTTTGAAA GATTTGGTAG
451 AAATGTGCCG TGGTGTGCAA CATCCCTTGA GGGGTCTGTT TCTTCGAAAT
501 TACCTTCTTC AGTGTAACAG AAATATCTTA CCTGATGAAG GAGAGCCAAC
551 AGATGAAGAA ACAACTGGTG ACATCAGTGA TTCCATGGAT TTTGTACTGC
601 TCACTTTTGC AGAAATGAAC AAGCTCTGGG TGCGAATGCA GCATCAGGGA
651 CATAGCCGAG ATAGAGAAAA AAGAGAACGA GAAAGACAAG AACTGAGAAT
701 TTTAGTGGTA ACAAAATTTGG TGCGCCTCAG TCAGTTGGAA GGTGTAATATG
751 TGGAACGTTA CAACACAGAT GTTTTGACTG GCATATTGGA GCAAGTTGTA
801 AACTGTAGGG ATGCTTTGGC TCAAGAATAT CTCATGGAGT GTATTATTCA
851 GGTTTTCCCT GATGAATTTT ACCTCCAGAC TTTGAATCCT TTTCTTCGGG
901 CCGTGGCTGA TTAGACCCAG AATGTAAATG TGAAGAACAT AATCATTGCT
951 TTAATTGATA GATTAGCTTT ATTTGCTCAC CGTGAAGATG GACCTGGAAT
1001 CCCAGCGGAT ATTTAACTTT TTGATATATT TTCACAGCAG GTGGCTACAG
1051 TGATACAGTC TAGACAAGAC ATGCCTTCAG AGGATGTTGT ATCTTTACAA
1101 GTCTCTCTGA TTAATCTTGC CATGAAATGT TACCCTGATC GTGTGGACTA
1151 TGTTGATAAA GTTCTAGAAA CAACAGTGGA GATATTCAAT AAGCTCAACC
1201 TTGAACATAT TTGTAACAGT AGTGCAAGTT CAAAGGAACAT CACCAGACTT
1251 TTGAAAATAC CAGTTGACAC TTACAACAAT ATTTTAACAG TCTTGAATTT
1301 AAAACATTTT CACCACTCTT TTGAGTACTT TGACTACGAG TCCAGAAAAG
1351 GCATGAGTTG TTATGTGCTT AGTAATGTTT TGGATTATAA CACAGAAATT
1401 GTCTCTCAAG ACCAGGTGGA TTCCATAATG AATTTGGTAT CCACGTTGAT
1451 TCAAGATCAG CCAGATCAAC CTGTAGAAGA CCCTGATCCA GAAGATTTTG
1501 CTGATGAGCA GAGCCTTGTG GGCCGCTTCA TTCATCTGCT GCGCTCTGAG
1551 GACCCTGACC AGCAGTACTT GATTTTGAAC ACAGCACGAA AACATTTTGG
1601 AGCTGGTGGA AATCAGCGGA TTCGCTTCAC ACTGCCACCT TTGGTATTTG
1651 CAGCTTACCA GCTGGCTTTT CGATATAAAG AGAATCTTAA AGTGGATGAC
1701 AAATGGGAAA AGAAATGCCA GAAGATTTT TCATTGCCCC ACCAGACTAT
1751 CAGTGCTTTG ATCAAAGCAG AGCTGGCAGA ATTGCCCTTA AGACTTTTTC
1801 TTCAAGGAGC ATAGCTGCTT GGGGAAATTG GTTTTGAAAA TCATGAGACA
1851 GTCGCATATG AATTCATGTC CCAGGCATTT TCTCTGTATG AAGATGAAAT
1901 CAGCGATTCC AAAGCACAGC TAGCTGCCAT CACCTTGATC ATTGGCACTT
1951 TTGAAGAGG AGAGTGCTTC AGTGAAGAGA ATCATGAACC TCTGAGGACT
2001 CAGTGTGCCC TTGCTGCATC CAAACTTCTA AAGAAACCTG ATCAGGGCCG
2051 AGCTGTGAGC ACCTGTGCAC ATCTCTTCTG GTCTGGCAGA AACACGGACA
2101 AAAATGGGGA AAGAGCTTCA GGAGGCAAGA GGGTAATGGA GTGCCATAAA
2151 AAAGCTCTAA AAATAGCAAA TCAGTGCATG GACCCCTCTC TACAAGTGCA
2201 GCTTTTATTA GAAATCTTGA ACAGATATAT CTATTTTATG AAAAAGGAAA
2251 ATGATGCGGT AACAAATTCAG GTTTTAAACC AGCTTATCCA AAAGATTCTGA
2301 GAAGACCTCC CGAATCTTGA ATCCAGTGAA GAAACAGAGC AGATTAAACA
2351 ACATTTTTCAT AACACACTGG AGCATTTCGG CTTGCGGCGG GAATCACCAG
2401 AACCCGAGGG GCCAATTTAT GAAGTCTCA TCCTTTAAAA AGGAAATAGC
2451 TCACCATACT CCTTTCCATG TACATCCAGT GAGGGTTTTA TTACGCTAGG
2501 TTTCCCTTCC ATAGATTGTG CCTTTCAGAA ATGCTGAGGT AGGTTTCCCA

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2551 TTTCTTACCT GTGATGTGTT TTACCCAGCA CCTCCGGACA CTCACCTTCA
 2601 GGACCTTAAT AAAATTATTC ACTTGGTAAG TGTTCAGTC TTTCTGATCA
 2651 CCCCAAGTAG CATGACTGAT CTGCAATTTA AAATTCCTGT GATCTGTAAA
 2701 AAAAAA

BLAST Results

Entry AC007225 from database EMBLNEW:
 Homo sapiens chromosome 16 clone 480G7, WORKING DRAFT SEQUENCE, 38
 unordered pieces.
 Score = 1081, P = 2.8e-217, identities = 219/221
 13 exons

Entry HS015146 from database EMBL:
 human STS WI-8848.
 Score = 2033, P = 2.9e-87, identities = 425/436

Medline entries

96327632:
 Genetic mapping and embryonic expression of a novel, maternally
 transcribed gene Mem3.

97258867:
 Endosome to Golgi retrieval of the vacuolar protein sorting receptor,
 Vps10p, requires the function of the
 VPS29, VPS30, and VPS35 gene products.

92360909:
 Alternative pathways for the sorting of soluble vacuolar proteins in
 yeast: a vps35 null mutant missorts and
 secretes only a subset of vacuolar hydrolases.

10198044:
 Distinct Domains within Vps35p Mediate the Retrieval of Two Different
 Cargo Proteins from the Yeast
 Prevacuolar/Endosomal Compartment

Peptide information for frame 3

ORF from 48 bp to 2435 bp; peptide length: 796
 Category: strong similarity to known protein
 Classification: unset

1 MPTTQOSPQD EQEKLDEAI QAVKVQSFQM KRCLDKNKLM DSLKHASNML
 51 GELRTSMLSP KSYELYMAI SDELHYLEVY LTDEFAGRK VADLYELVQY
 101 AGNIIPRLYL LITVGVVYVK SFPQSRKDIL KDLVEMCRGV QHPLRGLFLR
 151 NYLLQCTRNI LPDEGEPTDE ETTGDISDSM DFVLLNFAEM NKLWVRMQHQ
 201 GHSRDREKRE RERQELRILV GTNLVRLSQL EGVNVERYKQ IVLTGILEQV
 251 VNCRDALAQE YLMECIIQVF PDEFHLQTLN PFLRACAEH QNVNVKNIII
 301 ALIDRLALFA HREDGPGIPA DIKLFDFISQ QVATVQSRQ DMPSQDVVSL
 351 QVSLINLAMK CYPDRVDYVD KVLETTVEIF NKLNLHAIAT SSAVSKELTR
 401 LLKIPVDTYN NLTVLKLKH FHPLFEYFDY ESRKSMSCYV LSNVLDYNTE
 451 IVSQDQVDSI MNLVSTLIQD QPDQPVDPD PEDFADEQSL VGRFIHLLRS
 501 EDPDQOYLIL NTARKHFGAG GNQIRFTLP PLVFAAYQLA FRYKENSQVD
 551 DKWEKKCKQI FSFAHQITISA LIKAELAELP LRLFLQGALA AGEIGFENHE
 601 TVAYEFMSQA FSLYEDEISD SKAQLAAITL IIGTFERMKC FSEENHEPLR
 651 TQCALAASKL LKKPDQGRAV STCAHLFWG RNTDKNGEEL HGGKRVMECL
 701 KKALKIANQC MDPQLQVQLF IEILNRYIYF YEKENDAVTI QVLNQLIQKI
 751 REDLPNLESS EETEQINKHF HNTLEHLRLR RESPESEGPI YEGIL

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_72p16, frame 3

TREMBL:AF024504_3 gene: "A_TM017A05.7"; Arabidopsis thaliana BAC
 TM017A05., N = 2, Score = 927, P = 1.9e-162

PIR:S56936 vacuolar protein-sorting protein VPS35 - yeast
(Saccharomyces cerevisiae), N = 3, Score = 826, P = 1.5e-116

TREMBL:MM47024_1 gene: "Mem3"; product: "MEM3"; Mus musculus
maternal-embryonic 3 (Mem3) mRNA, complete cds., N = 1, Score = 3376, P
= 0

TREMBL:S42186_1 gene: "VPS35"; product: "Vps35p"; VPS35=vacuolar
protein sorting [Saccharomyces cerevisiae=yeast, Genomic, 3790 nt], N =
3, Score = 813, P = 4.4e-115

>TREMBL:MM47024_1 gene: "Mem3"; product: "MEM3"; Mus musculus
maternal-embryonic 3 (Mem3) mRNA, complete cds.
Length = 754

HSPs:

Score = 3376 (506.5 bits), Expect = 0.0e+00, P = 0.0e+00
Identities = 666/721 (92%), Positives = 682/721 (94%)

```
Query:      78 EVYLTDEFAGKGRKADLYELVQYAGNIIPRLYLLITVGVVYVKSFPQSRKDILKDLVEMC 137
              +VYLTDEFAGK ++ADLYELVQY+GNIIPRLYLLITVGVVYVKSFPQSRKDILKDLVEMC
Sbjct:      34 KVYLTDEFAGKERLADLYELVQYSGNIIPRLYLLITVGVVYVKSFPQSRKDILKDLVEMC 93

Query:     138 RGQVHPLRGLFLRNYLLQCTRNILPDEGEPTDEETTGDISDSMDVLLNFAEMNKLWVRM 197
              RGQVHPLRGLFLRNYLLQCTRNILPDEGEPTDEETTGDISDSMDVLLNFAEMNKLWVRM
Sbjct:      94 RGQVHPLRGLFLRNYLLQCTRNILPDEGEPTDEETTGDISDSMDVLLNFAEMNKLWVRM 153

Query:     198 QHQGHSRDREKRERERQELRILVGTNLVRLSQLEG-VNVERYKQIVLTGILEQVNVNCRDA 256
              QHQGHSRDREKRERERQELRILVGTNLV +QIVLTGILEQVNVNCRDA
Sbjct:     154 QHQGHSRDREKRERERQELRILVGTNLVALTLVSWRCKCGTLQIVLTGILEQVNVNCRDA 213

Query:     257 LAQEYLMECIIQVFPDEFHLQTLNPFRLRACAEHQNVNVKNIIIALIDRLALFAHREDGP 316
              LAQE MECIIQVFPDEFHLQTLNPFRLRACAEHQNVNVKNIIIALIDRLALFAHRE P
Sbjct:     214 LAQEISMECIIQVFPDEFHLQTLNPFRLRACAEHQNVNVKNIIIALIDRLALFAHREMEP 273

Query:     317 GIPADIKLFDIFSQQVATVIQSRQDMPSEDVVSQVSLINLAMKCYPDVVDYVDKVLETT 376
              GIPA++KLFDIFSQQVATVIQSR+DMPSEDVVSQVSLINLAMKCYPDVVDYVDKVLETT
Sbjct:     274 GIPAEKLKFDIFSQQVATVIQSRDMPSEDVVSQVSLINLAMKCYPDVVDYVDKVLETT 333

Query:     377 VEIFNKLNLHIATSSAVSKELTRLLKIPVDYNNILTVLKLKHFHPLFEYFDYESR--K 434
              VEIFNKLNLHIATSSAVSKELTRLLKIPVDYNNILTVLKLKHFHPLFEYFDYES K
Sbjct:     334 VEIFNKLNLHIATSSAVSKELTRLLKIPVDYNNILTVLKLKHFHPLFEYFDYESSPGK 393

Query:     435 SMSCYVLSNVLDYNTIEIVSQDQVDSIMNLVSTLIQDQDPQVEDPDPEDFADEQSLVGRF 494
              SMSCYVLSNVLDYNTIEIVSQDQVDSIMNLVSTLIQDQDPQVEDPDPEDFADEQSLVGRF
Sbjct:     394 SMSCYVLSNVLDYNTIEIVSQDQVDSIMNLVSTLIQDQDPQVEDPDPEDFADEQSLVGRF 453

Query:     495 IHLLRSEDPPDQYLIILNTARKHFGAGGNQIRFTLPPLVFAAYQLAFRYKENSKVDDKWE 554
              IHLLRS+DPDQYLIILNTARKHFGAGGNQIRFTLPPLVFAAYQLAFRYKENS +
Sbjct:     454 IHLLRSDPDQYLIILNTARKHFGAGGNQIRFTLPPLVFAAYQLAFRYKENS KWMTSKG 513

Query:     555 KKQKQIFSFHQITISALIKAEALPLRLFLQGALAAGEIGFENHETVAYEFMSQAFSLY 614
              + ++ F HQTISALIKAEALPLRLFLQGALAAGEIGFENHETVAYEFMSQAFSLY
Sbjct:     514 RNARRYFHLPHQTISALIKAEALPLRLFLQGALAAGEIGFENHETVAYEFMSQAFSLY 573

Query:     615 EDEISDSKAQLAAITLIIGTFERMKCFSEENHEPLRTQCALAASKLLKKPDQGRAVSTCA 674
              EDEISDSKAQLAAITLIIGTFERMKCFSEENHEPLRT+CALAASKLLKKPDQ C
Sbjct:     574 EDEISDSKAQLAAITLIIGTFERMKCFSEENHEPLRTECALAASKLLKKPDQAEREHMC 633

Query:     675 HLFWSGRNTDKNGEELHGGKRVMECLKKALKIANQCMDPSLQVQLFIEILNRYIYFYEKE 734
              L WSGRNTDKNGEELHGGKRVMECLKKALKIANQCMDPSLQVQLFIEILNRYIYFYEKE
Sbjct:     634 SL-WSGRNTDKNGEELHGGKRVMECLKKALKIANQCMDPSLQVQLFIEILNRYIYFYEKE 692

Query:     735 NDAVTIQLVNLQIQKIREDLNPLESSEETE QINKHFHNTLEHLRLRRESPESSEGPYIEGL 794
              NDAVTIQLVNLQIQKIREDLNPLESSEETE QINKHFHNTLEHLR RRESPESSEGPYIEGL
Sbjct:     693 NDAVTIQLVNLQIQKIREDLNPLESSEETE QINKHFHNTLEHLRTRRESPESSEGPYIEGL 752

Query:     795 IL 796
              IL
Sbjct:     753 IL 754
```

Pedant information for DKFZphtes3_72p16, frame 3

Report for DKFZphtes3_72p16.3

[LENGTH] 796

SEO IEILNRYIIFYEKENDAVTIOVLNQLIQKIREDLPNLESSEETEQINKHFHNTLEHLRLR

```

SEG      .....
PRD      hhhhhhhhhhhccccceeeehhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhh
MEM      .....

SEG      RESPESEGPIYEGIL
SEG      .....
PRD      hhccccccccceeeccc
MEM      .....

```

(No Prosite data available for DKFZphtes3_72p16.3)

(No Pfam data available for DKFZphtes3_72p16.3)

DKFZphtes3_7b22

group: cell structure and motility

DKFZphtes3_7b22 encodes a novel 443 amino acid protein with weak similarity to paramyosins.

The novel protein is related to paramyosin, a major structural component of thick filaments and invertebrate muscle. Paramyosins are promising antigens for immunization against several parasites, such as *Schistosoma mansoni*.

The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamic.

similarity to paramyosins

complete cDNA, complete cds, few EST hits

Sequenced by BMFZ

Locus: /map="3"

Insert length: 2291 bp

Poly A stretch at pos. 2241, polyadenylation signal at pos. 2213

```
1  GGAAGAAAGG CTAGCGGGCG TTGGCCGTAT GTGGGTGTCT TGAGGCAGTT
51  TTTCAGTTCT TTCATTTACC AAAGTGACAT GCACCTACTA GGTGCCAGGT
101 GTTTAGACGT ACATACAACC CTCTGCAAAA TCTTTCAGTG TAGTCCTCTG
151 TATGAAAGT TTCCAGCCAA GAATTGCCAC TGCACCTGAG ATAAGGGGGA
201 TCCTGGCCAT TAAGGAAACC TTGCCTTCGA AACTGAGCCG TGAGGAACTA
251 TACAAAATGG GAAATTGGGA CAAATCCCAG TGGCTCATGA CACTAAGAAAG
301 TAAAATTACG AACTCACTGA GCTGGAAGTC ATTCAACGGG AATTGAATAG
351 GTAACCTGCAC TTTTGTGAGA TTATAAATAT ACCACGGAGG GTAACGAAGC
401 TACAGAAAGAA TGGAAAGAAG CAGCCTGGAA GACTCAAACC TTCTCCAAA
451 AGTTTGGCAT TCTGAGATGA CGGTGTCAGT GACAGGCGAA CCACCTAGTA
501 CCGTAGAAGA AGAAGGAATA CCTAAAGAAA CAGACATAGA AATCATCCCA
551 GAAATCCCGG AAACCTCTAG GCCACTGTCC CTTCCAGATG TGCTGAGGAT
601 CTCGGCAGTT CTGGAGGACA CCACAGACCA GCTCTCTATT CTGAAGTACA
651 TCATGCCCGT TCAGTACGAA GGGAGACAGA GCATCTGCGT GAAAAGCAGA
701 GAAATGAATC TAAAGGAAGC GAATCTAGAC AAACCTCCAA TGGCCTCAAC
751 AATCACAATA ATTCCAGTGC CGTTAATAAC TGAGGAAGGA CCCAACTTGC
801 CAGAAATCAG ACACAGAGGC CGGTTGCGTG TGGAGTTTAA CAAAATGCAG
851 GATCTTGCTC TCAAAAAACC TACAAGGCAG ACCATCATGA CTACGGAGAC
901 ACTGAAGAAA ATTCAGATTG ATAGGCAGTT TTTGAGCGAT GTGATTGCAG
951 ATACCATTAA GGAGTTGCAA GATTCGGCCA CTTACAACAG TCTCTGCAA
1001 GCTTTGAGCA AAGAGAGGGA AAACAAAATG CATTTCTATG ACATCATTGC
1051 CAGGGAGGAA AAAGGAAGAA AACAGATAAT ATCACTTCAA AAACAGCTAA
1101 TTAATGTCAA AAAGGAATGG CAATTTGAAG TCCAGAGTCA GAATGAGTAT
1151 ATTGCTAACC TCAAGGACCA ACTGCAAGAG ATGAAGGCAA AATCCAACCT
1201 GGAGAATCGC TACATGAAAA CCAATACCGA GCTGCAGATT GCCCAGACCC
1251 AGAAAAAGTG TAACAGAACA GAGGAACCTT TGGTGGAAGA GATTGAGAAA
1301 CTCAGGATGA AAACCGAAGA AGAGGCCCGG ACTCATACAG AGATTGAAAT
1351 GTTCCTTAGA AAGGAGCAGC AGAACTTGA GGAGAGGCTG GAGTTCTGGA
1401 TGGAGAAATA CGATAAGGAC ACAGAAATGA AACAGAATGA ACTAAATGCT
1451 CTCAAAGCCA CAAAGGCCAG TGAATTAGCA CACCTTCAAG ACCTGGCAAA
1501 GATGATAAGA GAGTATGAAC AGGTCATCAT TGAAGATCGT ATAGAAAAGG
1551 AGAGGAGCAA GAAGAAGGTA AAACAGGATC TCTTGGAATT AAAGAGCGTT
1601 ATAAAGCTCC AGGCCCTGGT GCGAGGCACT ATGATACGGA GAGAAATTGG
1651 TGGTTTCAAG ATGCCTAAG ACAAGTTGA TAGCAAGGAT TCAAAAGGCA
1701 AAGGTAAAGG CAAGGATAAG AGGAGAGGCA AGAAGAAGTG ACCAAGTTCT
1751 CTTTTGTGTT TTCTGCTGGT ATTCTGGAGG TGGGAAGGAC TTGGAGAGTT
1801 AAGAAACACC TGGTACCTCA AAGATGACTC ATCTACAGGT TGTTCCTAT
1851 TGAGACTTTC CCAGGGAAGC CTGATTTTAC TTTGCCTGTT AATTTCACCT
1901 TGCCTGTTAG GTGGGTTTTT AAACCCTGAT TTAGGATTAC ACCATTGACT
1951 GATTGGCTTC TCATACCTTG CTGGGAAGAA GTTTCTAGTA GTCTGTGAA
2001 GATTCATTCT TCTTGCTCTT TCTCAGCAGA ACAAGGAGT TCACTGGCTT
2051 AGCTACAGTG ACGCATTGAA ACTTGAGTAA TTCCTGTAAT GTCAGATTTT
2101 GATTTTACCC AATTGTCTG TAGTGAAAAA ACTCTTATGA GCAAAAGTAT
2151 TCAGTAGGAA TTACAATATG ATGTTATTAG CTGTCCAGCA TAATATATAC
2201 ACAGCAAAGT TTTAATAAAT GTTGGTTCCT GCCTGCCTTT TAAAAAATAA
2251 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA A
```

BLAST Results

Entry G36731 from database EMBL:
SHGC-52923 Human Homo sapiens STS cDNA.

Score = 2262, P = 1.3e-97, identities = 462/468

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 410 bp to 1738 bp; peptide length: 443
Category: similarity to known protein

```

1 MEEDSLEDN LPPKVHSEM TVSVTGEPPS TVEEGIPKE TDIEIPEIP
51 ETLEPLSLPD VLRISAVLED TTDQLSILNY IMPVQYEGRO SICVKSREM
101 LEGTNLDKLP MASTITKIPS PLITEEGPNL PEIRHRGRFA VEFNKMQLV
151 FKKPTRQTIM TTETLKKIQI DRQFFSDVIA DTIKELQDSA TYNLLQALS
201 KERENKMHFY DIIAREEKGR KQIISLQKQL INVKKEWQFE VQSNEYIAN
251 LKDQLQEMKA KSNLENRYMK TTELQIAQT QKKNRTEEL LVEEIEKLRM
301 KTEEEARTH EITEMFLRKEQ QKLEERLEFW MEKYDKDTEM QNELNALK
351 TKASDLAHLQ DLAKMIREYE QVIIEDRIEK ERSKKVKQD LLELKSIVKL
401 QAWWRGTMIR REIGGFKMPK DKVDSKDSKG KGKGDKRRG KKK

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_7b22, frame 2

SWISSPROT:MYSP_BRUMA PARAMYOSIN., N = 1, Score = 158, P = 5.8e-08

PIR:A44972 paramyosin - nematode (*Dirofilaria immitis*) (fragment), N = 1, Score = 157, P = 7.1e-08

SWISSPROT:MYSP_ONCVO PARAMYOSIN., N = 1, Score = 157, P = 7.4e-08

PIR:S52537 emm L 15 protein - *Streptococcus pyogenes*, N = 1, Score = 151, P = 8.6e-08

>SWISSPROT:MYSP_BRUMA PARAMYOSIN.
Length = 880

HSPs:

Score = 158 (23.7 bits), Expect = 5.8e-08, P = 5.8e-08
Identities = 66/259 (25%), Positives = 125/259 (48%)

```

Query: 142 EFNKMQLVFKKPTRQTIMTTETLKKIQIDRQFFSDVIADTIKELQDSATYNLLQALS 201
      + K + L K R T E K++ + +D +A + LQ A N LL+ +
Sbjct: 169 QLKDKHLAEKAAERFEAQTVELSNKVEDLNRHVND-LAQQRQLQ--AENNDLLKEIHD 225

```

```

Query: 202 ER---ENKMHF-YDIIAREEKGRKQIISLQKQLINVKKEWQFEVQSNEYIANLKDQLQE 257
      ++ +N H Y + + E+ R+++ ++ + + +VQ + + + D+ E
Sbjct: 226 QKVQLDNLQHVKYQLAQQLLEEARRLEDAERERSQLQAQLH-QVQLELDSVRTALDE--E 282

```

```

Query: 258 MKAASNLENRYMKTTELQIAQTQKKNRTEELLVEEIEKLRMKT-EEEARHTTEIEMFL 316
      A++ E++ NTE I Q + K + L EE+E LR K +++A +IE+ L
Sbjct: 283 SAARAEAEHKLALANTE--ITQWKSQFDEVALHHEEVEDLRKKMLQKQAEYEEQIEIML 340

```

```

Query: 317 RKEQQ--KLEERLEFWMEKYDKDTEMKQNELNALKATKASDLAHLQDLAKMIREYEQVII 374
      +K Q K + RL+ +E D E QN + L+ K + L K + E + I
Sbjct: 341 QKISQLEKAKSRLQSEVEVLIVDLEKAQNTIAILERAK-----EQLEKTVNELKVRID 393

```

```

Query: 375 EDRIEKERSKKVKQDLELKSIVKL 400
      E +E E ++++ + L EL+ + L
Sbjct: 394 ELTVELEAAQREARAALAEQLKLN 419

```

Score = 118 (17.7 bits), Expect = 1.3e-03, P = 1.3e-03
Identities = 54/231 (23%), Positives = 108/231 (46%)

```

Query: 181 DTIKELQDSATYNLLQ----ALSKERENKMHFYDIIAREEKGRKQIISLQKQLINVKK 235
      D +KE+ D LQ L+++ E + RE + Q+ +Q +L +V+
Sbjct: 218 DLLKEIHQKVQLDNLQHVKYQLAQQLLEEARRLEDAERERSQLQAQLHQVQLELDSVRT 277

```

Query: 236 EWQFE--VQSQNEY-IANLKDQLQEMKAKSNLENRYMKTNTE-LQIAQTQKKCNRTTELL 291
 E +++ E+ +A ++ + K+K + E E L+ QK+ E++
 Sbjct: 278 ALDEESAARAEAEHKLALANTEITQWKSQFDEVALHHEEVEDLRKKMLQKQAEYEEQIE 337

Query: 292 VEEIEKLRMKTTEEEARTHTEIEMF---LRKEQQKLE--ERLEFWMEKYDKDTEMKQNELN 346
 + ++K+ + ++R +E+E+ L K Q + ER + +EK + +++ +EL
 Sbjct: 338 IM-LQKISQLEKAKSRLQSEVEVLIVDLEKAQNTIAILERAKEQLEKTVNELKVRIDELT 396

Query: 347 A-LKATKASDLAHLQDLAKMIREYEQVIEDRIEKERSKKKVKQDLELKSVI 398
 L+A + A L +L K+ YE+ + E + R KK++ DL E K +
 Sbjct: 397 VELEAAQREARAALAEQKLKNLYEKAV-EQKEALARENKKLQDDLHEAKEAL 448

Score = 107 (16.1 bits), Expect = 2.1e-02, P = 2.1e-02
 Identities = 49/279 (17%), Positives = 124/279 (44%)

Query: 123 ITEEGPNLPEIRHRGRFAV-EFNKMODLVFKKPTRQTIMTTETLKKIQIDRQFFSDVIAD 181
 I E L + R A+ E K+++L K ++ + E KK+Q D + +AD
 Sbjct: 392 IDELTVELEAAQREARAALAEQKLKNLYEKAVEQKEALAREN-KKLQDDLHEAKEALAD 450

Query: 182 TIKELQDSATYNSLLQALSKERENKMHFYDIIAREEKGRKQ--IISLQQLINVKKEWQF 239
 ++L + N+ L +E + + + R+ + R Q + LQ+ I +++ Q
 Sbjct: 451 ANRKLHIELDLENARLAGEIRELQTALKESEAARRDAENRAQRALAEQLQRIEMERRLQE 510

Query: 240 EVQSQNEYIANLKDQLQEMKAKSNLENRYMKTNTELOIAQTQKKCNRTTE-ELLVEEIEKL 298
 + + N++ ++ + A L + + E+ + + + E E+ V+ + +
 Sbjct: 511 KEEEMEALRKNMQFEIDRLTAA--LADAEARMKAEISRLKKKYQAEIAELEMTVDNLNRA 568

Query: 299 RMKTEEEARTHTEIEMFLRKEQQKLEERLEFWMEKYDKDTEMKQNELNALKATKASDLAH 358
 ++ ++ + +E L+ + + +L+ +++Y + Q +++AL A + +
 Sbjct: 569 NIEAQTMIKKQSEQLKILQASLEDTRQLQTLQDY---ALAQKVSALSA-ELEECKV 623

Query: 359 LQDLAKMIREYEQVIEDRIEKERSKKKVKQDLELKSVIKQ 401
 D A R+ ++ +E+ + V +L +K+ ++ +
 Sbjct: 624 ALDNAIRARKQAEIDLEEANGRITDLVSVNNNLTAIKNKLETE 666

Pedant information for DKFZphtes3_7b22, frame 2

Report for DKFZphtes3_7b22.2

[LENGTH] 443
 [MW] 51917.95
 [pI] 6.18
 [HOMOL] PIR:S28589 trichohyalin - rabbit 2e-08
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 7e-07
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 7e-07
 [FUNCAT] 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1322] 5e-06
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 11.01 stress response [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR141c] 1e-05
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR216c] 3e-05
 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 6e-05
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w] 6e-05
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YER008c] 1e-04
 [FUNCAT] 08.16 extracellular transport [S. cerevisiae, YER008c] 1e-04
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YER008c] 1e-04
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YDR356w] 2e-04
 [FUNCAT] 08.01 nuclear transport [S. cerevisiae, YDL207w] 4e-04
 [FUNCAT] 04.07 rna transport [S. cerevisiae, YDL207w] 4e-04
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YKL201c] 5e-04
 [EC] 3.6.1.32 Myosin ATPase 3e-08
 [PIRKW] phosphotransferase 6e-06
 [PIRKW] citrulline 8e-06
 [PIRKW] tandem repeat 1e-07
 [PIRKW] heart 6e-06
 [PIRKW] polymorphism 4e-06
 [PIRKW] serine/threonine-specific protein kinase 6e-06
 [PIRKW] DNA binding 8e-08

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[PIRKW]      muscle contraction 1e-07
[PIRKW]      actin binding 3e-08
[PIRKW]      ATP 3e-08
[PIRKW]      thick filament 1e-07
[PIRKW]      phosphoprotein 3e-08
[PIRKW]      glycoprotein 4e-06
[PIRKW]      skeletal muscle 1e-07
[PIRKW]      calcium binding 8e-06
[PIRKW]      alternative splicing 3e-08
[PIRKW]      coiled coil 3e-08
[PIRKW]      P-loop 3e-08
[PIRKW]      heptad repeat 4e-06
[PIRKW]      methylated amino acid 3e-08
[PIRKW]      basement membrane 4e-06
[PIRKW]      cardiac muscle 6e-06
[PIRKW]      extracellular matrix 4e-06
[PIRKW]      hydrolase 3e-08
[PIRKW]      membrane protein 4e-06
[PIRKW]      EF hand 8e-06
[PIRKW]      cytoskeleton 8e-06
[PIRKW]      hair 8e-06
[SUPFAM]     myosin heavy chain 3e-08
[SUPFAM]     unassigned Ser/Thr or Tyr-specific protein kinases 6e-06
[SUPFAM]     calmodulin repeat homology 8e-06
[SUPFAM]     myosin motor domain homology 3e-08
[SUPFAM]     trichohyalin 8e-06
[SUPFAM]     protein kinase homology 6e-06
[PROSITE]    AMIDATION 2
[PROSITE]    CAMP_PHOSPHO_SITE 1
[PROSITE]    CK2_PHOSPHO_SITE 12
[PROSITE]    TYR_PHOSPHO_SITE 2
[PROSITE]    PKC_PHOSPHO_SITE 4
[PROSITE]    ASN_GLYCOSYLATION 1
[KW]         All_Alpha
[KW]         LOW_COMPLEXITY 10.61 %

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```

SEQ  MEEDSLEDSNLPKPVHSEMTVSVTGEPSTVEEEGIPKETDIEIIPETLEPLSLPD
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxx.
PRD  cccccccccccccccccceeeccccccccceeeccccceeecccccccccccccc

SEQ  VLRISAVLEDTTDQLSILNYIMPVQYEGRQSIKVSREMNLGNTDKLPMASTITKIPS
SEG  .....
PRD  chhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  PLITEEGPNLPEIRHRGRFAVEFNKMQDLVFKKPTRQTIMTTETLKKIQIDRQFFSDVIA
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  DTIKELQDSATYNSLLQALSKERENKMHFYDIIAREEKGRKQIISLQKQLINVKKEWQFE
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  VQSQNEYIANLKDQLQEMKAKSNLENRYMKTNTLQIAQTQKKCNRTTEELLVEEIEKLRM
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  KTEEEARTHTEIEMFLRKEQQKLEERLEFWMKEYDKDTEMKQNELNALKATKASDLAHLQ
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  DLAKMIREYEQVIIEDRIEKERSKKKVKQDLLELKSIVIKLQAWRGTMIRREIGGFKMPK
SEG  .....x
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ  DKVDSKDSKGGKGGKDKRRGKKK
SEG  xxxxxxxxxxxxxxxxxxxxxxxxx
PRD  ccccccccccccccccccccccc

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Prosites for DKFZphtes3_7b22.2

PS00001	285->289	ASN_GLYCOSYLATION	PDOC00001
PS00004	152->156	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00005	182->185	PKC_PHOSPHO_SITE	PDOC00005
PS00005	280->283	PKC_PHOSPHO_SITE	PDOC00005
PS00005	383->386	PKC_PHOSPHO_SITE	PDOC00005
PS00006	5->9	CK2_PHOSPHO_SITE	PDOC00006
PS00006	30->34	CK2_PHOSPHO_SITE	PDOC00006

PS00006	41->45	CK2_PHOSPHO_SITE	PDOC00006
PS00006	57->61	CK2_PHOSPHO_SITE	PDOC00006
PS00006	104->108	CK2_PHOSPHO_SITE	PDOC00006
PS00006	182->186	CK2_PHOSPHO_SITE	PDOC00006
PS00006	243->247	CK2_PHOSPHO_SITE	PDOC00006
PS00006	262->266	CK2_PHOSPHO_SITE	PDOC00006
PS00006	271->275	CK2_PHOSPHO_SITE	PDOC00006
PS00006	302->306	CK2_PHOSPHO_SITE	PDOC00006
PS00006	308->312	CK2_PHOSPHO_SITE	PDOC00006
PS00006	310->314	CK2_PHOSPHO_SITE	PDOC00006
PS00007	261->269	TYR_PHOSPHO_SITE	PDOC00007
PS00007	184->193	TYR_PHOSPHO_SITE	PDOC00007
PS00009	218->222	AMIDATION	PDOC00009
PS00009	439->443	AMIDATION	PDOC00009

(No Pfam data available for DKFZphtes3_7b22.2)

DKFZphtes3_7d17

group: testes derived

DKFZphtes3_7d17 encodes a novel 633 amino acid protein with weak similarity to human KIAA0454.

Pfam predicts a TNFR/NGFR cysteine-rich region.

No informative BLAST results; No predictive prosite or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to KIAA0454

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 3608 bp

Poly A stretch at pos. 3587, polyadenylation signal at pos. 3570

```
1 GGGGAAGTTAC GGC GAAGTCC ACCCAGCGTT TCTCAGGCAA TCTGAAGGCA
51 AATCCTGTTT AGACCCAGGC GAAGGTCCT GGTGACCCAG GCTCTCACCA
101 GCCAATTGTC CCTTGCCGTC CTCCTGAGGG TATCTGGAGC TTCAGTGCTG
151 TGTGCTCTTG GCCTCCACAC TGGGGATGCC ACTGACTCCC ACTGTCCAGG
201 GCTTCCAGTG GACTCTCCGA GGCCCTGATG TAGAACTTC CCCATTCGGT
251 GCACCAAGAG CAGCCTCACA TGGTGTGGGC CGACATCAAG AGCTGCCGAGA
301 TCCAACAGTC CCTGGCCCCA CCTTTCTGTC CACAAACGTC AGCATGGTGG
351 TATCTGCCGG CCCTTGGTCC GGTGAGAAGG CAGAGATGAA CATTCTAGAA
401 ATCAACAAGA AATCGCGCCC CCAGCTGGCA GAGAACAAC AGCAGTTCAG
451 AAACCTCAAA CAGAAATGTC TTGTAAC TCA AGTGGCCTAC TTCCTGGCCA
501 ACCGGCAAAA TAATTACGAC TATGAAGACT GCAAAGACCT CATAAAATCT
551 ATGCTGAGGG ATGAGCGGCT GCTCACAGAA GAGAAGCTTG CAGAGGAGCT
601 CGGGCAAGCT GAGGAGCTCA GGCAATATAA AGTCCTGGTT CACTCTCAGG
651 AACGAGAGCT GACCCAGTTA AGGGAGAAGT TACAGGAAGG GAGAGATGCC
701 TCCCGCTCAT TGAATCAGCA TCTCCAGGCC CTCCTCACTC CGGATGAGCC
751 GGACCACTCC CAGGACGCGG ACCTCCGAGA ACAGCTGGCT GAGGGATGTA
801 GGCTGGCACA GCACCTCGTC CAAAAGCTCA GCCCAGAAAA TGATGACGAT
851 GAGGATGAAG ATGTTAAAGT TGAGGAGGCT GAGAAAGTAC AGGAATTATA
901 TGCCCCCAGG GAGGTGCAGA AGGCTGAAGA AAAGGAAGTC CCTGAGGACT
951 CACTGGAGGA GTGTGCCATC ACTTGTTCAA ATAGCCACCA CCCTTGTGAG
1001 TCCAACCAGC CTTACGGGAA CACCAGAATC ACATTTGAGG AAGACCAAGT
1051 CGACTCAACT CTCATTGACT CATCCTCTCA TGATGAATGG TTGGATGCTG
1101 TATGCATTAT CCCAGAAAAT GAAAGTGATC ATGAGCAAGA GGAAGAAAAA
1151 GGGCCAGTGT CTCCCAGGAA TCTGCAGGAG TCTGAAGAGG AGGAAGCCCC
1201 CCAGGAGTCC TGGGATGAAG GTGATTGGAC TCTCTCAATT CCTCCTGACA
1251 TGTCTGCCTC ATACCACTCT GACAGGAGCA CCTTTCCTC AGTAGAGGAA
1301 CAGCAAGTCG GCTTGGCTCT TGACATAGGC AGACATTGGT GTGATCAAGT
1351 GAAAAAGGAG GACCAAGAGG CCACAAGTCC CAGGCTCAGC AGGGAGCTGC
1401 TGGATGAGAA AGAGCCTGAA GTCTTGCAAG ACTCACTGGA TAGATTTTAT
1451 TCAACTCCTT TTGAGTACCT GGAAGTGCCT GACTTATGCC AGCCCTACAG
1501 AAGTGACTTT TATCATTGTC AGGAACAACA CCTTGGCTTG GCTCTTGACT
1551 TGGACAGAAT GAAAAAGGAC CAAGAAGAGG AAGAAGACCA AGGCCACCA
1601 TGCCCCAGGC TCAGCAGAGA GCTGCCGGAG GTAGTAGAGC CTGAGGACTT
1651 GCAGGACTCA CTGGATAGAT GGTATTGAC TCCCTTTCAGT TATCCAGAAC
1701 TGCCGTGATTC ATGCCAGCCC TACGGAAGTT GCTTTTACTC ATTGGAGGAA
1751 GAACACGTTG GCTTTTCTCT TGACGTGGAT GAAATTGAAA AGTACCAAGA
1801 AGGGGAAGAA GATCAAAAGC CACCATGCCC CAGGCTCAAC GAGGTGCTGA
1851 TGGAAAGCAGA AGAGCCTGAA GTCTTGCAAG ACTCACTGGA TAGATGTTAT
1901 TCGACTACTT CAACTTACTT TCAACTACAT GCCTCATTC AGCAGTACAG
1951 AAGTGCCCTT TACTCATTTG AGGAACAGGA CGTCAGCTTG GCCCTTGACG
2001 TGGACAATAG GTTTTTTACT TTGACAGTGA TAAGGCACCA CCTGGCCTTC
2051 CAGATGGGAG TCATATTCCC AACTAAGCA GCCCTTACTA AGCTGAGAGA
2101 TGTCATTGCT GCAGGCAGGA CCTATAGGCA CATGTAGGTT TGAATGAAAC
2151 TGATAGTTCCC TTTGGAAGCC CAGTCATAGG ATGGGAAAGT GGGCATGGCT
2201 CTATTCTTAT TCTCAGACCA TGCCAGTGGC CACCTGTGCT CAGTCTGAAG
2251 ACGTTGGACC CAAGTTAGGT GTGACACGTT CACACGACTA TGTAGCACAT
2301 GCCGGGAGTG ATCTGCCAGA CATTCTAATT TGAACAGAT ATCTCTGGGT
2351 AGCTACAAAG TTCTCAGGG GTTTTCAATTT GCAGGCATGT CTCTGAGCTT
2401 CTATACCTGC TCAAGGTCAG TGTCATCTTT GTGTTTAGCT CATCCAAAGG
2451 TGTTACCCTG GTTTCATTGA ACCTAACCCC ATTCTTTGTA TCTTCAGTGT
2501 TGGTTTGTTT TGCTGATCC ATCTGTAACA CAGGAGGGAT CCTTGGCTGA
2551 GGATTGTATT TCAGAACCAC TGACTGCTCT TGACAGTTGT TAACCCACTA
2601 GGCTCCTTTG AGTAGAGAAG CCATAGTCCT TCAGCCTCCA ATTGATATCA
2651 ATACTTAGGA AGACCACAGC TAGACGGACA AACAGCATTG GGAGGCCTTA
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2701 GTCCTGCTCC TTTCAATTCC ATCCTGTAAA GAACAGGAGT CAGGAGCCGC
2751 TGGCAAGAGA CAGCATGTCA CCTGGGACTC TGCCAGTGCA GAATATGAAC
2801 AATGCCATGT TCTTGCAGAA AATGCTTAGC CTGAGTTTCA TAGGAGGTAA
2851 TCACCAGACA ACTGCAGAA GTAGAACT GAGCAGGACA ACTGACCTGT
2901 CTCCTTCACA CAGTCCACGT CACCACGAAT CACACAACAA AAAGGAGGAG
2951 AGATATTTTG GGTTCAGAAG AAGTAAATGA TAATGTAGCT ACATTCTTTT
3001 AGTTATTTTG AACCCCAAT ATTTCTCAT CTTTTTGTG TTGTCATTGA
3051 TTTTGGTGAC ATGGACTTGT TTGTAGAGGA CAGGTGAGCT GTCTGGCTCA
3101 ATGGTCTACA TTCTGAAGTT GTCTGAAAAT GTCTTCATGA TTAAATTCAG
3151 CCTAACGTT TCATCAAGAA CACTACAGAG TCGATACTGT GAGTTTCCAA
3201 CCTCAGCCCA TCTGTGGGCA GAGAAGGTCT AGTTTGTCCA TCAGCATTAT
3251 CATGATATCA GCACTGGTTA CTTGGTTAAG GAGGGGTCTA GGAGATCTGT
3301 CCCTTTTAGA GACACCTTAC TTATGATGAA GTATTGGGA GAGTGGTTT
3351 TCAAAGTAGA AATGTCCTGT ATTCCAGTGA TCATCCTCTA AACGTTTTAT
3401 CATTATTATA TCATCCCTGC CTGTGTCTAT TATTATATTC ATATCTCTAC
3451 GCTGGAAATT TGCTGCCTCA ATGTTTACTG TGCCTTGTG TTTGCTAGTG
3501 TGTGTGTTG AAAAAAAAC ATTCTCTGCC TGAGTTTAA TTTTGTCCA
3551 AAGTTATTTT AATCTATACA ATTA AAAACT TTTGCCTATC AAAAAAAAC
3601 AAAAAAAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 176 bp to 2074 bp; peptide length: 633
 Category: similarity to known protein

```

1  MPLTPTVQGF QWTLRGPDVE TSPFGAPRAA SHGVGRHQEL RDPTVPGPTS
51  SATNVSMVVS AGPWSGEKAE MNILEINKKS RPQLAENKQO FRNLKQKCLV
101  TQVAYFLANR QNNYDYEDCK DLIKSMRLRDE RLLTEEKLA E LGQAEELRQ
151  YKVLVHSQER ELTQLREKLO EGRDASRSLN QHLOALLTPD EPDNSQGRDL
201  REQLAEGCRL AQHLVQKLSP ENDDDEDEDV KVEEAQVQOE LYAPREVQKA
251  EEKEVPEDSL EECAITCSNS HHPCESNQPY GNTRITFEED QVDSTLIDSS
301  SHDEWLDAVC IIPENESDHE QEEKEGPVSP RNLQSEEEEE APQESWDEGD
351  WTLSIPPDM SASYQSDRSTF HSVEEQVGL ALDIGRHWCD QVKKEDQEAT
401  SPRLSRELLD EKEPEVLQDS LDRFYSTPFE YLELPDLCPQ YRSDFYSLQE
451  QHLGLALDLD RMKKDQEEEE DQGPPCPRLS RELPEVVEPE DLQDSLDRWY
501  STPFSPYELP DSCQPYGSCF YSLEEEHVGF SLDVDEIEKY QEGEEDQKPP
551  CPRLNEVLME AEEPEVLQDS LDRCYSTTST YFQLHASFQQ YRSFYFEE
601  QDVSLALDLD NRFFTLTVIR HHLAFQMGVI FPH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_7d17, frame 2

PIR:T00069 hypothetical protein KIAA0454 - human (fragment), N = 1,
 Score = 199, P = 1e-11

PIR:A45592 liver stage antigen LSA-1 - Plasmodium falciparum, N = 1,
 Score = 158, P = 2.7e-07

>PIR:T00069 hypothetical protein KIAA0454 - human (fragment)
 Length = 1,882

HSPs:

Score = 199 (29.9 bits), Expect = 1.0e-11, P = 1.0e-11
 Identities = 74/261 (28%), Positives = 122/261 (46%)

Query: 117 EDCKDLIKSMRLDERLLT---EEKLAELGQAEELRQYKVLVHSQERELTQLREKLQEG 172
 +D + LI+ + + E L EEKLAEL A +Y L+ Q REL+ LR+K++EG
 Sbjct: 964 KDLESILQRVSQLAQLPKNGLEEKLAELRSASWPGKYDSLQDQARELSYLRQKIREG 1023

Query: 173 RDASRSLNQH-----LQALLTPDEPDNSQGRDLREQLAEGCRLAQHLVQKLSPENDDD 225
 R + +H + LL ++ D G+ REQLA+G +L + L KLS ++
 Sbjct: 1024 RGICYLITRHA KDTVKS FEDLLRSNDI DYLLGQS FREQLAQGSQ LTERLTSKLSTKD HKS 1083

Query: 226 EDEDVKVEEA EK VQELYAPREVQKAE EK-EVPEDSLEEC AITCSNSHHPCESNQPYGNTR 284
 E + +E L RE+Q+ E+ EV + L+ ++T S+SH +S++ +T
 Sbjct: 1084 EK DQAGLEPLA----LRLSRELQEKEKVIEVLQAKLDARSLTPSSSHALSDSHRSPSSTS 1139

Query: 285 ITFEEDQV--DSTLIDSSSHDEWLD A VCIIPENESDHEQE EEEKGPVSPRNLQESEEEEEAP 342
 +E + D ++ +H E A P + +S + S + A
 Sbjct: 1140 FLSDELEACSDMDIVSEYTHYEEKKAS---PSHSDSIHHSSHS AVLSKSPSSTSASQ GAK 1196

Query: 343 QESWDEGDWTL SIPPDM SASYQSDRSTFH 371
 ES + +L P + S FH
 Sbjct: 1197 AES-NSNPISLPTPQNTPK EANAQAHSGFH 1224

Score = 89 (13.4 bits), Expect = 1.1e-01, P = 1.0e-01
 Identities = 35/89 (39%), Positives = 44/89 (49%)

Query: 464 KDQEEEEEDQG---PPCPRLSRELPEVVEP-EDLQDSLDRWYSTPFSYP ELPDSCQ-PYGS 518
 KD + E+DQ P RLSREL E + E LQ LD TP S L DS + P +
 Sbjct: 1079 KDHKSEKDQAGLEPLALRLSRELQEKEKVIEVLQAKLDARSLTPSSSHALSDSHRSPSSTS 1138

Query: 519 CFYSLEEEHVGFSLD VDEIEKYEGEEDQKPP 550
 F S E E D+D + +Y EE + P
 Sbjct: 1139 SFLSDELEACS---DMDIVSEYTHYEEKKASP 1167

Score = 73 (11.0 bits), Expect = 4.8e+00, P = 9.9e-01
 Identities = 31/88 (35%), Positives = 40/88 (45%)

Query: 390 DQVKKEDQEATSP---RLSRELLD-EKEPEVLQDSLDRFYSTPFEYLELPDLCQ-PYRSD 444
 D ++DQ P RLSREL + EK EVLQ LD TP L D + P +
 Sbjct: 1080 DHKSEKDQAGLEPLALRLSRELQEKEKVIEVLQAKLDARSLTPSSSHALSDSHRSPSSTS 1139

Query: 445 FYSLQEQLGLGLDLDLDRMKKDQEEEEEDQGPP 475
 F S L D+D + + EE + P
 Sbjct: 1140 FLS---DELEACSDMDIVSEYTHYEEKKASP 1167

Score = 68 (10.2 bits), Expect = 1.1e-01, P = 1.0e-01
 Identities = 36/156 (23%), Positives = 68/156 (43%)

Query: 31 SHGVGRHQELRDPTV---PGPTSSATNVSMVVSAGPWS-----GEKAEMNILEINKK 79
 S G +HQE + TV P P S + V A G ++ ++ +
 Sbjct: 684 SPGKHQHQEEGNVTVRPFPRPQSLDLGATFTVDAHQLDNQSQPRDPGPQSAFSLPGSTQH 743

Query: 80 SRPQLAENKQQRNLKQKCLVTQVAYFL-ANRQNNYDYE-DCKDLIKSMLRDERLLTEEK 137
 R QL++ KQ++++L++K L+++ F AN Y + L+K + ++ ++
 Sbjct: 744 LRSQLSQCKQRYQDLQEKLLSEATVFAQANELEKYRVMLTGESLVKQDSKQIQVDLQDL 803

Query: 138 LAEELGQAEELRQYKVLVHSQERELTQLREK-LQEG 172
 E G++E + + + E L+E L EG
 Sbjct: 804 GYETCGRSENEAEREETTSPECEEHNSLKEMVLM EG 839

Score = 65 (9.8 bits), Expect = 2.2e-01, P = 2.0e-01
 Identities = 23/96 (23%), Positives = 52/96 (54%)

Query: 123 IKSMRLRDERLLTEEKLAELGQAE-----LRQYKVLVHSQERELTQLREKLQEGRDASRS 178
 ++ + D+ + E + E+ EE LRQ ++ V ++ +L +LR+ L ++ +
 Sbjct: 5 LRQRIHDKAVALERAIDEKFSALEEKELRQLRLAVRERDHDLERLRDVL S-----SNEA 60

Query: 179 LNQHLLQALLTPDEPDNSQGRDLREQLAEGCRLAQHLVQKL 218
 Q +++LL ++G ++ EQL+ C+ Q L +++
 Sbjct: 61 TMQSMESLL-----RAKGLEV-EQLSTTCQNLQWLKEEM 93

Score = 61 (9.2 bits), Expect = 5.5e-01, P = 4.2e-01
 Identities = 27/95 (28%), Positives = 47/95 (49%)

Query: 134 TEEK-LAEELGQAEELRQY----KVLVHSQERELTQLREKLQEGRDASRSLNQHLLQALLT 188
 +E K L +LG+ EE R Y ++L +LQ ++L +++L
 Sbjct: 855 SERKPLENQLGKQEEFRVYGKSENILV--LRKDIKDLKAQLQANANKVIQNLKSRVRSLSV 912

Query: 189 PDEPDNSQGRDLREQLAEGCRLAQHLVQKLSPENDDDDEDE 228
 + +S R R+ A G ++ SP + DEDE
 Sbjct: 913 TSDYSSSLERP-RKLRAVGT-----LEGSSPHSVPEDE 945

Score = 57 (8.6 bits), Expect = 1.4e+00, P = 7.5e-01
 Identities = 26/92 (28%), Positives = 47/92 (51%)

Query: 127 LRDERLLTEEKLAELGQAEEL---RQYKVLVHSQERELTQLREKLQEGRDASRSLNQHLL 183
 L E LL EK+A Q +E+ R+ ++L+ + L R +L E A R L L
 Sbjct: 358 LTOEVL LREKVASVESQGEISGNRRQQLLNLLEG--LVDERSRLNEALQAE RQLYSSL 415

Prosites for DKFZphtes3 7d17.2

Pfam for DKF2phtes3 7d17.2

941

DKFZphtes3_7j3

group: cell cycle

DKFZphtes3_7j3.2 encodes a novel 628 amino acid putative protein kinase, which is related to the C-TAK1 Cdc25C associated protein kinase.

Cdc25C is a protein kinase that controls entry into mitosis by dephosphorylation of Cdc2. Cdc25C function is regulated by phosphorylation, too. Serine 216 phosphorylation of Cdc25C mediates the binding of 14-3-3 protein to Cdc25C. C-TAK1 (Cdc twenty-five C associated protein kinase) phosphorylates Cdc25C on serine 216 in vitro. The new protein is closely related to C-Tak1 and therefore should be involved in cell-cycle regulation, too.

The new protein can find application in modulating/blocking the cell cycle.

strong similarity to serine/threonine-specific protein kinases

complete cDNA, complete cds, potential start at Bp 128, few EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 3443 bp

Poly A stretch at pos. 3399, polyadenylation signal at pos. 3376

```
1 GTGCTTTACT GCGCGCTCTG GTACTGCTGT GGCTCCCCGT CCTGGTGCGG
51 GACCTGTGCC CCGCGCTTCA GCCCTCCCCG CACAGCCTAC TGATTCCTCT
101 GCCGCCCTTG CTCACCTCCT GCTCGCCATG GAGTCGCTGG TTTCGCGCGG
151 GCGCTCCGGC CCACTCCCTT CGGCCCGAGA GCTAGCCCGG CCGCTGGCGG
201 AAGGGCTGAT CAAGTCGCCC AAGCCCCTAA TGAAGAAGCA GCGGTGAAG
251 CGGCACCACC ACAAGCACA CCGCGGCGAC CGCTACGAGT TCCTGGAGAC
301 CCTGGGCAAA GGCACCTACG GGAAGGTGAA GAAGGCGCGG GAGAGCTCGG
351 GCGCCTCTGT GGCATCAAG TCAATCCGGA AGGACAAAAT CAAAGATGAG
401 CAAGATCTGA TGCACATACG GAGGGAGATT GAGATCATGT CATCACTCAA
451 CCACCCCTAC ATCATTGCCA TCCATGAAGT GTTTGAGAAC AGCAGCAAGA
501 TCGTGATCGT CATGGAGTAT GCCAGCCGGG GCGACCTTTA TGAATACATC
551 AGCGAGCGGC AGCAGCTCAG TGAGCGCGAA GCTAGGCATT TCTCCGCGCA
601 GATCGTCTCT GCCGTGCACT ATTGCCATCA GAACAGAGTT GTCCACCGAG
651 ATCTCAAGCT GGAGAACATC CTCTTGATG CCAATGGGAA TATCAAGATT
701 GCTGACTTCG GCCTCTCCAA CCTCTACCAT CAAGGCAAGT TCCTGCAGAC
751 ATTCTGTGGG AGCCCCCTCT ATGCCTCGCC AGAGATTGTC AATGGGAAGC
801 CCTACACAAA CCCAGAGGTG GACAGCTGGT CCTGGGTGT TCTCCTCTAC
851 ATCCTGGTGC ATGGCACCAT GCCCTTTGAT GGGCATGACC ATAAGATCCT
901 AGTGAACACG ATCAGCAACG GGGCCTACCG GGAGCCACCT AAACCTCTG
951 ATGCCTGTGG CCTGATCCGG TGCTGTGTA TGGTGAACCC CACCCGCGCG
1001 GCCACCCTGG AGGATGTGGC CAGTCACTGG TGGGTCAACT GGGGCTACGC
1051 CACCCGAGTG GGAGAGCAGG AGGCTCCGCA TGAGGGTGGG CACCCTGGCA
1101 GTGACTCTGC CCGCGCCTCC ATGGCTGACT GGCTCCGGCG TTCTCCCGC
1151 CCCCTCTGG AGAATGGGGC CAAGGTGTGC AGCTTCTTCA AGCAGCATGC
1201 ACCTGGTGGG GGAAGCACC AACCCTGGCT GGAGCGCCAG CATTGCTCA
1251 AGAAGTCCCG CAGGAGAAT GACATGGCCC AGTCTCTCCA CAGTGACACG
1301 GCTGATGACA CTGCCATCG CCTGGCAAG AGCAACCTCA AGCTGCCAAA
1351 GGGCATTTCT AAGAAGAAGG TGTCAGCCTC TGCAGAAGGG GTACAGGAGG
1401 ACCCTCCGGA GCTCAGCCCA ATCCCTGCGA GCCCAGGGCA GGCTGCCCG
1451 CTGCTCCCCA AGAAGGGCAT TCTCAAGAAG CCCCAGACGC GCGAGTCTGG
1501 TACTACTTCC TCTCCCGAGC CCAGTGAATC TGGGGAGCTC TTGGACGCAG
1551 GCGACGTGTT TGTGAGTGGG GATCCCAAGG AGCAGAAGCC TCCGCAAGCT
1601 TCAGGGGTGC TCCTCCATCG CAAAGGCATC CTCAAACTCA ATGGCAAGTT
1651 CTCCAGACA GCCTTGAGC TCGCGGCCCC CACCACCTTC GGCTCCCTGG
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1751 GCTGTGAGCG AGGACAGCAT CCTGTCTCTT GAGTCTCTTG ACCAGCTGGA
1801 CTTGCCTGAA CGGCTCCAG AGCCCCCACT GCGGGGCTGT GTGTCTGTGG
1851 ACAACCTCAC GGGGCTTGAG GAGCCCCCTT CAGAGGGGCC TGAAGCTGC
1901 CTGAGGCGCT GCGGCGAGGA TCCTTTGGGG GACAGCTGCT TTCCCTGAC
1951 AGACTGCCAG GAGGTGACAG CGACCTACCG ACAGGCACTG AGGGTCTGCT
2001 CAAAGCTCAC CTGAGTGGAG TAGGCATTGC CCCAGCCCGG TCAGGCTCTC
2051 AGATGCAGCT GGTGACCCC CGAGGGGAGA TGCTTCTTCC CCCACCTCCC
2101 AGGACCTGCA TCCAGCTCA GAAGGCTGAG AGGGTTTGCA GTGGAGCCCT
2151 GAGCAGGGCT GGCATGGGA AGTAGGCAAA TGAATGCGC CAAGGGTTCA
2201 GTGTCTGTCT TCAGCCCTGC TGAACGAAGA GGATACTAAA GAGAGGGGAA
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2501 GCATCCTGGG AATGGTCTGG AGTAACGCTT CGTTATTTT ATTTTATTT
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2551 TTATTTATTT ATTTATTTT TTGAGACGGA GTTTCGCTCT TGGTGCCAG
2601 GCTAGAGTGC AATGGCGCGA TCTCAGCTCA CCTCAACCTC CGCTCCCGG
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2801 CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCCC
2851 CACCTAACCC TTCCTTATT AGCCTAGGAG TAAGAGAACA CAATCTCTGT
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2951 TCCTGAAGTT GCTGCTGTGA ATCTGAAAGA CTGAAAAGC CTCGCGCTGC
3001 TGTGTGGACT TCATCTCAAG GGGCCAGCC TCCTCTGGAC TCCACCTTGG
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3101 ATGGATGTGT TCTCTAGGCC TTCAGGACTC TAGAATGTCC ATATTTATTT
3151 TTATGTCTTT GGCTTTGTGT TTAGGAAAA GTGAATCTTG CTGTTTCAA
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3351 ATGGACCTCC GTGGCCAAA AGTACCATTA AAACCAGAAA GGTGATTGGA
3401 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

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BLAST Results

No BLAST result

Medline entries

98202387:
C-TAK1 protein kinase phosphorylates human Cdc25C on serine 216 and promotes 14-3-3 protein binding.

Peptide information for frame 2

ORF from 128 bp to 2011 bp; peptide length: 628
Category: strong similarity to known protein

```

1 MESLVFARRS GPTPSAAELA RPLAEGLIKS PKPLMKKQAV KRHHKHNLR
51 HRYEFLETLG KGYGKVKKA RESSGRLVAI KSIRKDKIKD EQDLMHIRRE
101 IEIMSSLNHP HIIAIEVFE NSSKIVIVME YASRGDLYDY ISERQQLSER
151 EARHFFRQIV SAVHYCHQNR VVHRDLKLEN ILLDANGNIK IADFGLSNLY
201 HQGKFLQTFE GSPLYASPEI VNGKPYTGPE VDSWSLGVLL YILVHGTMPE
251 DGHDKILVK QISNGAYREP PKPSDACGLI RWLLMVNPTR RATLEDVASH
301 WWVNWGYATR VGEQEAPHEG GHPGSDSARA SMADWLRRSS RPLENGAKV
351 CSFFKQHAPG GGSTTPGLER QHSLKKSKE NDMAQSLHSD TADDTAHRPG
401 KSNLKLPGKI LKKKVSASAE GVQEDPPELS PIPASPGQAA PLLPKKGILK
451 KPRQRESGYI SSPEPSESGE LLDAGDVFVS GDPKEQKPPQ ASGLLLHRKG
501 ILKLNGKFSQ TALELAAPTT FGSLDELAPP RPLARASRPS GAVSEDSILS
551 SESFDQLDLP ERLPEPPLRG CVSVDNLTGL EEPPSEGPGS CLRRWRQDPL
601 GDSCFSLTDC QEVATYRQA LRVCSKLT

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_7j3, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3_7j3, frame 2

Report for DKFZphtes3_7j3.2

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[LENGTH]      628
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[pI]           9.01
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mRNA for KIAA0537 protein, complete cds. 1e-152
[FUNCAT]       01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDR477w]
5e-66
[FUNCAT]       11.01 stress response [S. cerevisiae, YDR477w] 5e-66

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[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDR477w] 5e-66
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YLR096w] 6e-54
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YLR096w] 6e-54
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YDR507c] 8e-52
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YDR507c] 8e-52
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YKL101w] 9e-51
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKL101w] 9e-51
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 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YPL153c] 6e-44
 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YPL153c] 6e-44
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YPL153c] 6e-44
 [FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YMR001c] 2e-42
 [FUNCAT] 10.02.11 key kinases [S. cerevisiae, YBL105c] 3e-34
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YKL139w CTK1 - carboxy-terminal domain] 2e-28
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YFR014c] 4e-28
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YGL180w] 2e-26
 [FUNCAT] 06.13.04 lysosomal and vacuolar degradation [S. cerevisiae, YGL180w] 2e-26
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 [FUNCAT] 01.04.04 regulation of phosphate utilization [S. cerevisiae, YPL031c] 5e-24
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YHL007c] 6e-24
 [FUNCAT] 10.05.11 key kinases [S. cerevisiae, YHL007c] 6e-24
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YNR031c] 1e-22
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 [FUNCAT] 03.13 meiosis [S. cerevisiae, YDR523c] 8e-22
 [FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YDL108w] 6e-21
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 [FUNCAT] 01.02.04 regulation of nitrogen and sulphur utilization [S. cerevisiae, YNL183c] 1e-17
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 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YBR097w] 2e-08
 [FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YBR097w] 2e-08
 [FUNCAT] 30.08 organization of golgi [S. cerevisiae, YBR097w] 2e-08
 [FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YHR079c] 8e-05
 [FUNCAT] 01.06.10 regulation of lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YHR079c] 8e-05
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 [BLOCKS] BL00239B Receptor tyrosine kinase class II proteins
 [BLOCKS] BL00107A Protein kinases ATP-binding region proteins
 [SCOP] dlgol_ 5.1.1.1.9 MAP kinase Erk2 [rat Rattus norvegicus] 1e-77
 [SCOP] dlwfc_ 5.1.1.1.8 MAP kinase p38 [human (Homo sapiens)] 4e-68
 [SCOP] dlkoa_2 5.1.1.1.7 (1-350) Twitchin, kinase domain [Caenorhabditis] 2e-85
 [SCOP] dlkoba_ 5.1.1.1.6 Twitchin, kinase domain [california sea har] 1e-80
 [SCOP] dlphk_ 5.1.1.1.5 gamma-subunit of glycogen phosphorylase kinase 2e-76
 [SCOP] dlirk_ 5.1.1.2.4 insulin receptor [Human (Homo sapiens)] 1e-69
 [SCOP] dlapme_ 5.1.1.1.4 cAMP-dependent PK, catalytic subunit [mouse (Mu)] 1e-84
 [SCOP] dlfgka_ 5.1.1.2.3 Fibroblast growth factor receptor 1 [human (Hom)] 1e-68
 [SCOP] dlydre_ 5.1.1.1.3 cAMP-dependent PK, catalytic subunit [bovine (Bo)] 9e-85
 [SCOP] dlfmk_3 5.1.1.2.2 (168-437) c-src tyrosine kinase [human (Hom)] 1e-69
 [SCOP] dlcdka_ 5.1.1.1.2 cAMP-dependent PK, catalytic subunit [pig (Su)] 1e-85
 [SCOP] d2hcka3_ 5.1.1.2.1 (167-437) Haemopoietic cell kinase Hck [huma] 5e-66
 [SCOP] dlcsn_ 5.1.1.1.11 Casein kinase-1, CK1 [Schizosaccharomyces pombe] 9e-47
 [SCOP] dljsua_ 5.1.1.1.1 Cyclin-dependent PK [Human (Homo sapiens)] 1e-75
 [SCOP] dlckja_ 5.1.1.1.10 Casein kinase-1, CK1 [rat (Rattus norvegicus)] 5e-54
 [EC] 2.7.1.38 Phosphorylase kinase 1e-36
 [EC] 2.7.1.123 Ca2+/calmodulin-dependent protein kinase 4e-40

[EC] 2.7.1.128 [Acetyl-CoA carboxylase] kinase 1e-61
 [EC] 2.7.1.117 Myosin-light-chain kinase 2e-40
 [EC] 2.7.1.109 [Hydroxymethylglutaryl-CoA reductase(NADPH)] kinase 1e-61
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 [SUPFAM] protein kinase C mu 4e-33
 [PROSITE] PROTEIN_KINASE_ATP 2
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 [PROSITE] MYRISTYL 4
 [PROSITE] CAMP_PHOSPHO_SITE 3
 [PROSITE] CK2_PHOSPHO_SITE 13
 [PROSITE] TYR_PHOSPHO_SITE 2
 [PROSITE] PKC_PHOSPHO_SITE 12

[PROSITE] ASN_GLYCOSYLATION 2
 [PROSITE] PROTEIN_KINASE_ST 1
 [PFAM] Eukaryotic protein kinase domain
 [KW] All_Alpha
 [KW] 3D
 [KW] LOW_COMPLEXITY 10.51 %

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 SEG
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 SEG
 lctpe ETTEEEEEECCTTTTBHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHCCCECCCCGGG

SEQ ILLDANGNIKIADFGLSNLYHQKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL
 SEG
 lctpe EEETTTTCEEECTTTTTEET-TTT-BCCCCCGGGCCHHHHHCCBC-HHHHHHHHHHH

SEQ YILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASH
 SEG
 lctpe HHHHHCCTTTTTTTHHHHHHHHHHCCCCCTTCHHHHHHHHHHTTTTGGGTTTHHHHHHC

SEQ WWVNWGYATRVGEQAPHEGGHPGSDSARASMADWLRRSSRPLENGAKVCSFFKQHAPG
 SEG
 lctpe GG.....

SEQ GGSTTPGLERQHSLLKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGKILKKKVSASAE
 SEG
 lctpe

SEQ GVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYSSPEPSESSELLDAGDVFS
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 lctpe

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 SEGXXXXXXXXXXXXX.....
 lctpe

SEQ GDSCFSLTDCQEVATYRQALRVCSKLT
 SEG
 lctpe

Prosites for DKFzphes3_7j3.2

PS00001	121->125	ASN_GLYCOSYLATION	PDOC00001
PS00001	576->580	ASN_GLYCOSYLATION	PDOC00001
PS00004	290->294	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	337->341	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	413->417	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	30->33	PKC_PHOSPHO_SITE	PDOC00005
PS00005	74->77	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	122->125	PKC_PHOSPHO_SITE	PDOC00005
PS00005	142->145	PKC_PHOSPHO_SITE	PDOC00005
PS00005	148->151	PKC_PHOSPHO_SITE	PDOC00005
PS00005	289->292	PKC_PHOSPHO_SITE	PDOC00005
PS00005	327->330	PKC_PHOSPHO_SITE	PDOC00005
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PS00005	373->376	PKC_PHOSPHO_SITE	PDOC00005
PS00005	377->380	PKC_PHOSPHO_SITE	PDOC00005
PS00005	616->619	PKC_PHOSPHO_SITE	PDOC00005
PS00006	15->19	CK2_PHOSPHO_SITE	PDOC00006
PS00006	133->137	CK2_PHOSPHO_SITE	PDOC00006
PS00006	148->152	CK2_PHOSPHO_SITE	PDOC00006
PS00006	227->231	CK2_PHOSPHO_SITE	PDOC00006
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PS00006	461->465	CK2_PHOSPHO_SITE	PDOC00006
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PS00006	523->527	CK2_PHOSPHO_SITE	PDOC00006
PS00006	578->582	CK2_PHOSPHO_SITE	PDOC00006
PS00006	606->610	CK2_PHOSPHO_SITE	PDOC00006
PS00007	453->460	TYR_PHOSPHO_SITE	PDOC00007
PS00007	453->461	TYR_PHOSPHO_SITE	PDOC00007
PS00008	320->326	MYRISTYL	PDOC00008
PS00008	324->330	MYRISTYL	PDOC00008
PS00008	347->353	MYRISTYL	PDOC00008
PS00008	360->366	MYRISTYL	PDOC00008
PS00016	134->137	RGD	PDOC00016
PS00107	59->82	PROTEIN_KINASE_ATP	PDOC00100
PS00107	59->86	PROTEIN_KINASE_ATP	PDOC00100
PS00108	171->184	PROTEIN_KINASE_ST	PDOC00100

Pfam for DKFZphtes3_7j3.2

HMM_NAME	Eukaryotic protein kinase domain		
HMM	*YeigRiIGeGsFGtVYkCiWrtGeIVAIIkkkrms.....FlREI		
	YE+++++G+G+G+V+K+++ +G++VAIK I+K++++ ++REI		
Query	53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREI	101	
HMM	qIMRrLnHPNIIRFYDwFedddDHIYMIMEYMeGGDLFDYIrrngpMsEw		
	+IM +LNHP+II + ++FE ++ I ++MEY+ GDL+DYI+++ ++SE+		
Query	102 EIMSSLNHPHIIAIHEVFE-NSSKIVIVMEYASRGDLYDYISERQQLSER	150	
HMM	eIrfIMyQILrGMeYLHSMgIIHRDLKPENILIDeNgqIKIcDFGLARqM		
	E+R++++QI++++ Y+H ++++HRDLK ENIL+D NG+IKI+DFGL+ ++		
Query	151 EARHFFRQIVSAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLY	200	
HMM	nnYerMttfCGTPWYMMAPEVIMg.nyYttkVDMWSFGCILWEMMTGep		
	+ + ++ TFCG+P Y +PE+ ++G +Y +++VD WS+G++L++++ G+		
Query	201 HQGKFLQTFCGSPLYA-SPEI-VNGKPYTGPEVDSWSLGVLLYILVHGTM	248	
HMM	PFyddnMemImrIiqrfrfpfWpnCSeElyDFMrwCWnyDPekRPTFrQI		
	PF+++ ++ I + +++ +P S+ + ++RW++ ++P++R T +++		
Query	249 PFDGHDHKILVKQISNGAYREPPKPSD-ACGLIRWLLMVNPTRRATLEDV	297	
HMM	LnHPWF*		
	H W+		
Query	298 ASHWWV	303	

DKFZphtes3_7j8

group: testes derived

DKFZphtes3_7j8 encodes a novel 410 amino acid protein nearly identical to human
WUGSC:H_DJ1159004.1.

The novel protein contains an additional C-terminal domain, which is not present in
WUGSC:H_DJ1159004.1.
No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific
genes.

WUGSC:H_DJ1159004.1 similarity to YBL104p

verifies and extends the genmodel WUGSC:H_DJ1159004.1
similarity to *S.cerevisiae* YBL104p

Sequenced by BMFZ

Locus: /map="7p21-p22"

Insert length: 3353 bp

Poly A stretch at pos. 3231, no polyadenylation signal found

```
1  GCAAAATATG TTGTATTTGT GGCATAGTTC ATATTTACAC TATCATAAAA
51 TTATGGCCGA GAAGTTAAAT ATTCTAAATG TGTCAACATA GTTCTCTGTA
101 AAACGTGACT ATTTTCCAAA TATATTTTGA AATAAAACAA TATAAAATATG
151 TTTTCTGTTT TTAGGAATGG TGGAAAGCAG CAGACATAAT TGGAGTGGGT
201 TGGATAAGCA AAGTGATATT CAAAATTAA ATGAAGAGAG AATCTTAGCT
251 TTACAGCTTT GTGGGTGGAT AAAGAAAGGA ACGGATGTAG ACGTGGGGCC
301 ATTTTGAAC TCCCTTGATC AAGAAGGGGA ATGGGAAAGA GCTGCTGCTG
351 TGGCATTGTT CAACCTGGAT ATTCCCGGAG CAATCCAAAT CCTGAATGAA
401 GGGGCATCTT CTGAAAAGG AGATCTGAAT CTCAATGTGG TAGCAATGGC
451 TTTATCGGGT TATACGGATG AGAAGAACTC CCTTGGAGA GAAATGTGTA
501 GCACACTGCG ATTACAGCTA AATAACCCGT ATTTGTGTGT CATGTTTGCA
551 TTTCTGACAA GTGAAACAGG ATCTTACGAT GGAGTTTTGT ATGAAAACAA
601 AGTTGCAGTA CGTGACAGAG TGGCATTTCG TTGTAATTC CTTAGTGATA
651 CTCAGTTAA TAGATACATC GAAAAGTTGA CCAATGAAAT GAAAGAGGCT
701 GGAATTTGG AAGGAATTTT GCTTACAGGC CTTACTAAAG ATGGAGTGGG
751 CTTAATGGAG AGTTATGTTG ATAGAAGTGG AGATGTTCAA ACAGCAAGTT
801 ACTGTATGTT ACAGGGTTCA CCTTTAGATG TTCTTAAAGA TGAAGGGT
851 CAGTACTGGA TTGAGAATTA TAGAAATTTA TTAGATGCCT GGAGGTTTTG
901 GCATAAACGA GCTGAATTTG ATATTCACAG GACTAAGTTG GATCCAGTT
951 CCAAGCCTTT AGCACAAAGT TTTGTGAGTT GCAATTTCTG TGGCAAGTCA
1001 ATCTCTTACA GCTGTTTCA GGTGCTCAT CAGGGCAGAG GTTTTAGTCA
1051 GTATGGTGTG AGTGGCTCAC CAACGAAATC TAAAGTCACA AGTTGCTCTG
1101 GCTGTGCGAA ACCACTTCCT CGATGTGCGC TTTGTCTCAT TAATATGGGA
1151 ACACCACTTT CTAGCTGTCC TGGAGGAACC AAATCAGATG AAAAAGTGGG
1201 CTTGAGCAAG GACAAAAAAT TAGCCCAATT TAACAAGTGG TTTACATGGT
1251 GTCATAATTG CAGGCACGGT GGACATGCTG GACATATGCT TAGTTGGTTC
1301 AGGGACCATG CAGAGTGCCC TGTGTCTGCA TGCACGTGTA AATGTATGCA
1351 GTTGATACA ACGGGGAATC TGGTACCTGC AGAGACTGTC CAGCCATAAA
1401 ATGTTACCA CTTAAGAGAA CCCTTCAAGT GTGGAGCTTT CTAGTAGGTG
1451 TCCTTCATAG CTCAGAAACA TACCTCAGAA CAAGCCATTC ATGACTTACC
1501 TGTAATGGGA AATAAATCA TTCTATCAGA TCAGCAGTTT TGATGTTTGA
1551 GTGATTTTGA TATGCTTCAC AGAGACAAAT GCTGCCAAAA TAAACATCGA
1601 AGTATAGACA TGAGTTCTGT TCAGCAGGTT GAAAAGTCTG ATTTAGAAAA
1651 ACTTTCTAAG TTTTGTTGA AATTATGAAC ACTCTAGAAG CAGAATTTCT
1701 GGAAGAGCCA AGAACAGACT TTGAGCCTAT ATCTTCAAAG CTGAAACTGG
1751 ATATCTTTCA ATAAAAATG TGCACTTTAA AAATAAAATG ACTAATTCCTG
1801 TGATTTCAGC AATAGTTTAA AGTTCAGCTG TGCTTAGATT TCTTTCAGAT
1851 TAATTTAAAA TTATAGATTT TACTTTTGTG AATTGCAGAG CCCCTATCCC
1901 ACACCTGAGA ATATTTTATA TACTGTCTGT TTATATATGT GTCTATGTGT
1951 GTGTGTATAT TTATGTGTGT ATGTATAAAT ATGTACTTTT TAAAGGAGCC
2001 TTTTCCCTCC TTTGATTTTA AGATAAGCAA TCTTTTGGCA TAACATTATC
2051 GTCTTCTTAG AAAAGCCAAG ATGAAGAATC TATCTTACAA CTTTTCCTCT
2101 TCAGTAGAGA AAAACATGTA CCATTTTCAGG TGAACATACA AAATTTTCAC
2151 TTTCTACCTT TTGCTTCCA ATGTCCTGAT TTGTCTTCAA AGGTTTTTCT
2201 CCATATTAAT TTGTCATCTT ATCCTCATCA CCTGAGAAGA TTTTACTGCA
2251 TACAAAGTCT ATGCAAGATT ATATGTAAGT AGCCATTAGT TATAATCTAT
2301 GTCAGTGTGT CTGTGCTGTC AAATTCCTGT CTGATTTGGA ATACCATACC
2351 TTGTTCTTTC CAAGGTAGAG TAGGAAGTGT TGGGGAAATA GGGTCACTTC
2401 AGAGACCATT TTAGTGTAAT GTTTTAAAT GTAAGTGTTA TGGGGCTAA
2451 GTCAGGGACT TTATTTAAAA CATTTTTTTT TTCTCATTTT ATAGCTAGAT
2501 AGTTGTAAGA GAAATACAAA GAATTTACAA GATGCTTCTC TGTCATCTGC
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2551 CGTATGCAGA GGGACTGAAC TAGGAATTTT GTAGTTGAAG CTGTGTTTCAT
2601 AAAGAGTAAA TCTTATTTTA TAGATTTTGG AGAAATAAAA CAAGAATTTT
2651 AAGAGCTTTC GTATTAGCAG TTTTGCCTTA TAAAAACTAA GATTTGTCAG
2701 ATTAGTTTGA GGTGTAACCT AAATATTAAA AGTAGATTAA ATTTATTTT
2751 TACCTTGAGT GTCTGATACA TAAACCCTT TTCTAGGAAA ACATTGGAAG
2801 TAGTACATAT TTACTCTAAA TGTCTCACCT GCATGACAGT CTTTCAAAT
2851 GAAAGACATG GTAATTGCAA TTTTTTTTTA AAGATTGCTA TTAAGGGTAC
2901 TTTTCCAGC CTTCATTGTA GTAAATCTTA ATTGATTTC AATTATTAA
2951 ATATACCCTT TACCTTTAAT ATTCATTG AAGTGTTCTT TCAAACTTA
3001 CTGTCTTAAA TATGAAAGTC AGCTTTAAGT AATGTCAGAC TCATATGCAT
3051 TTTCATTCTC ATTAGCTAAA GTAAATGTA AAATTATCTC AAATAGTTAC
3101 AAGTTTTTGA AATACAGTAT AAAACATGAA TGTAAAGTCT ATTATGTAAT
3151 ATGCTTATTT GTAATCCTAA TATATGAGGG TGACATTTT AAGATTGTAT
3201 GTATGTGTCA ACCTCTTAAA TGTTTTCTGT GAAAAAAAAA AAAAAAAAAA
3251 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3301 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3351 AAA

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 167 bp to 1396 bp: peptide length: 410
 Category: known protein
 Classification: unclassified

```

1 MVESSRHNWS GLDKQSDIQN LNEERILALQ LCGWIKKGTD VDVGPFLNSL
51 VQEGEWERAA AVALFNLDIR RAIQILNEGA SSEKGDNLN VVAMALSGYT
101 DEKNSLWREM CSTLRLQLNN PYLCVMFAFL TSETGSYDGV LYENKVAVRD
151 RVAFACKFELS DTQLNRYIEK LTNEMKEAGN LEGILLTGLT KDGVDLMESY
201 VDRTGVDVQTA SYCMLQGSPL DVLKDERVQY WIENYRNLDD AWFVHKKRAE
251 FDIHRSKLDP SSKPLAQVFV SCNFCGKSI YSCSAVPHQG RGFSQYGVSG
301 SPTKSKVTSC PGCRKPLPRC ALCLINMGTP VSSCPGGTKS DEKVDLSKDK
351 KLAQFNNWFT WCHNCRHGGH AGHMLSWFRD HAECFVSACT CKCMQLDITG
401 NLVPAETVQP

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_7j8, frame 2

PIR:S45391 probable membrane protein YBL104c - yeast (*Saccharomyces cerevisiae*), N = 2, Score = 446, P = 4.5e-47

TREMBL:AC004982_1 gene: "WUGSC:H_DJ1159004.1"; Homo sapiens PAC clone
 DJ1159004 from 7p21-p22, complete sequence., N = 1, Score = 2038, P = 7.6e-211

>TREMBL:AC004982_1 gene: "WUGSC:H_DJ1159004.1"; Homo sapiens PAC clone
 DJ1159004 from 7p21-p22, complete sequence.
 Length = 379

HSPs:

Score = 2038 (305.8 bits), Expect = 7.6e-211, P = 7.6e-211
 Identities = 379/379 (100%), Positives = 379/379 (100%)

```

Query:      1 MVESSRHNWSGLDKQSDIQNLNEERILALQLCGWIKKGTDDVDVGPFLNSLVQEGEWERAA 60
            MVESSRHNWSGLDKQSDIQNLNEERILALQLCGWIKKGTDDVDVGPFLNSLVQEGEWERAA
Sbjct:      1 MVESSRHNWSGLDKQSDIQNLNEERILALQLCGWIKKGTDDVDVGPFLNSLVQEGEWERAA 60

Query:      61 AVALFNLDIRRAIQILNEGASSEKGDNLNVVAMALSGYTDEKNSLWREMCSTLRLQLNN 120
            AVALFNLDIRRAIQILNEGASSEKGDNLNVVAMALSGYTDEKNSLWREMCSTLRLQLNN
Sbjct:      61 AVALFNLDIRRAIQILNEGASSEKGDNLNVVAMALSGYTDEKNSLWREMCSTLRLQLNN 120

```


DKF2phtes3_7p10

group: Cell Cycle

DKF2phtes3_7p10.1 encodes a novel 422 amino acid putative protein, which is closely related to the *Xenopus laevis* XPMC2 protein.

In fission yeast the kinases Wee1 and Mik1 control that initiation of mitosis starts after completion of DNA synthesis. Yeast in which both Wee1 and Mik1 kinases are defective exhibit a mitotic catastrophe phenotype. XPMC2 of *xenopus* rescues several different yeast mitotic catastrophe mutants defective in Wee1/Mik1 kinase function. The XPMC2 protein is localised in the nucleus in *Xenopus* oocytes. The new protein is the human orthologue of this gene.

The new protein can find application in modulating/blocking the cell cycle.

strong similarity to XPMC2 protein

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: /map="9q34"

Insert length: 2380 bp

Poly A stretch at pos. 2341, polyadenylation signal at pos. 2318

```
1 AGCGTGC GTG CTGAGGTATG CGCAACGCGT GCGGGGTCTC TTCCGGAGTC
51 TTTTCTTGA CGGGGTCCCT GCGGTGGGTG TGTTCGGCC TGGCCTGGGC
101 AGGCGCTTGT GCTGCCAGGG GCGCGGGCCC GGGGAGGCCG GGGTCTCGGG
151 TGGCCGCCGG CCCAGGCGCT GGACGGCAGC AGGATGGGGA AGGCGAAGGT
201 CCCC GCCCTCC AAGCGCGCCC CGAGCAGCCC CGTGGCTAAG CCGGGTCTGT
251 TCAAGACGCT CACTCGGAAG AAAACAAGA AGAAAAAAG GTTTTGAAA
301 AGCAAGGCGC GGAAGTAAG CAAGAAGCCA GCAAGCGGCC CCGGTGCTGT
351 GTGCGGACCT CCAAAGGCAC CAGAAGACTT TTCTCAAAAC TGAAGGCGC
401 TGCAAGAGTG GCTGCTGAAA CAAAAATCTC AGGCCCCAGA AAAGCCTCTT
451 GTCATCTCTC AGATGGGTTC CAAAAAGAAG CCCAAATTA TCCAGCAAAA
501 CAAAAAAGAG ACCTCGCCTC AAGTGAAGGG AGAGGAGATG CCGGCAGGAA
551 AAGACCAGGA GGCACAGAGG GGCTCTGTTC CTTAGGTTT CAAGATGGAC
601 AGGAGGGCGC CAGTACCTCG CACCAAGGCC AGTGAACAG AGCACAATAA
651 GAAAGGAACC AAGGAAAGGA CAAATGGTGA TATTGTTCCA GAACGAGGGG
701 ACATCGAGCA TAAGAAGCGG AAAGCTAAGG AGGCAGCCCC AGCCCCACCC
751 ACCGAGGAAG ACATCTGGTT TGACGACGTG GACCCAGCGG ATATCGAAGC
801 TGCCATAGGT CCAGAGGCGG CCAAGATAGC GAGGAAACAG TTGGGTGAGA
851 GCGAGGGGAG CGTCAGCCTC AGCCTCGTGA AAGAGCAGGC CTTGCGCGGC
901 CTGACAAGAG CCTTAGCCTT GGA CTGTGAG ATGGTGGGCG TGGGCCCTAA
951 GGGGGAGGAG AGCATGGCCG CCCGTGTGTC CATCGTGAAC CAGTATGGGA
1001 AGTGCCTTTA TGACAAGTAC GTCAAACCAA CTGAGCCCGT GACGACTAT
1051 AGGACAGCGG TCAGTGGGAT TCGGCCTGAG AACCTCAAGC AGGGAGAAGA
1101 GCTTGAAGTT GTTCAGAAAG AAGTGGCAGA GATGCTGAAG GGCAGAATTC
1151 TAGTGGGGCA CGCTCTGCAT AATGACCTAA AGGTACTATT TCTTGATCAT
1201 CCAAAAAAGA AGATTCGGGA CACACAGAAA TATAAACCTT TCAAGAGTCA
1251 AGTAAAGAGT GGAAGGCCGT CTCTGAGACT ACTTTCAGAG AAGATCCTTG
1301 GGCTCCAGGT CCAGCAGGCG GAGCACTGTT CAATTCAGGA TGCCCAAGGA
1351 GCAATGAGGC TGTACGTCAT GGTGAAGAAG GAGTGGGAGA GCATGGCCCG
1401 AGACAGGCGC CCCTGCTGA CTGCTCCAGA CCACTGCAGT GACGACGCCT
1451 AGCAGTCTG CCGTGTGCT GCTGCCGCCG CGCTACAGAG GCAATGTGAC
1501 CAGTCACAGG GACAGATCAC ATCTCCCCAG AGTGGCAACT CTGGTGAAAC
1551 CTTTTCAGAA TCATGGCAGA GGGGCGTGCC GTGGTGCTAC TGAGAAGGTC
1601 CTCCTTCTC TTGACTTTGT GGTCTGAAAC CTGGTCTTAC TGTCCATGTG
1651 TGTTTGGGCC CGGATGGTCA GGGTGGGGAG CAGGGACGGC CATGGGCACG
1701 CTTGGCCACG CTTTACCGAC TGCTGACCCC CTGGGCCAGG TGAGGTTGGG
1751 GCCTGTGGGC CGCCAGTCCA TACGGTGCTG TCACTGCCCC TCTTCGGTGA
1801 CACCCTGGGG TGAGGTGCTC AGCACCTTCC TCTCGAGGAG CCACATTTTC
1851 CTCCTTTGTG TTAGGGGACA TAACAAGCTC TGCTGGGCTT GAGGGACCCA
1901 GACCAGGTGT GTCAGTCAG CTCCTGAGAC ACAGCTGGCC GGCACAACAG
1951 GTGTTACATC AGGGGTTTCC TGTGGCCGTT TGAACCTTGA GCATTTATCT
2001 AATATAAATT GGGCCAGGGT TGCTGGTGG GTACCCAGC AGAGGCTTCT
2051 CCAATAGCA CAGGATGTG TTGCTGGGC ACCGTGACTG CGGTATTTC
2101 TGGAGTCCG CAGACATGCC AACCTTGGGC TATTTGAGCT GGAGAAGCTA
2151 TGTGATGCTA GCCGGTGGCT TTCTGGGCTA GGGCCAGTT TGAGGCTCCC
2201 CTGGGAAC TA GCCCAGGAA CAGCCAGTGG CACTGACAAG GGGACGGAGT
2251 CCAAGGCGTT ATTTGGCCAC CTGACAGCTG GACAGAAAAG GGGCAGACAC
2301 ACCGAGGATG CGATTTAAAA TAAATGCAGA TGTTTACTTG GAAAAAATAA
2351 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

Medline entries

Peptide information for frame 1

1	MGKAKVPASK	RAPSSSPVAKP	GPVKTLTRKK	NKKKKRFWKS	KAREVSKKPA
51	SGPGAPVRRP	KAPEDFSONW	KALQDEWLLQ	KSQAPKPLP	ISQMGSKKKP
101	KIIQQNKKRT	SPQVKGEEMP	AKGDQEAESQ	SVPSGSKMDR	RAPVPRTKAS
151	GTEHNKKGTK	ERTNGDIVPE	RGDIEHKKRK	AKEAAPAPPT	EEDIWFDDVD
201	PADIEAIAIGP	EAAKIAKRLQ	GQSGESVLSL	LKPEQAFGGL	TRALALDCEN
251	VGVGPKGEES	MAARVSIVNQ	GKGCVYDKYV	KPTPEVTDYR	TVASGIRPEN
301	LKQGEELLEV	QKEVAEMLKG	RILVGHALHN	DLKVLFLDHP	KKKIRDQTKY
351	KPFKSQVSKS	RPSRLRLSEK	ILGLQVQAAE	HCSIQDAQAA	MRLYVMVKKE
401	WESMARDRRP	LLTAPLHCHD	DA		

Pedant information for DKFZphtes3_7p10, frame 1

```

[LENGTH]      422
[MW]           46671.91
[pI]           9.79
[HOMOL]        PIR:S53818 XPMC2 protein - African clawed frog 7e-96
[FUNCAT]       03.22 cell cycle control and mitosis [S. cerevisiae, YOL080c] 2e-42
[FUNCAT]       01.03.16 polynucleotide degradation [S. cerevisiae, YGR276c] 2e-19
[FUNCAT]       05.04 translation (initiation, elongation and termination) [S. cerevisiae,
YGL094c] 7e-13
[FUNCAT]       04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S.
cerevisiae, YGL094c] 7e-13
[FUNCAT]       99 unclassified proteins [S. cerevisiae, YLR107w] 6e-10
[PROSITE]      RGD 1
[PROSITE]      MYRISTYL 4
[PROSITE]      CAMP_PHOSPHO_SITE 2
[PROSITE]      CK2_PHOSPHO_SITE 6
[PROSITE]      TYR_PHOSPHO_SITE 2
[PROSITE]      GLYCOSAMINOGLYCAN 1
[PROSITE]      PKC_PHOSPHO_SITE 8
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY 11.37 %

```

BNSDOCID: <WO_0112659A2_I_>

```
SEQ      AGKDQEASRGSVPSGSKMDRRAPVPRTKASGTEHNKKGTKERTNGDIVPERGDIEHKRRK
SEG      .....xxxxxxxxx
PRD      eccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhh

SEQ      AKEAAPAPPTEEDIWFDDVPADIEAAIGPEAAKIARKQLGQSEGSVLSLVKEQAFGGGL
SEG      xxxxxxxxxxxxxxx.....
PRD      hhhhhccccccccceeeccccccchhhhhhhcccchhhhhhhhhhhhhccccccchhhhhhhhhhhhhh

SEQ      TRALALDCEMVGVPKGEESMAARVSIVNQY GKCVYDKYVKPTPEVTDYRTAVSGIRPEN
SEG      .....
PRD      hhhccccccccccccccchhhhhhhhhhhccccccccceeeeecccccccccccccccccccc

SEQ      LKQGEELEVQKEVAEMLKGRILVGHALHNDLKVFLFDHPKKKIRDQTQKYKPKFSQVKSGL
SEG      .....
PRD      cccccchhhhhhhhhhhhhhhcccceeecccchhhhhhhhhhhccccccccccccceeccccccccccc

SEQ      RPSRLRLSEKILGLQVQQAEHC SIQDAQAAMRLYVMVKKEWESMARDRRPLLTAPDHCS D
SEG      .....
PRD      chhhhhhhhhhhhhhhhhccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccc

SEQ      DA
SEG      ..
PRD      CC
```

Prosites for DKFZphtes3_7p10.1

PS000002	51->55	GLYCOSAMINOGLYCAN	PDOC000002
PS000004	107->111	CAMP_PHOSPHO_SITE	PDOC000004
PS000004	156->160	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	9->12	PKC_PHOSPHO_SITE	PDOC000005
PS000005	27->30	PKC_PHOSPHO_SITE	PDOC000005
PS000005	46->49	PKC_PHOSPHO_SITE	PDOC000005
PS000005	96->99	PKC_PHOSPHO_SITE	PDOC000005
PS000005	347->350	PKC_PHOSPHO_SITE	PDOC000005
PS000005	359->362	PKC_PHOSPHO_SITE	PDOC000005
PS000005	363->366	PKC_PHOSPHO_SITE	PDOC000005
PS000005	368->371	PKC_PHOSPHO_SITE	PDOC000005
PS000006	136->140	CK2_PHOSPHO_SITE	PDOC000006
PS000006	150->154	CK2_PHOSPHO_SITE	PDOC000006
PS000006	163->167	CK2_PHOSPHO_SITE	PDOC000006
PS000006	190->194	CK2_PHOSPHO_SITE	PDOC000006
PS000006	383->387	CK2_PHOSPHO_SITE	PDOC000006
PS000006	413->417	CK2_PHOSPHO_SITE	PDOC000006
PS000007	343->351	TYR_PHOSPHO_SITE	PDOC000007
PS000007	342->351	TYR_PHOSPHO_SITE	PDOC000007
PS000008	130->136	MYRISTYL	PDOC000008
PS000008	151->157	MYRISTYL	PDOC000008
PS000008	221->227	MYRISTYL	PDOC000008
PS000008	239->245	MYRISTYL	PDOC000008
PS000016	171->174	RGD	PDOC000016

(No Pfam data available for DKFZphtes3_7p10.1)

DKFZphtes3_7p9

group: nucleic acid management

DKFZphtes3_7p9 encodes a novel 691 amino acid protein with similarity to human nuclear domain 10 protein NDP52.

The nuclear domain (ND)10 also described as POD or Kr bodies is involved in the development of acute promyelocytic leukemia and virus-host interactions. The NDP52 protein is part of this complex structure. In vivo, NDP52 is transcribed in all human tissues, but is redistributed upon viral infection and interferon treatment. ND10 plays an important role in the viral life cycle.

The novel protein is similar to NDP52. It contains three leucine zippers and a RGD cell attachment site. This protein seems to be a novel part of the ND819 complex.

The new protein can find application in modulation of viral infections and tumour events.

similarity to nuclear domain 10 protein NDP52

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: /map="329.1 cR from top of Chr12 linkage group"

Insert length: 3003 bp

Poly A stretch at pos. 2957, no polyadenylation signal found

```
1 AAGGTGAGGG GAACAGCTGA TCCGTCTGTT GGGAGGACAG ATATCTCAAG
51 GCCAGGATGG AAGAATCACC ACTAAGCCGG GCACCATCCC GTGGTGGAGT
101 CAACTTTCTC AATGTAGCCC GGACCTACAT CCCCACACAC AAGGTGGAAT
151 GTCACTACAC CCTTCCCCCA GGCACCATGC CCAGTGCCAG TGACTGGATT
201 GGCATCTTCA AGGTGGAGGC TGCCTGTGTT CGGGATTACC ACACATTTGT
251 GTGGTCTTCC GTGCCTGAAA GTACAACCTGA TGGTCCCCC ATTACACCA
301 GTGTCCAGTT CCAAGCCAGC TACCTGCCCA AACCAGGAGC TCAGCTCTAC
351 CAGTTCCGAT ATGTGAACCG CCAGGGCCAG GTGTGTGGGC AGAGCCCCC
401 TTTCCAGTTC CGAGAGCCAA GGCCCATGGA TGAAGTGGT ACCCTGGAGG
451 AGGCTGATGG GGGCTCTGAC ATCCTGCTGG TTGTCCCCA GGCAACTGTG
501 TTACAGAACC AGCTCGATGA GAGCCAGCAA GAACGGAATG ACCTGATGCA
551 GCTGAAGCTA CAGCTGGAGG GACAGGTGAC AGAGCTGAGG AGCCGAGTGC
601 AGGAGCTCGA GAGGGCTCTG GCAACTGCCA GGCAGGAGCA CACGGAGCTG
651 ATGGAACAGT ACAAGGGGAT TTCCCGGTCC CATGGGGAGA TCACAGAAGA
701 GAGGGACATC CTGAGCCGGC AACAGGGAGA CCATGTGGCA CGCATCCTGG
751 AGCTAGAGGA TGACATCCAG ACCATCAGTG AGAAAGTGCT GACGAAGGAA
801 GTGGAGCTGG ACAGGCTTAG AGACACAGTG AAGGCCCTGA CTCGGGAACA
851 AGAGAAGTTC CTTGGGCAAC TGAAAGAAGT ACAAGCAGAC AAGGAGCAAA
901 GTGAGGCTGA GCTCCAAGTG GCACAACAGG AGAACCATCA CTTAAATTTG
951 GACCTGAAGG AGGCGAAGAG CTGGCAAGAG GAGCAGAGTG CTCAGGCTCA
1001 GCGAGTGAAA GACAAGGTGG CCCAGATGAA GGACACCCCTA GGCCAGGCCC
1051 AGCAGCGGGT GGCCGAGCTG GAGCCCTTGA AGGAGCAGCT TCGAGGGGCC
1101 CAGGAGCTTG CAGCCTCAAG CCAGCAGAAA GCCACCCTTC TTGGGGAGGA
1151 GTTGGCCAGC GCAGCAGCAG CCAGGGACCG CACCATAGCC GAACTACACC
1201 GCAGCCGCCT GGAAGTGGCT GAAGTTAACG GCAGGCTGGC TGAGCTCGGT
1251 TTGCACTTGA AGGAAGAAAA ATGCCAATGG AGCAAGGAGC GGGCAGGGCT
1301 GCTGCAGAGT GTGGAGGCAG AGAAGGACAA GATCCTGAAG CTGAGTGCAG
1351 AGATACTTCG ATTGGAGAAG GCAGTTCAGG AGGAGAGGAC CCAAACCAA
1401 GTGTTCAAGA CTGAGCTGCC CCGGGAGAAG GATTCTAGCC TGGTACAGTT
1451 GTCAGAAAGT AAGCGGGAGC TGACAGAGCT GCGGTCAGCC CTGCGTGTGC
1501 TCCAGAAGGA AAAGGAGCAG TTACAGGAGG AGAAACAGGA ATTGCTAGAG
1551 TACATGAGAA AGCTAGAGGC CCGCCTGGAG AAGGTGGCAG ATGAGAAAGT
1601 GAATGAGGAT GCCACCACAG AGGATGAGGA GGCCGCTGTG GGGCTGAGCT
1651 GCCCGGCAGC TGTGACAGAC TCAGAGGACG AGTCCCCAGA AGACATGAGG
1701 CTCCCACCCT ATGGCCTTTG TGAGCGTGGA GACCCAGGCT CCTCTCTGC
1751 TGGGCCCTCA GAGGCTTCTC CCCTTGTTGT CATCAGCCAG CCGGCTCCCA
1801 TTTCTCCTCA CCTCTCTGGG CCAGCTGAGG ACAGTAGCTC TGACTCGGAG
1851 GCTGAAGATG AGAAGTCAGT CCTGATGGCA GCTGTGAGA GTGGGGTGA
1901 GGAGGCCAAC TTACTGCTTC CTGAAGTGGG CAGTGCCTTC TATGACATGG
1951 CAGTGGCTT TACAGTGGGT ACCCTGTGAG AAACCAGCAC TGGGGGCCCT
2001 GCCACCCCCA CATGGAAGGA GTGTCCTATC TGTAAGGAGC GCTTCTCTGC
2051 TGAGAGTGAC AAGGATGCCC TGGAGGACCA CATGGATGGA CACTTCTTTT
2101 TCAGCACCCA GGACCCCTTC ACCTTTGAGT GATCTTACTC CCTCGTACAT
2151 GCACAAATAC ACACCTATGC ACACACACAC TCACACACAT GCATACACTT
2201 AGGTTTCTAT CCCATTTTCT ATCACACTGG GCTCCATGAT ATTCTGTTCC
2251 CTAAGAAGTG CTTCTGTGTG CCCTGTTTTC ATCCCAAGAT TTCTCACTTC
2301 ATCCTCTCCT ACCTGGCTCT TTTGTCCCAG GGAGGGGTCC TGTTCCGAAG
2351 CAGTGGCTGA ATTTATCCCC TGAAAGTGGT TTTGGAGGAA CCGGGATGGA
2401 GGAGGCCTTC CCCTGTGGGA ATAGAATCGT CCACCTCTAG CCCTGGTTGC
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2451 TTCTGATACA CAGCCACTGC ACACACACAC TCACACTCAC ACTCCCTTGT
2501 CTGATGCCCC AAAGCCAATT CCTGGGGCAC CCTACCTCT CTTATTGGA
2551 GTTTCCTGTT GTTTACCTGA GTTTTCTCTG GGGTCTGCAC AGAGGCAGCA
2601 GCATGGACAT CATGGCCTCT CAGGTCCCTT TTGGTTCTCA GTTTCATTGG
2651 TTCCTCTTTC TGTTCCCCCA TTGACTTCTG TGCCCCACCC TAGCCTTTTC
2701 CATAACCTTA GGTATTCACT TTGGAGGGGT TTTTGTATT TTTGAGGATT
2751 CCTGTATTCT GTATCCTCTC CTCGCATCTC CTCACATGGA AAGAAATAAT
2801 GTATTTGTGC CTTCTGTGAG GAATGGGGGG AACAAGTGGT CCCAGGTATC
2851 CCCATTTCCT AGGCCCCCTT CCCTCTCCAG GTCCCCCAC AGCAATAAAA
2901 GCTTCCCCCT GATATCCATC CCTTTGTAGT TTGAACAAAT ATATTATAT
2951 GATATGTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3001 AAA

```

BLAST Results

Entry HS189353 from database EMBL:
human STS WI-11261.
Score = 2191, P = 1.4e-92, identities = 463/485

Medline entries

95310349:
Molecular characterization of NDP52, a novel protein of the nuclear domain 10, which is redistributed upon virus infection and interferon treatment.

97375672:
Cellular localization, expression, and structure of the nuclear dot protein 52.

Peptide information for frame 3

ORF from 57 bp to 2129 bp; peptide length: 691
Category: similarity to known protein
Prosite motifs: RGD (557-560)
LEUCINE_ZIPPER (163-185)
LEUCINE_ZIPPER (475-497)
LEUCINE_ZIPPER (482-504)

```

1 MEESPLSRAP SRGGVNFLNV ARTYIPNTKV ECHYTLPPGT MPSASDWIGI
51 FKVEAACVRD YHTFVWSSVP ESTTDGSPH TSVQFQASYL PKPGAQLYQF
101 RYVNRQGVQC GQSPPFQFRE PRPMDELVTI EEADGGSFIL LVVPKATVLQ
151 NQLDESQWER NDLMQLKLQL EGQVTELRSR VQELERLAT ARQHTLME
201 QYKGISRSYG EITEERDILS RQGGDHVARI LELEDDIQT SEKVLTKVEE
251 LDRLRDTVKA LTREQEKLGL QLKEVQADKE QSEAEQVAQ QENHHLNLDL
301 KEAKSWQEEQ SAQAQRLKDK VAQMKDTLGQ AQORVAELEP LKEQLRGAQE
351 LAASSQKQAT LLGEELASAA AARDRTIAEL HRSRLEVAEV NGRLELGLH
401 LKEEKCQWSK ERAGLLQSV EAKDKILKLS AEILRLEKAV QEERTQNVF
451 KTELAREKDS SLVQLSESKR ELTELRSALR VLQKEKEQLQ EEKQELLEYM
501 RKLEARLEKV ADEKWNEDAT TEDEEAAVGL SCPAALTDE DESPEMRLP
551 PYGLCERQGP GSSPAGPREA SPLVVISQPA PISPHLSGPA EDSSSDSEAE
601 DEKSVLMAAV QSGGEEANLL LPELGSAFYD MASGFTVGT SETSTGGPAT
651 PTWKECPICK ERFPAESDKD ALEDHMDGHF FFSTQDPFTF E

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_7p9, frame 3

PIR:A56733 nuclear domain 10 protein NDP52 - human, N = 2, Score = 307,
P = 7.7e-28

TREMBL:AB008852_1 gene: "NDP"; product: "NDP52"; Bos taurus mRNA for NDP52, complete cds., N = 2, Score = 302, P = 4e-27

TREMBL:AC004549_1 gene: "WUGSC:H_RG459N13.1"; product: "TXBP151"; Homo sapiens BAC clone RG459N13 from 7p15, complete sequence., N = 2, Score = 275, P = 2.3e-25

PIR:G02043 TXBP151 - human, N = 2, Score = 270, P = 8.5e-25

TREMBL:DM35816_4 gene: "zip"; product: "nonmuscle myosin-II heavy chain"; Drosophila melanogaster nonmuscle myosin-II heavy chain (zip) gene, complete cds., N = 1, Score = 254, P = 1.4e-17

>PIR:A56733 nuclear domain 10 protein NDP52 - human
Length = 446

HSPs:

Score = 307 (46.1 bits), Expect = 7.7e-28, Sum P(2) = 7.7e-28
Identities = 104/323 (32%), Positives = 158/323 (48%)

Query: 15 VNFLNVARTYIPNTKVECHYTLPPGTMPASDWIGIFKVEAACVRDYHTFVWSSVPESTT 74
V F +V + YIP V CHYT +P DWIGIF+V R+Y+TF+W ++P
Sbjct: 23 VIFNSVEKFYIPGGDVTCHYTFTQHFIPRRKDWIGIFRVGWKTTREYYTFMWVTLPIDLN 82

Query: 75 DGSPIHTSVQFQASYLPKPGAQLYQFRYVNRQGVCGQSPFPQFREPRPMDELVTLEAD 134
+ S VQF+A YLPK + YQF YV+ G V G S PFQFR D LV +
Sbjct: 83 NKSAAQQEVQFKAYYLPKDD-EYYQFCYVDEGTVRGASIPFQFRENEEDILVVTQ-- 139

Query: 135 GGS DILLVVPKATVLQNQ-LDES---QQERN DLMQLKLQLEGQVTE-LRSRVQELERALA 189
G + + K +NQ L +S Q++N MQ +LQ + + E L+S ++LE +
Sbjct: 140 GEVEEIEQHKNELCKENQELKDSCISLQKQNSDMQAE LQKKQEELETLSINKKLELVK 199

Query: 190 TARQE-HTELMEQYKGISRSHGEITEERDI-LSRQQGDHVARILELEDDIQTISEKVLTK 247
+ TEL+ Q K ++ E+ I + + Q + E+E +Q +K T+
Sbjct: 200 EQKDYWETELL-QLKEQNQKMSSSENEKMGIRVDQLQAQLSTQEKEMEKLVQGDQDK--TE 256

Query: 248 EVE-LDRLDTVKALTREQEKLKGQLKEVQADKEQSEAELQVAQQENHHLNLDLKEAKSW 306
++E L + D + EQ K +L++ +Q+E QQE N DL + S
Sbjct: 257 QLEQLKKENDHFLSLTEQRKDQKKLEQTVEQMKQNETTAMKKQQLMDENFDLSKRLSE 316

Query: 307 QEEQSAQAQRLKDKVAQM KDTLGQAQQRV 335
E QR K+++ D L + R+
Sbjct: 317 NEIICNALQRQKERLEGENDLLKRENSRL 345

Score = 304 (45.6 bits), Expect = 2.1e-27, Sum P(2) = 2.1e-27
Identities = 98/337 (29%), Positives = 163/337 (48%)

Query: 15 VNFLNVARTYIPNTKVECHYTLPPGTMPASDWIGIFKVEAACVRDYHTFVWSSVPESTT 74
V F +V + YIP V CHYT +P DWIGIF+V R+Y+TF+W ++P
Sbjct: 23 VIFNSVEKFYIPGGDVTCHYTFTQHFIPRRKDWIGIFRVGWKTTREYYTFMWVTLPIDLN 82

Query: 75 DGSPIHTSVQFQASYLPKPGAQLYQFRYVNRQGVCGQSPFPQFREPRPMDELVTLEAD 134
+ S VQF+A YLPK + YQF YV+ G V G S PFQFR P +E
Sbjct: 83 NKSAAQQEVQFKAYYLPKDD-EYYQFCYVDEGTVRGASIPFQFR---PENE----- 130

Query: 135 GGS DILLVVPKATVLQNQLDESQQERN DLMQLKLQLEGQVTELSRVQELERALATARQE 194
DIL+V Q +++E +Q +L + +L+ L+ + +++ L +QE
Sbjct: 131 --EDILVVT-----QGEVEEIEQHKNELCKENQELKDSCISLQKQNSDMQAE LQK-KQE 182

Query: 195 HTELMQYKGISRSHGEITEERDILSRQQGDH-VARILELEDDIQTISEKVLTKVELDR 253
E ++ I ++ ++ ++Q D+ +L+L++ Q +S + + +D+
Sbjct: 183 ELETQS-----INKKLELVKVEKQKDYWETELLQLKEQNQKMSSSENEKMGIRVDQ 232

Query: 254 LRDTVKALTREQEKL--GQLKEVQAD---KEQSEAELQVAQQENHHLNLDLKEAKSWQE 308
L+ + +E EKL+ Q K Q + KE L + +Q L+ + Q
Sbjct: 233 LQAQLSTQEKEMEKLVQGDQDKTEQLEQLKKENDHFLSLTEQRKDQKKLEQTVEQMKQN 292

Query: 309 EQSA--QAQRLKDKVAQM KDTLGQAQQRVAELEPLKEQLRGAQEL 351
E +A + Q L D+ + L + + L+ KE+L G +L
Sbjct: 293 ETTAMKKQQLMDENFDLSKRLSENEIICNALQRQKERLEGENDL 337

Score = 124 (18.6 bits), Expect = 2.3e-06, Sum P(2) = 2.3e-06
Identities = 53/227 (23%), Positives = 113/227 (49%)

Query: 138 DILLVVPKATVLQNQLDESQQERN DLMQLKLQLEGQVTELSRVQELERALATARQEHT 197
DIL+V Q +++E +Q +L + +L+ L+ + +++ L +QE E
Sbjct: 132 DILVVT-----QGEVEEIEQHKNELCKENQELKDSCISLQKQNSDMQAE LQK-KQEELE 185

Query: 198 LMEQYKGISRSHGEITEERDILSRQQGDH-VARILELEDDIQTISEKVLTKVELDR 256
++ I ++ ++ ++Q D+ +L+L++ Q +S + + +D+L+
Sbjct: 186 TLQS-----INKKLELVKVEKQKDYWETELLQLKEQNQKMSSSENEKMGIRVDQLQA 235

Query: 257 TVKALTREQEKLKGQLKEVQADKEQSEAELQVAQQENHHLNLDLKEAKSWQEEQSAQQR 316
+ +E EKL VQ D++++E +L+ ++EN HL L L E + Q++ ++
Sbjct: 236 QLSTQEKEMEKL-----VQGDQDKTE-QLEQLKKENDHFLSLTEQRKDQKKLEQTVEQ 288

Query: 317 LK-DKVAQMKDTLGQAQQRVAELEPLKEQLRGAQELA-ASSQKATLLGE 364
 +K ++ MK + Q+ + E L ++L + + A +OK L GE
 Sbjct: 289 MKQNETTAMK----KQELMDENFDLSKRLSENEIICNALQRQKERLEGE 334

Score = 103 (15.5 bits), Expect = 4.4e-04, Sum P(2) = 4.4e-04
 Identities = 63/278 (22%), Positives = 123/278 (44%)

Query: 299 DLKEAKSWQEEQSAQAQRLKDKVAQMK---DTLGQAQQRVAELEPLKEQLRGAQELAAS 354
 +++E + +E + Q LKD ++ D + Q++ ELE L + + EL
 Sbjct: 141 EVEEIEQHNLCKENQELKDSCISLQKQNSDMQAELOKKQEELET--QSINKKLELKV 199

Query: 355 SQKATLLGEELASAAAARDRTIAELHRSRLEVAEVNGLRLAELGLHLKEEKQWSKERAG 414
 Q+ EL + +E + + V ++ +L+ + E+ Q +++
 Sbjct: 200 EQKD--YWETELLQLKEQNQKMSSENEKMGIRVDQLQAQLSTQEKEM-EKLVQGDQDKTE 256

Query: 415 LQSVAEAEKDKI-LKLSAEIL---RLEKAVQEERTQNVFKTELAREKDSSLVQLSESKR 470
 L+ ++ E D + L L+ + +LE+ V E+ QN+ T + +++ SKR
 Sbjct: 257 QLEQLKKENDHFLSLTEQRKDQKKLEQTV-EQMKQNET--TAMKKQELMDENFDLSKR 313

Query: 471 ELTELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN---DATEDEEAA 527
 L+E LQ++KE+L+ E +LL ++ +RL +N T DE A
 Sbjct: 314 -LSENEIICNALQRQKERLEGEN-DLL---KRENSRLLSYMGDLFNSLPYQVPTSDEGGA 368

Query: 528 ---VGLSCPAALTD-SEDESPEDMRPPYGLCERDGPSSPAGPREASPL 573
 GL+ + E SP + + +C+ D ++ PL
 Sbjct: 369 RQNPGLAYGNPYSGIQESSSPSLSIKKCPICKADDICDHTLEQQQMQL 418

Score = 64 (9.6 bits), Expect = 7.7e-28, Sum P(2) = 7.7e-28
 Identities = 13/29 (44%), Positives = 17/29 (58%)

Query: 651 PTWKECPICKERFPAESDKDALEDHMDGH 679
 P CPIC + FPA ++K EDH+ H
 Sbjct: 417 PLCFNCPICDKIFPA-TEKQIFEDHVFCH 444

Score = 64 (9.6 bits), Expect = 5.8e+00, Sum P(2) = 1.0e+00
 Identities = 26/90 (28%), Positives = 45/90 (50%)

Query: 470 RELTELRSALRVLQKEKEQLQEE---KQELLEYMRKLEARLE-KVADEK--W----- 515
 +E EL+ + LQK+ +Q E KQE LE ++ + +LE KV ++K W
 Sbjct: 154 KENQELKDSCISLQKQNSDMQAELOKKQEELETLSINKKLELKVKEQKDYWETELLQLK 213

Query: 516 --NEDATTEDEEAAVGLS-CPAALTDSEDE 542
 N+ ++E+E+ + + A L+ E E
 Sbjct: 214 EQNQKMSSENEKMGIRVDQLQAQLSTQEKE 243

Score = 47 (7.1 bits), Expect = 4.6e-26, Sum P(2) = 4.6e-26
 Identities = 11/30 (36%), Positives = 17/30 (56%)

Query: 631 MASGFTVGTLSSTSTGGPATPTWKECPICK 660
 +A G + E+S+ P + K+CPICK
 Sbjct: 374 LAYGNPYSGIQESSSPSLSI--KKCPICK 401

Pedant information for DKFZphtes3_7p9, frame 3

Report for DKFZphtes3_7p9.3

[LENGTH] 691
 [MW] 77336.52
 [pI] 4.77
 [HOMOL] PIR:A56733 nuclear domain 10 protein NDP52 - human 2e-29
 [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 2e-11
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YDR356w] 2e-11
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 2e-11
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR356w] 2e-11
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 2e-11
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR309c] 2e-08
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-07
 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-07
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-07
 [FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YJL074c] 4e-07
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YNL250w] 4e-06
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YBR289w] 4e-06

[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YBR289w]
4e-06

[FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YBR289w] 4e-06

[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 4e-06

[FUNCAT] 03.13 meiosis [S. cerevisiae, YNL250w] 4e-06

[FUNCAT] 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1643] 1e-05

[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR134c] 4e-05

[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 4e-05

[FUNCAT] 08.19 cellular import [S. cerevisiae, YNL243w] 7e-05

[FUNCAT] 01.03.16 polynucleotide degradation [S. cerevisiae, YNL243w] 7e-05

[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YNL243w] 7e-05

[FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL079c] 2e-04

[FUNCAT] 03.01 cell growth [S. cerevisiae, YNL079c] 2e-04

[BLOCKS] BL00682B ZP domain proteins

[EC] 3.6.1.32 Myosin ATPase 1e-13

[PIRKW] nucleus 6e-10

[PIRKW] phosphotransferase 2e-07

[PIRKW] duplication 9e-07

[PIRKW] citrulline 1e-09

[PIRKW] tandem repeat 1e-13

[PIRKW] heart 5e-11

[PIRKW] endocytosis 5e-09

[PIRKW] polymorphism 3e-06

[PIRKW] cornified cell envelope 1e-06

[PIRKW] transmembrane protein 6e-12

[PIRKW] serine/threonine-specific protein kinase 2e-07

[PIRKW] cell wall 1e-06

[PIRKW] zinc finger 5e-09

[PIRKW] metal binding 5e-09

[PIRKW] DNA binding 8e-08

[PIRKW] muscle contraction 1e-11

[PIRKW] IgG constant region-binding 1e-06

[PIRKW] acetylated amino end 4e-09

[PIRKW] actin binding 1e-13

[PIRKW] mitosis 9e-09

[PIRKW] microtubule binding 9e-09

[PIRKW] ATP 1e-13

[PIRKW] thick filament 1e-10

[PIRKW] phosphoprotein 1e-13

[PIRKW] epidermis 1e-06

[PIRKW] leucine zipper 1e-07

[PIRKW] glycoprotein 4e-07

[PIRKW] skeletal muscle 4e-10

[PIRKW] disulfide bond 1e-07

[PIRKW] calcium binding 1e-09

[PIRKW] alternative splicing 1e-10

[PIRKW] coiled coil 1e-13

[PIRKW] P-loop 1e-13

[PIRKW] heptad repeat 6e-10

[PIRKW] methylated amino acid 1e-13

[PIRKW] basement membrane 3e-06

[PIRKW] immunoglobulin receptor 2e-07

[PIRKW] peripheral membrane protein 5e-09

[PIRKW] dimer 1e-07

[PIRKW] cardiac muscle 1e-10

[PIRKW] extracellular matrix 3e-06

[PIRKW] hydrolase 1e-13

[PIRKW] microtubule 6e-10

[PIRKW] muscle 2e-09

[PIRKW] membrane protein 3e-06

[PIRKW] EF hand 1e-09

[PIRKW] cytoskeleton 6e-12

[PIRKW] hair 1e-09

[PIRKW] calmodulin binding 5e-09

[PIRKW] Golgi apparatus 3e-08

[SUPFAM] myosin heavy chain 1e-13

[SUPFAM] conserved hypothetical P115 protein 1e-08

[SUPFAM] hypothetical protein YJL074c 5e-07

[SUPFAM] centromere protein E 9e-09

[SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 2e-07

[SUPFAM] calmodulin repeat homology 1e-09

[SUPFAM] myosin motor domain homology 1e-13

[SUPFAM] alpha-actinin actin-binding domain homology 3e-13

[SUPFAM] tropomyosin 3e-07

[SUPFAM] plectin 3e-13

[SUPFAM] trichohyalin 1e-09

[SUPFAM] pleckstrin repeat homology 4e-06

[SUPFAM] ribosomal protein S10 homology 3e-13

[SUPFAM] giantin 3e-08
 [SUPFAM] protein kinase homology 2e-07
 [SUPFAM] protein kinase C zinc-binding repeat homology 4e-06
 [SUPFAM] involucrin 1e-06
 [SUPFAM] kinesin motor domain homology 9e-09
 [SUPFAM] human early endosome antigen 1 5e-09
 [SUPFAM] unassigned kinesin-related proteins 8e-08
 [SUPFAM] M5 protein 3e-08
 [SUPFAM] cytoskeletal keratin 3e-08
 [PROSITE] LEUCINE_ZIPPER 3
 [PROSITE] RGD 1
 [PROSITE] MYRISTYL 6
 [PROSITE] CK2_PHOSPHO_SITE 25
 [PROSITE] PKC_PHOSPHO_SITE 6
 [KW] All_Alpha
 [KW] LOW_COMPLEXITY 9.12 %
 [KW] COILED_COIL 39.36 %

SEQ MEESPLSRAPSRGGVNFNLNVRTYIPNTKVECHYTLPPGTMPASDWIGIFKVEAACVRD
 SEG
 PRD ccc
 COILS
 SEQ YHTFVWSSVPESTTDGSPHITSVQFQASYLPKPGAQLYQFRYVNRQGVCGQSPFPQFRE
 SEG
 PRD eeeeeeeeecc
 COILS
 SEQ PRPMDLVLTLEADGGSDILLVVPKATVLQNQLDESQQRNDLMQLKLQLEGQVTELSR
 SEG
 PRD cccccceehhhhhchhh
 COILSCC
 SEQ VQELERALATARQEHTELMEQYKGISRSHGEITEERDILSRQGDHVARILELEDDIQT
 SEG
 PRD hhh
 COILS CC
 SEQ SEKVLTKVELDRLRDTVKALTREQEKLGLQKEVQADKEQSEAEQVAQENHHLNLDL
 SEG
 PRD hhh
 COILSCC
 SEQ KEAKSWQEEQSAQAORLKDVAQMDTLGQAQORVAELEPLKEQLRGAQELAASSQKAT
 SEG
 PRD hhh
 COILS CCCCC..CC
 SEQ LLGEELASAAAARDRTIAELHRSRLVAEVNGLRLAELGLHLKEEKQWSKERAGLLQSVE
 SEG xxx
 PRD hhh
 COILS CCCCCCCC.....CCCCCCCCCCCC
 SEQ AEKDKILKLSAEILRLKAVQEERTQNVFKTELAREKDSLSVQLSESKRELTELSALR
 SEG
 PRD hhh
 COILS CC
 SEQ VLQKEKEQLQEEKQELLEMYMRKLEARLEKVADEKWNEDATTEDEEAAGLSCPAALTDSE
 SEG .xx
 PRD hhh
 COILS CC
 SEQ DESPEDMRLPPYGLCERDGPSSPAGPREASPLVVISQAPISPHLSGPAEDSSSDSEAE
 SEG
 PRD hhhhhccch
 COILS
 SEQ DEKSVLMAAVQSGGEEANLLPELGSAFYDMASGFTVGTLSSETSTGGPATPTWKECPICK
 SEG xx.....
 PRD hhhhhhhhhhhhhcc
 COILS
 SEQ ERFPAESDKDALEDHMDGHFFSTQDPFTFE
 SEG
 PRD cccccccchhhhhhhcccccecccccccccc
 COILS

Prosites for DKFZphtes3_7p9.3

PS000005	190->193	PKC_PHOSPHO_SITE	PDOC000005
PS000005	241->244	PKC_PHOSPHO_SITE	PDOC000005
PS000005	257->260	PKC_PHOSPHO_SITE	PDOC000005
PS000005	468->471	PKC_PHOSPHO_SITE	PDOC000005
PS000005	652->655	PKC_PHOSPHO_SITE	PDOC000005
PS000005	667->670	PKC_PHOSPHO_SITE	PDOC000005
PS000006	28->32	CK2_PHOSPHO_SITE	PDOC000006
PS000006	43->47	CK2_PHOSPHO_SITE	PDOC000006
PS000006	68->72	CK2_PHOSPHO_SITE	PDOC000006
PS000006	72->76	CK2_PHOSPHO_SITE	PDOC000006
PS000006	129->133	CK2_PHOSPHO_SITE	PDOC000006
PS000006	156->160	CK2_PHOSPHO_SITE	PDOC000006
PS000006	208->212	CK2_PHOSPHO_SITE	PDOC000006
PS000006	239->243	CK2_PHOSPHO_SITE	PDOC000006
PS000006	282->286	CK2_PHOSPHO_SITE	PDOC000006
PS000006	305->309	CK2_PHOSPHO_SITE	PDOC000006
PS000006	376->380	CK2_PHOSPHO_SITE	PDOC000006
PS000006	383->387	CK2_PHOSPHO_SITE	PDOC000006
PS000006	468->472	CK2_PHOSPHO_SITE	PDOC000006
PS000006	520->524	CK2_PHOSPHO_SITE	PDOC000006
PS000006	537->541	CK2_PHOSPHO_SITE	PDOC000006
PS000006	539->543	CK2_PHOSPHO_SITE	PDOC000006
PS000006	543->547	CK2_PHOSPHO_SITE	PDOC000006
PS000006	593->597	CK2_PHOSPHO_SITE	PDOC000006
PS000006	595->599	CK2_PHOSPHO_SITE	PDOC000006
PS000006	597->601	CK2_PHOSPHO_SITE	PDOC000006
PS000006	612->616	CK2_PHOSPHO_SITE	PDOC000006
PS000006	639->643	CK2_PHOSPHO_SITE	PDOC000006
PS000006	652->656	CK2_PHOSPHO_SITE	PDOC000006
PS000006	667->671	CK2_PHOSPHO_SITE	PDOC000006
PS000006	683->687	CK2_PHOSPHO_SITE	PDOC000006
PS000008	39->45	MYRISTYL	PDOC000008
PS000008	107->113	MYRISTYL	PDOC000008
PS000008	204->210	MYRISTYL	PDOC000008
PS000008	414->420	MYRISTYL	PDOC000008
PS000008	561->567	MYRISTYL	PDOC000008
PS000008	613->619	MYRISTYL	PDOC000008
PS000016	557->560	RGD	PDOC000016
PS000029	163->185	LEUCINE_ZIPPER	PDOC000029
PS000029	475->497	LEUCINE_ZIPPER	PDOC000029
PS000029	482->504	LEUCINE_ZIPPER	PDOC000029

(No Pfam data available for DKFZphtes3_7p9.3)

DKFZphtes3_8e24

group: signal transduction

DKFZphtes3 8e24.3 encodes a novel 658 amino acid putative GTP-binding protein, related to yeast YGL099w and mouse MMRL putative GTP-binding proteins.

GTP-binding proteins are involved in various signal transduction pathways, transferring the signal of a cellular receptor to an intracellular signal cascade.

The new protein can find clinical application in modulating/blocking the response to a cellular receptor.

strong similarity to guanine nucleotide binding proteins

complete cDNA, complete cds, potential start at Bp 31, EST hits

Sequenced by MediGenomix

Locus: unknown

Insert length: 3290 bp

Poly A stretch at pos. 3269, polyadenylation signal at pos. 3251

```
1 CGTCCAGCGG TCGTGTGGCC ATGGGCCGGA GGAGAGCCCC GGCCGGTGGG
51 TCGCTGGGAC GGGCCCTTAT GCGCCATCAG ACTCAGCGGA GCCGAAGCCA
101 TCGTCACACT GACTCCTGGT TGCACACAAG TGAATCAAT GATGGCTATG
151 ATTGGGGTCG TCTTAATCTT CAGTCAGTGA CTGAACAGAG CTCCCTTGAT
201 GACTTCCTTG CTACTGCAGA ACTTGCAGGA ACAGAGTTTG TAGCTGAAAA
251 ACTTAATATT AAGTTTGTGC CTGCTGAGGC TAGAACTGGA CTACTGTCTT
301 TCGAGGAGAG CCAGAGAATT AAGAAGCTCC ATGAAGAAAA CAAACAGTTC
351 TTGTGTATAC CGAGGAGACC AAACCTGGAAC CAAAATACTA CCCCAGAAGA
401 ACTCAACAA GCAGAGAAAG ATAACCTTCT AGAATGGAGA CGTCAGCTTG
451 TCCGGCTAG AGAGGAACAG AAGCTGATAT TGACTCCATT TGAACGAAAT
501 TTGGACTTTT GCGCCAGCT CTGGAGAGTC ATTGAGAGAA GTGATATTGT
551 GGTCCAGATA GTAGATGCTC GAAACCCACT CCTGTTTAGA TGTGAGGATT
601 TGGAAATGTTA TGTGAAAGAA ATGGATGCCA ATAAGGAGAA CGTCATTCTG
651 ATCAACAAGG CAGACTTGCT GACTGCTGAG CAGCGGAGTG CCTGGGCCAT
701 GTACTTCGAA AAAGAAGATG TGAAGGTTAT TTTCTGGTCA GCTTTGGCCG
751 GAGCCATTCC CCGTAATGGT GACTCTGAGG AAGAGGCAAA CAGAGATGAT
801 AGACAAAGCA ACACAACCTGA GTTTGGACAT TCCAGTTTCG ACCAGGCTGA
851 AATTTCACAC AGTGAATCCG AACATCTCCC AGCTAGGGAT TCTCCTTCAC
901 TTAGTGAAAA TCCCACAACG GATGAAGATG ACAGTGAGTA TGAGGACTGT
951 CCAGAGGAGG AGGAAGACGA CTGGCAGACG TGCTCAGAAG AAGACGGTCC
1001 CAAGGAAGAG GACTGCAGCC AGGACTGGAA GGAAGCTCT ACTGCAGATT
1051 CTGAGGCTCG GAGCAGGAAA ACCCCACAGA AGAGGCAGAT ACACAATTTT
1101 AGCCATCTGG TATCCAAGCA GGAGTTACTG GAGCTCTTTA AGGAGCTACA
1151 CACTGGGAGA AAGGTGAAAG ATGGGCAACT TACGGTCGGA CTGGTGGGCT
1201 ACCCTAATGT TGGTAAGAGT TCAACAATCA ACACCATCAT GGGCAACAAG
1251 AAAGTATCTG TGTCTGCCAC ACCTGGTCAC ACAAAGCACT TTCAGACTCT
1301 CTATGTGGAG CTGGCCTCT GCCTGTGTGA CTGTCTGGC TTGGTGATGC
1351 CATCTTTTGT GTCTACCAAG GCAGAAATGA CTTGCAGCGG AATCCTCCCA
1401 ATTGATCAGA TGAGAGATCA TGTTCTCCT GTATCACTAG TTTGCCAGAA
1451 TATTCCAAGA CATGTTTTAG AAGCTACCTA TGCCATTAC ATCATAACGC
1501 CTAGAGAGGA TGAAGATCCC CACCGACCTC CAACATCGGA AGAACTGTTG
1551 ACAGCTTATG GATACATGCG AGGATTCATG ACAGCGCATG GACAGCCAGA
1601 CAGGCTCGA TCTGCGCGCT ACATCCTGAA GGACTATGTC AGTGGTAAGC
1651 TGCTGTACTG CCATCCTCCT CCTGGAAGAG ATCCTGTAAC TTTTCAGCAT
1701 CAACACCAGC GACTCCTAGA GAACAAAATG AACAGTGATG AAATAAAAAAT
1751 GCAGCTAGCG AGAAATAAAA AAGCAAAGCA GATTGAAAAT ATCGTTGACA
1801 AAACTTTTTT CCATCAAGAG AATGTGAGGG CTTTGACCAA AGGAGTCCAG
1851 GCTGTGATGG GTTACAAGCC CGGGAGTGGT GTAGTGACTG CATCCACTGC
1901 GAGCTCTGAG AATCGGGCGG GGAAGCCCTG GAAAAAACAT GGCACAGAA
1951 ATAAAAAGA AAAAAGTCGT AGACTCTACA AGCACCTGGA TATGTGAGGT
2001 TGGGCTGCAA CAGAAATGTC ATCTGCATTG TGCAGATGGA AAAGAGCAGA
2051 AGCTGCCTGT TGCCTGTGGA ACTGTCCCAA GACACTAGCA CTGTAGAACG
2101 GGCCCTGCTC TTGCAGAGCA CGGCTGCACC CAACAGTCTC CATGTCAAGA
2151 CCAAGGGCCT CTTGGAAACA CCAGCTCTGA CAAAAGGAG TCATCTGGGA
2201 CCCCAGAAAT CCTACTCCTG GCCGGGCACA GTGGCTCAGC CACCAACATG
2251 GAGAAACCCC GTCTCTACTA AAAATACAAA AAAATTAGCC AGGCGTGGTG
2301 GCGCGCACCT GTAATCCCAG TACTCGGGA GGCTGAGGCA GGAGAATCAC
2351 TTGAACCAAG GAGCAGAGT TTGCAGTGAA TGGAGATTGC GCCGCTGCAC
2401 TCCAGCCTGG GCGACAGAGT GAGACTGCAT CACAAGAAAA AAAATTGCA
2451 AGGGATGGT CACGAGACAC ATTTGGGACG AAGGTGAAAG AGAAATTCCC
2501 CATTCCTGAT GTCCTAGTTG GGTTCCTCCG ACTCTAAACA AGGGACTTGG
2551 GTTCAAGTTAG TGTACAGCGG GGGCTCACGT CCACTAAGGA ACATGTAGAA
2601 TGTAACCACC GGGTGACAGG GAAGCTGCGG TATTTACTAC CTAGCCCCCA
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2651 TCTTCACTGG TTATTCCACT TATTTAAAT GTCCAGAATA AGCAAATCTC
2701 CATATAGAGG AAGTAGATTA GTGGTTGCTT CGGGATGGGA GGAATGGGAA
2751 GATTGAGGTC TTTCTTTTGC AGTGATAAAA ATGTCTTAAA ATTGACTGTA
2801 GCGATGGTCA CACAACTCTG AATATGCTTA AGACCATTGA ATTACACACT
2851 TTACGTTGGT GAATTGTATG GTATGTAAAT TATAGTTCAA TAACATAGTT
2901 ACAAAGATA ATCAAAGCA TGAAAGCACT ATGTATGTGG TTGGATCTG
2951 TGCTCTCACC GAGTCTCATG TTGAAATGTA AGCCCCCTGG TGGGAGGCGA
3001 TGGGATTATG GGGCAGAGTC CTCACAAACG GTTAGCACC ACCCGCTCAG
3051 TGCTGTTCTC CTGATATTGA GTCCTCATCA CATCTGGTTG CTTCAAAGTG
3101 TGTGGTGCCT CCCCTCTGTC TCCCTCCTGC TCTGGCCATA TAAGATGTGC
3151 CTGCTTCTCC TTCGCCTTCT AACATGATTG TAAGTTTCCT GAGGCCTCCC
3201 TAGAAGCAAA AGCTGCTGTG CTTCTGTAC CATCTACTGG ACCGTGAGCC
3251 AATTAAACCT CTTTCTTTA TAAAAAAGG AAAAAAAGG

```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 21 bp to 1994 bp; peptide length: 658
 Category: strong similarity to known protein

```

1 MGRRRAPAGG SLGRALMRHQ TQSRSRHRHT DSWLHTSELN DGYDWGRNLN
51 QSVTEQSSLD DFLATAELAG TEFVAEKLNI KFPVPAEARTG LLSFEESQRI
101 KKLHEENKQF LCIPRRPNWN QNTTPEELKQ AEKDNFLEWR RQLVRLEEEQ
151 KLILTPFERN LDFWRQLWRV IERSDIVVQI VDARNPLLFR CEDLECYVKE
201 MDANKENVIL INKADLLTAE QRSAWAMYFE KEDVKVIFWS ALAGAIPLNG
251 DSEEEANRDD QSNNTTEFGH SSFDQAEISH SESEHLPARD SPSLSENPTT
301 DEDDSEYEDC PEEEDDWQT CSEEDGPKEE DCSQDWKESS TADSEARSRK
351 TPQKRQIHNF SHLVSKQELL ELFKELHTGR KVKDQQLTVG LVGYPNVGKS
401 STINTIMGNK KVSVSATPGH TKHFQTLTYVE PGLCLDCDPCG LVMPSEFVSTK
451 AEMTCSGILP IDQMRDHVPP VSLVCQNIPIR HVLEATYGIN IITPREDEDP
501 HRPPTSEELL TAYGYMRGFM TAHGQPDQPR SARYILKDYV SGKLLYCHPP
551 PGRDPVTFQH QHORLLENKM NSDEIKMQLG RNKKAKQIEN IVDKTFHHQE
601 NVRALTKGVQ AVMGYKPGSG VVTASTASSE NGAGKPWKKH GNRNKKKESR
651 RLYKHLDM

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_8e24, frame 3

SWISSPROT:YAWG_SCHPO HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN
 CHROMOSOME I., N = 3, Score = 560, P = 1.6e-111

PIR:S64106 hypothetical protein YGL099w - yeast (Saccharomyces
 cerevisiae), N = 2, Score = 544, P = 2.6e-105

TREMBL:CEAF3143_1 gene: "C53H9.2"; Caenorhabditis elegans cosmid
 C53H9., N = 1, Score = 551, P = 2.9e-53

SWISSPROT:MMR1_MOUSE POSSIBLE GTP-BINDING PROTEIN MMR1., N = 2, Score =
 311, P = 7.5e-31

>SWISSPROT:YAWG_SCHPO HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN
 CHROMOSOME I.
 Length = 616

HSPs:

Score = 560 (84.0 bits), Expect = 1.6e-111, Sum P(3) = 1.6e-111
 Identities = 119/253 (47%), Positives = 163/253 (64%)

Query: 12 LGRALMRHQ TQSRSRHRHT DSWLHTSELN DGYDWGRNLN QSVTEQSSLD DFLATAELAGT 71
 LGRA+ T+ R+ + H + + R L+SVT ++ LD+FL TAEI

Sbjct: 12 LGRAIQSDFTKNRRNRK--GGLKHIVSDPKAH--RAALRSVTHETDLDEFNLTAELGEV 67

Query: 72 EFVAEKLNIKFVP-AEARTGLLSFEESQRIKKLHEENKQFLCIPRRPNWNQNTTPEELKQ 130
EF+AEK N+ + E LLS EE+ R K+ E+NK L IPRRP+W+Q TT EL +

Sbjct: 68 EFIAEKQNVTVIQNPQNPFLLSKEEAARSKQKQEKNDRLTIPRRPHWDQTTTAVELDR 127

Query: 131 AEKDNFLEWRRQLVRLEEEQKLITPFFERNLDFWRQLWRVIERSDIVVQIVDARNPLLFR 190
E+++FL WRR L +L++ + I+TPFFERNL+ WRQLWRVIERSD+VVQIVDARNPL FR

Sbjct: 128 MERESFLNWRRLAQLQDVEGFIVTPFFERNLEIWRQLWRVIERSDVVVQIVDARNPLFFR 187

Query: 191 CEDLECYVKEMDANKENVILINKADLLTAEQRSAWAMYFEKEDVKVIFWSALAGAIPLNG 250
LE YVKE+ +K+N +L+NKAD+LT EQR+ W+ YF + ++ +F+SA A N

Sbjct: 188 SAHLEQYVKEVGPSKKNFLLVNKADMLTEEQRNYWSSYFNENNIPFLFFSARMAA-EANE 246

Query: 251 DSEEEANRDDRQSN 264
E+ + SN

Sbjct: 247 RGEDLETYESTSSN 260

Score = 532 (79.8 bits), Expect = 1.6e-111, Sum P(3) = 1.6e-111
Identities = 131/323 (40%), Positives = 192/323 (59%)

Query: 340 STADSEARSRKTPQKRQIHNFSLVSKQELLELFKELHTGRKVKDGO--LTVGLVGYPNV 397
ST+ +E + +H+ S + + + L +F++ + + DG+ +T GLVGYPNV

Sbjct: 256 STSSNEIPESLQADENDVHS-SRIATLKVLEGIFEKFA--TLPDGKTKMTFGLVGYPNV 312

Query: 398 GKSSTINTIMGNKKVSVSATPGHKTGHFQTLVEPGLCLDCPGLVMPSEVSTKAEMTCSG 457
GKSSTIN ++G+KKVSVS+TPG TKHFQT+ + + L DCPGLV PSF +T+A++ G

Sbjct: 313 GKSSTINALVSGSKVSVSTPGKTKHFQTLINLSEKVSLLDCPGLVFPFATQADLVLDG 372

Query: 458 ILPIDQMRDHPVPSLVLCQNIPIRHVLEATYGINI-ITPREDEDPHRPPTSEELLTAYGYM 516
+LPIDQ+R++ P +L+ + IP+ VLE Y I I I P E E P+++E+L +

Sbjct: 373 VLPIDQLREYTGPSALMAERIPKEVLETLYTIRIRIKPIE-EGGTGVPSAQEVLPFARS 431

Query: 517 RGFMTAH-GQPDQPRSARYILKDYVSGKLLYCHPPPG--RDPVTFQHQHQRLLLENKMNSD 573
RGFM AH G PD R+AR +LKDYV+GKLLY HPPP F +H + + + SD

Sbjct: 432 RGFMAAHGTPDDSRARILLKDYVNGKLLYVHPPPNYPNSGSEFNKEHHQKIVSA-TSD 490

Query: 574 EIKMQLGR---NKKAKQIEN-IVDKTFFHQEN--VRALTQGVQAVM-G--YKPGSGVVTA 624
I +L R + E+ +VD +F QEN VR + KG M G YK + +

Sbjct: 491 SITEKLQRTAISDNTLSAESQLVDDEYF-QENPHVRPMVKGTAVAMQGPVYKGRNTMQPF 549

Query: 625 STASSENGAGK-PWKKHGNRNKKEKSRL 652
+++ + K P G + K+R+L

Sbjct: 550 QRRLLNDASPKYPMNAQKGKPLSRKARQL 578

Score = 47 (7.1 bits), Expect = 1.3e-60, Sum P(3) = 1.3e-60
Identities = 21/84 (25%), Positives = 35/84 (41%)

Query: 552 GRDPVTFQHQHQRLLLENKMNSDEIKMQLGRNKKAKQIENIVDKTFFHQENVRALTQGVQA 611
G D T++ + + +DE + R K +E I +K F TK

Sbjct: 248 GEDLETYESTSSNEIPESLQADENDVHSSRIATLKVLEGIFEK--FASTLPDGKTKMTFG 305

Query: 612 VMGYKPGSGVVTASTASSENGAGK 635
++GY P G +ST ++ G+ K

Sbjct: 306 LVGY-PNVG--KSSTINALVSGSK 326

Score = 43 (6.5 bits), Expect = 1.6e-111, Sum P(3) = 1.6e-111
Identities = 7/13 (53%), Positives = 9/13 (69%)

Query: 638 KKHGNRNKKEKSR 650
KKH +NK+ K R

Sbjct: 596 KKHNNKKNRSKQR 608

Pedant information for DKFZphtes3_8e24, frame 3

Report for DKFZphtes3_8e24.3

[LENGTH] 658
[MW] 75226.58
[pI] 5.86
[HOMOL] SWISSPROT:YAWG_SCHPO HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME
I. 5e-56
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL099w] 3e-55
[FUNCAT] r general function prediction [M. jannaschii, MJ1464] 1e-16
[FUNCAT] 08.16 extracellular transport [S. cerevisiae, YER006w] 3e-09
[PIRKW] P-loop 1e-27
[PIRKW] GTP binding 1e-27
[SUPFAM] conserved hypothetical protein MG442 7e-08

[PROSITE]	ATP_GTP_A	1
[PROSITE]	MYRISTYL	3
[PROSITE]	AMIDATION	2
[PROSITE]	CAMP_PHOSPHO_SITE	1
[PROSITE]	CK2_PHOSPHO_SITE	19
[PROSITE]	TYR_PHOSPHO_SITE	2
[PROSITE]	PKC_PHOSPHO_SITE	10
[PROSITE]	ASN_GLYCOSYLATION	2
[KW]	Alpha_Beta	
[KW]	LOW_COMPLEXITY	4.56 %

```

SEQ      MGRRRAPAGGSLGRALMRHQTRSRSRHRHTDSDLHTSELNDGYDWGRNLNQSVEQSSLD
SEG      .....XXXXXXXXXXXXXXXX.....
PRD      cccccccccccccchhhhhhhhhhhccccccccccccccccccccccccchhhhhhhhhccccch

SEQ      DFLATAELAGTEFVAEKLNIKFPVPAEARTGLLSFEESQRIKKLHEENKQFLCIPRRPNWN
SEG      .....
PRD      hhhhhhhhhhhheeeecceeeeeeccccccchhhhhhhhhhhhhhhhhhhhhhhcccccccccc

SEQ      QNTTPEELKQAEKDNFLEWRRQLVRLEEEQKLILTPFERNLDFWRQLWRVIERSDIVVQI
SEG      .....
PRD      cccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccc

SEQ      VDARNPLLFRCDELECYVKEMDANKENVILINKADLLTAEQRSAWAMYFEKEDVKVIFWS
SEG      .....
PRD      eccccccccchhhhhhhhhhhccccceeeeeeccccchhhhhhhhhhhhhhhhhhhhhhhcccccccc

SEQ      ALAGAIPLNGDSEEEANRRDRQSNTEFGHSSFDQAEISHSESEHLPARDSPSLSENPTT
SEG      .....
PRD      cccccccccccccchhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccc

SEQ      DEDDSEYEDCPEEEEDDWQTCSEEDGPKEEDCSQDWKESSTADSEARSRKTPOKRQIHNF
SEG      .....
PRD      cccccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhcccccccccc

SEQ      SHLVSKQELLELFKELHTGRKVKDQGLTVGLVGYPNVGKSTINTIMGNKKVSVSATPGH
SEG      .....
PRD      cccccchhhhhhhhhhhhhhhhhhhhhccccceeeeeeccccccccccccceeeccccceeecccccc

SEQ      TKHFQTLTYVEPLCLCDCPGLVMPFSFVSTKAEMTCSGILPIDQMRDHVPPVSLVCQNIPR
SEG      .....
PRD      cceeeeeeccccceccccccccccccchhhhhhhhhccccccccccccccccceeeccccch

SEQ      HVLEATYGINIITPREDEDPHRPPTSEELLTAYGYMRGFMTAHGQPDQPRSARYILKDYV
SEG      .....
PRD      hhhhhhhhhccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhcc

SEQ      SGKLLYCHPPPGRDPVTFQHQHQRLLENKMNSDEIKMQLGRNKKAKQIENIVDKTFFHQE
SEG      .....
PRD      cceeeeeeccccccccccccchhhhhhhhhhhccccchhhhhhhhhccchhhhhhhhhhhhhhhhhhhccch

SEQ      NVRALTKGVQAVMGYKPGSGVVTASTASSENGAGKPWKKHGNRNKKEKSRRLYKHLDM
SEG      .....
PRD      hhhhhhhhhceeeeeeccccccccceccccccccccccccccccccccccccccchhhhhhhhhhhhhcc

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Prosite for DKF2phtes3 8e24.3

PS000001	264->268	ASN_GLYCOSYLATION	PDOC000001
PS000001	359->363	ASN_GLYCOSYLATION	PDOC000001
PS000004	410->414	CAMP_PHOSPHO_SITE	PDOC000004
PS000005	21->24	PKC_PHOSPHO_SITE	PDOC000005
PS000005	26->29	PKC_PHOSPHO_SITE	PDOC000005
PS000005	97->100	PKC_PHOSPHO_SITE	PDOC000005
PS000005	348->351	PKC_PHOSPHO_SITE	PDOC000005
PS000005	378->381	PKC_PHOSPHO_SITE	PDOC000005
PS000005	448->451	PKC_PHOSPHO_SITE	PDOC000005
PS000005	493->496	PKC_PHOSPHO_SITE	PDOC000005
PS000005	531->534	PKC_PHOSPHO_SITE	PDOC000005
PS000005	541->544	PKC_PHOSPHO_SITE	PDOC000005
PS000005	649->652	PKC_PHOSPHO_SITE	PDOC000005
PS000006	52->56	CK2_PHOSPHO_SITE	PDOC000006
PS000006	57->61	CK2_PHOSPHO_SITE	PDOC000006
PS000006	93->97	CK2_PHOSPHO_SITE	PDOC000006
PS000006	123->127	CK2_PHOSPHO_SITE	PDOC000006
PS000006	155->159	CK2_PHOSPHO_SITE	PDOC000006
PS000006	252->256	CK2_PHOSPHO_SITE	PDOC000006
PS000006	271->275	CK2_PHOSPHO_SITE	PDOC000006
PS000006	279->283	CK2_PHOSPHO_SITE	PDOC000006

PS00006	281->285	CK2_PHOSPHO_SITE	PDOC00006
PS00006	293->297	CK2_PHOSPHO_SITE	PDOC00006
PS00006	299->303	CK2_PHOSPHO_SITE	PDOC00006
PS00006	305->309	CK2_PHOSPHO_SITE	PDOC00006
PS00006	320->324	CK2_PHOSPHO_SITE	PDOC00006
PS00006	322->326	CK2_PHOSPHO_SITE	PDOC00006
PS00006	340->344	CK2_PHOSPHO_SITE	PDOC00006
PS00006	365->369	CK2_PHOSPHO_SITE	PDOC00006
PS00006	449->453	CK2_PHOSPHO_SITE	PDOC00006
PS00006	493->497	CK2_PHOSPHO_SITE	PDOC00006
PS00006	505->509	CK2_PHOSPHO_SITE	PDOC00006
PS00007	480->488	TYR_PHOSPHO_SITE	PDOC00007
PS00007	190->198	TYR_PHOSPHO_SITE	PDOC00007
PS00008	9->15	MYRISTYL	PDOC00008
PS00008	432->438	MYRISTYL	PDOC00008
PS00008	620->626	MYRISTYL	PDOC00008
PS00009	1->5	AMIDATION	PDOC00009
PS00009	378->382	AMIDATION	PDOC00009
PS00017	393->401	ATP_GTP_A	PDOC00017

(No Pfam data available for DKFZphtes3_8e24.3)

DKFZphtes3_8g11

group: testes derived

DKFZphtes3_8g11 encodes a novel proline-rich 939 amino acid protein without similarity to known proteins.

The novel protein contains an ATP/GTP-binding site motif A (P-loop).
No informative BLAST results; No predictive prosite, pfam or SCOP motive.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown, prolin rich protein

1 EST hit (from testis library)

Sequenced by MediGenomix

Locus: unknown

Insert length: 3100 bp

Poly A stretch at pos. 3056, polyadenylation signal at pos. 3041

```
1 AGAGTCTTCC CTCAGCATAT TTTACGATAG AGAAGATCTT GTTCCAATGG
51 AAGAAAGTGA GGACTCACAG AGTGATTCCC AGACAAGGAT TTCTGAGTCC
101 CAACACTCCC TCAAGCCAAA TTATCTTTCC CAGGCCAAGA CTGACTTCTC
151 AGAACAGTTC CAGTTGCTAG AAGATCTGCA GCTAAAAATA GCAGCAAAAC
201 TCTTAAGGAG TCAAAATACCC CCCGATGTGC CTCCACCTCT AGCTTCAGGT
251 CTAGTCTTAA AATACCCTAT CTGCCTACAG TGTGGCCGAT GTTCAGGACT
301 TAATTGCCAT CATAAATTAC AGACCACTTC GGGGCCTTAT CTCTTATCT
351 ATCCACAGCT CCACCTTGTA CGCACTCCTG AAGGCCATGG TGAGGTTCCG
401 TTGCATCTTG CCTTTAGGCT GAGAATTGGG AAAAGATCCC AAATCTCAAA
451 GTATCGTGAA AGAGATAGAC CCGTCATACG GAGAAGCCCT ATATCACCAT
501 CACAAAGGAA AGCTAAAAATC TATACTCAAG CTTCCAAGAG TCCTACTTCC
551 ACAATAGATT TGCAGTCTGG GCCTTCCCAG TCCCCTGCTC CTGTACAAGT
601 CTACATCAGG CGAGGACAAC GCAGCAGGCC TGACTTAGTA GAAAAGACAA
651 AAAGTAGAGC ACCTGGGCAC TATGAATTCA CTCAAGTTCA CAACCTACCA
701 GAGAGTGACT CTGAAAGCAC TCAGAAATGAA AAACGGGCTA AAGTGAGAAC
751 CAAAAAGACC TCTGATTCAA AATATCCAAT GAAGAGAATC ACCAAGCGAC
801 TTAGAAAACA CAGAAAGTTC TACACAAACA GTAGAACCAC AATAGAGAGT
851 CCTTCTAGGG AATTAGCAGC CCATTTAAGA AGGAAGAGGA TTGGAGCAAC
901 TCAGACAAGT ACTGCCTCTT TAAAAAGACA ACCTAAGAAA CCTTCCCAAC
951 CCAAGTTCAT GCAACTGCTT TTTCAGAGCC TAAAGCGGGC ATTCCAAACA
1001 GCACACAGAG TTATAGCTTC TGTTGGGCGG AAGCCTGTGG ACGGACAAG
1051 GCCAGACAAAT TTGTGGGCAA GCAAAAACCTA TTATCCAAAA CAAAATGCCA
1101 GGGACTATTG CTTACCAAGC AGTATCAAAA GAGACAAGAG GTCAGCTGAC
1151 AAGCTAACGC CAGCAGGCTC AACCATTAAAG CAGGAGGACA TATTGTGGGG
1201 AGGAACGGTC CAGTGCAGAT CAGCTCAACA GCCAAGAAGA GCTTACTCTT
1251 TCCAACCCAG ACCTCTTCGA CTGCCCAAGC CCACAGATTG CCAAAGTGGT
1301 ATTGCTTTCC AAAGTGCCTC AGTGGGGCAG CCTCTGAGAA CTGTTCAAAA
1351 GGACAGTAGT AGCAGATCAA AGAAAACTTT CTATAGAAAT GAAACCTCCA
1401 GCCAGGAGTC TAAGAACTTG TCCACACCAG GAACCAAGAT TCAGGCCCGA
1451 GGAAGAATCC TACCTGGTTC CCTGTGAAG AGAACCTGGC ACCGACATCT
1501 TAAAGACAAA CTCACACACA AGGAGCATAA CCACCCAGC TTCTATAGGG
1551 AGAGAACCCC ACGCGGTCCT TCTGAGAGAA CCGTCAATAA CCCCTCTTGG
1601 AGAAACCATC GCAGTCCCTC TGAGAGAAGC CAACGCAGTT CCTTGGAGAG
1651 AAGACATCAC AGTCCCTCTC AGAGGAGCCA CTGCAGTCCC TCTAGGAAAA
1701 ACCATTCCAG TCCTTCTGAG AGAAGCTGGC GCAGTCCGTC TCAGAGAAAT
1751 CACTGCAGTC CCCCCGAGAG GAGCTGTAC AGTCTCTCTG AAAGGGGCCCT
1801 TCACAGTCCC TCTCAGAGGA GCCATCGCGG TCCCTCTCAG AGAAGACATC
1851 ACAGTCCCTC AGAGAGAAGC CATCGCAGTC CCTCAGAGAG AAGCCATCGC
1901 AGTCCCTCTG AGAGAAGACA TCGCAGTCCC TCCCAGAGGA GCCATCGCGG
1951 TCCCTCAGAG AGAAGCCATT GCAGTCCCTC TGAGAGAAGA CATCGCAGTC
2001 CCTCTCAGAG GAGCCATCGT GGTCCCTCTG AGAGAAGACA TCACAGTCCC
2051 TCTAAGAGAA GCCATCGCAG TCCCGCTCGG AGGAGCCATC GCAGTCCCTC
2101 AGAGAGAAGC CATCACAGTC CCTCTGAGAG AAGCCATCAC AGTCCCTCTG
2151 AGAGAAGACA TCACAGTCCC TCTGAGAGAA GCCATTGCAG TCCCTCTGAG
2201 AGAAGCCATT GCAGTCCCTC TGAGAGAAGA CATCGCAGTC CCTCTGAGAG
2251 AAGACATCAC AGTCCCTCAG AGAAAAGCCA TCACAGTCCC TCTGAGAGAA
2301 GCCATCACAG TCCCTCTGAG AGAAGACGTC ACAGTCCCTT GGAGAGGAGC
2351 CGTCACAGTC TCTTGAGAG GAGCCATCGC AGTCCCTCTG AGAGGAGATC
2401 TCACAGGTCC TTTGAGAGGA GCCATCGTAG GATTCTGAG AGAAGTCACA
2451 GTCCCTCAGA GAAGAGCCAC CTCAGTCCCT TGGAAAGAAG CCGTTGCAGT
2501 CCCTCTGAGA GGAGAGGACA CAGTTCCCTT GGGAAAACCT GTCACAGTCC
2551 CTCTGAGAGA AGCCATCGCA GTCCCTCCGG GATGAGGCAA GGGAGGACCT
2601 CTGAGAGGAG CCATCGCAGT TCCTGTGAGA GAACCCGTCA CAGTCCCTCT
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2651 GAGATGAGGC CAGGGAGGCC CTCTGGGAGG AACCATTGCA GTCCCTCTGA
2701 GAGGAGCCGA CGCAGTCCCC TTAAGGAGGG ACTCAAGTAC AGTTTCCCTG
2751 GAGAGAGGCC CAGCCATAGT TTGTCTAGAG ATTTCAAGAA TCAAACAAC
2801 CTCTCGGGGA CCACACATAA AAATCCCAAA GCAGGGCAAG TGTGGAGGCC
2851 TGAAGCTACT CGATGAGGCG AGGTCCGCCC CTATTATTCA TTGTCTAAG
2901 TCTTCATCGT GCTGCCCTTT CCAGGCTTCT TTCCTGCTCA GCCACTGCCT
2951 CCAATTCCTG CGCCCCCAGC GTGGAAAGGC TTCCATTCT CTCTACCGGG
3001 GGGGAGGCGG GTGAGAATGG GTCTGTAATT TCTCTAAGAT GAATAAAGGG
3051 GCAGTTAATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAGG

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BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 47 bp to 2863 bp; peptide length: 939
 Category: similarity to unknown protein
 Classification: unclassified
 Prosite motifs: ATP_GTP_A (824-832)

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1 MEESEDSQSD SQTRISESQH SLKPNYLSQA KTDSEQFQL LEDLQKIAA
51 KLLRSQIPPD VPPPLASGLV LKYPICLQCG RCGLNCHHK LQTTSGPYLL
101 IYPQLHLVRT PEGHGEVRLH LGFRLRIGKR SQISKYERD RPVIRSPIS
151 PSQRKAKIYT QAKSPTSTI DLQSGPSQSP APVQVYIRRG QRSRPDLVEK
201 TKTRAPGHYE FTQVHNPES DSESTQNEKR AKVRTKKTSD SKYPMKRITK
251 RLRKHKRFYT NSRTTIESPS RELAAHLRRK RIGATQTSTA SLKRQPKKPS
301 QPKFMQLLFQ SLKRAFQTAH RVIASVGRKP VDGTRPDNLW ASKNYYPKQN
351 ARDYCLPSSI KRDKRSADKL TPAGSTIKOE DILWGGTVQC RSAQQPRRAY
401 SFQPRPLRLP KPTDSQSGIA FQTASVGQPL RTVQKDSSSR SKKNFYRNET
451 SSQESKNLST PGTRVQARGR ILPGSPVKRT WHRHLKDKLT HKEHNHPSFY
501 RERTPRGPSE RTRHNPSWRN HRSPSERSQR SSLERRHHSP QRSCHCSPSR
551 KNHSPSERS WRSPSQRNHC SPPERSCHSL SERGLHSPSQ RSHRGPSQRR
601 HHSPSERSHR SPERSHRSP SERRHRSPSQ RSHRGPSERS HCSPSERRHR
651 SPSPSRSHRG SPERRHSPSK RSHRSPARRS HRSPSERSHH SPERSHHSP
701 SERRHHSPSE RSHCSPSERS HCSPSERRHR SPERRHHSP SEKSHHSPSE
751 RSHHSPSERR RSHPLERSRH SLLERSHRSP SERRSHRSFE RSHRISERS
801 HSPSEKSHLS PLERSRCSPS ERRGHSSSGK TCHSPSERSH RSPSGMRQGR
851 TSERSHRSSC ERTRHSPSEM RPGRPSGRNH CSPSERSRRS PLKEGLKYSF
901 PGERPSHSLs RDFKNQTLL GTTHKNPKAG QWRPEATR

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BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_8g11, frame 2

TREMBL:AF061185_1 gene: "car90"; product: "cyst germination specific acidic repeat protein precursor"; *Phytophthora infestans* cyst germination specific acidic repeat protein precursor (car90) gene, complete cds., N = 1, Score = 457, P = 2.3e-39

TREMBL:AC004561_38 gene: "F16P2.41"; product: "putative proline-rich protein"; *Arabidopsis thaliana* chromosome II BAC F16P2 genomic sequence, complete sequence., N = 1, Score = 340, P = 4.2e-27

TREMBL:AF062655_1 product: "plenty-of-prolines-101"; *Mus musculus* plenty-of-prolines-101 mRNA, complete cds., N = 1, Score = 313, P = 3.6e-24

PIR:PN0099 son3 protein - human (fragment), N = 1, Score = 292, P = 1.2e-22

>TREMBL:AF061185_1 gene: "car90"; product: "cyst germination specific acidic repeat protein precursor"; *Phytophthora infestans* cyst germination specific acidic repeat protein precursor (car90) gene, complete cds.

Length = 1,489

HSPs:

Score = 457 (68.6 bits), Expect = 2.3e-39, P = 2.3e-39
 Identities = 91/444 (20%), Positives = 239/444 (53%)

Query: 475 SPVKRTWHRHLKDKLTHKEHNHPSFY-RERTPRGPSETRHNPSWRNHRSPSERSQRSSL 533
 +P + T + +++ T+ ++ E TP P+E T + P+ +P+E + +S
 Sbjct: 584 APTEETMYAPIET-TYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETTYAST 642

Query: 534 ERRHHSQSQRSHCSPSRKNHSSPSERSWRSPSQNRHCSPPERSCHLSERGLHSPSQSRSH 593
 E ++P++ + +P+ + P+E + +P++ +P E + ++ +E ++P++ +
 Sbjct: 643 EETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETTYAPTEETTYAPTEETT 702

Query: 594 RGPSQRRHHSERSHRSPERSHRSPERRHRSQSRSHRGPSERSHCSPSERRHRS 653
 P++ + P+E + +P+E + +P+E +P + + GP+E + +P+E +P+
 Sbjct: 703 YAPAEETPYEPTETTYAPTEETTYAPTEETMYAPIETTYGPTEETTYAPTEATTYAPT 762

Query: 654 QSRHSGPSERRHHSKRSRSHRSPARRSHRSPERSHHSPERSHHSPERRHHSERSH 713
 + + P+E + P+ + +P + +P+E + ++P+E + +P+E +
 Sbjct: 763 EETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTETT 822

Query: 714 CSPSERSHCSPSERRHRSPEKSHHSPERSHHSPERRHRSPLERSRHSL 773
 +P+E + P+E +P+E ++P+E++ ++P+E++ ++P+E ++P E + +
 Sbjct: 823 YAPTEETPYEPTETTYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPT 882

Query: 774 ERSRSPSERRSHRSFERS-HRRISERSHSPSEKSHLSPLERSRCSPSERRGHSSSGKTC 832
 E + +P++ ++ E + + E +++P+E++ +P E + P+E ++ + +T
 Sbjct: 883 EETTYAPTKETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETT 942

Query: 833 HSPSERSHRSPSGMRQRTSERSHRSSCERTRHSPSEMRPGRPSGRNHCSPSERSRRSPL 892
 ++P+E + +P+ +E + + E T + P+E P+ +P+E + +P+
 Sbjct: 943 YAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETMYAPI 1002

Query: 893 KEGLKYSFPGERPSHLSRDFKNQTT 918
 +E Y+ P E +++ + + + T
 Sbjct: 1003 EE-TTYA-PTEETTYAPAEETPYEPT 1026

Score = 445 (66.8 bits), Expect = 4.5e-38, P = 4.5e-38
 Identities = 83/394 (21%), Positives = 212/394 (53%)

Query: 502 ERTPRGPSETRHNPSWRNHRSPSERSQRSSLERRHHSQSQRSHCSPSRKNHSSPSERSW 561
 E TP P+E T + P+ +P+E + + E ++P++ + +P+ + P+E +
 Sbjct: 763 EETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTETT 822

Query: 562 RSPSQNRHCSPPERSCHLSERGLHSPSQSRHSGPSQRRHHSERSHRSPERSHRSPS 621
 +P++ P E + ++ +E ++P++ + P+++ ++P+E + +P+E + P+
 Sbjct: 823 YAPTEETPYEPTETTYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPT 882

Query: 622 ERRHRSQSQRSHRGPSERSHCSPSERRHRSQSRSHRGPSERRHHSKRSRSHRSPARRSH 681
 E +P++ + P+E + + +E +P++ + P+E + P++ + +P +
 Sbjct: 883 EETTYAPTKETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETT 942

Query: 682 RSPERSHHSPERSHHSPERRHHSERSHCSPSERSHCSPSERRHRSPEKSHHSPERSH 741
 +P+E + ++P+E + ++P+E ++P+E + P+E + +P+E +P+E ++P
 Sbjct: 943 YAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETMYAPI 1002

Query: 742 EKSHHSPERSHHSPERRHHSPLERSRHSLERSHRSPERRSHRSFERS-HRRISERS 800
 E++ ++P+E + ++P+E + P E + ++ E + +P+E ++ S E + + E +
 Sbjct: 1003 EETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETTYASTEETTYAPTEETT 1062

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCCHSPERSHRSPSGMRQRTSERSHRSSC 860
 ++P+E++ P E + +P+E ++ + +T ++P+E + +P+ +E +
 Sbjct: 1063 YAPAEETPYEPTETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPT 1122

Query: 861 ERTSRSPSEMRPGRPSGRNHCSPSERSRRSPLKE 894
 E T ++P+E P+ +P E + P +E
 Sbjct: 1123 EETTYAPTEETTYAPTEETMYAPIETTYGPTEE 1156

Score = 439 (65.9 bits), Expect = 2.0e-37, P = 2.0e-37
 Identities = 86/421 (20%), Positives = 223/421 (52%)

Query: 475 SPVKRTWHRHLKDKLTHKEHNHPSFY-RERTPRGPSETRHNPSWRNHRSPSERSQRSSL 533
 +P + T + +K T+ ++ E TP P+E T + P+ +P+E + +S
 Sbjct: 848 APTEETTYAPT-EKTTYAPTEETTYAPTEETPYEPTETTYAPTKETTYAPTEETTYAST 906

Query: 534 ERRHHSQSQRSHCSPSRKNHSSPSERSWRSPSQNRHCSPPERSCHLSERGLHSPSQSRSH 593
 E ++P++ + +P+ + P+E + +P++ +P E + ++ +E ++P++ +
 Sbjct: 907 EETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETTYAPTEETTYAPTEETT 966

Query: 594 RGPSQRRHSPSERSHRSPSERSHRSPSERRHRSPSQRSHRGPSERSHCSPSERRHRSPS 653
 P++ + P+E + +P+E + +P+E +P + + P+E + +P+E P+
 Sbjct: 967 YAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPT 1026

Query: 654 QRSHRGPSERRHHSPSKRSHRSPARRSHRSPSERSHHSPSERSHHSPSERRHHSPSERSH 713
 + + P+E ++P++ + + + +P+E + ++P+E + + P+E ++P+E +
 Sbjct: 1027 EETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETT 1086

Query: 714 CSPSERSHCSPSERRHRSPSERRHHSPSEKSHHSPSERSHHSPSERRHSPLEERSHSL 773
 +P+E + +P+E +P+E ++P+E++ + P+E + ++P+E ++P E + ++ +
 Sbjct: 1087 YAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPI 1146

Query: 774 ERSRSPSERRSHRSFERS-HRRISERSHSPSEKSHLSPLERSRCSPPSERRGHSSSGKTC 832
 E + P+E ++ E + + E ++P+E++ P + +P+E ++ + +T
 Sbjct: 1147 EETTYGPTTEETTYAPTEATTYAPTEETTYAPTEETTYEPTGETTYAPTEETTYAPTEETT 1206

Query: 833 HSPSERSHRSPSGMRQGRTERSRRSSCERTRHSPSEMRPGRPSGRNHCSPPSERSRRSPL 892
 ++P+E + +P+ +E + + E T + P+E P+ +P+E + +P
 Sbjct: 1207 YAPTEETTYAPTEETPYEPTTEETTYAPTEETTYEPTTEETTYAPTEETTYAPTEETTYAPT 1266

Query: 893 KE 894
 +E
 Sbjct: 1267 EE 1268

Score = 439 (65.9 bits), Expect = 2.0e-37, P = 2.0e-37
 Identities = 91/434 (20%), Positives = 232/434 (53%)

Query: 475 SPVKRTWHRHLKDKLTHKEHNHPSFY-RERTPRGPSETRHNPSWRNHRSPSERSQRSSL 533
 +P + T + +K T+ ++ E TP P+E T + P+ +P+E + +S
 Sbjct: 440 APTEETTYAPT-EKTTYAPTEETTYAPTEETPYEPTTEETTYAPTEETTYAPTETTYAPTETTYAST 498

Query: 534 ERRHHSQSRSHCSPPSRKNHSSPERSWRSPSQRNHCSPPERSCHLSERGLHSPSQRSH 593
 E ++P++ + +P+ + P+E + +P++ +P E + ++ +E ++P++ +
 Sbjct: 499 EETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETT 558

Query: 594 RGPSQRRHSPSERSHRSPSERSHRSPSERRHRSPSQRSHRGPSERSHCSPSERRHRSPS 653
 P++ + P+E + +P+E + +P+E +P + + P+E + +P+E P+
 Sbjct: 559 YAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPT 618

Query: 654 QRSHRGPSERRHHSPSKRSHRSPARRSHRSPSERSHHSPSERSHHSPSERRHHSPSERSH 713
 + + P+E ++P++ + + + +P+E + ++P+E + + P+E ++P+E +
 Sbjct: 619 EETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETT 678

Query: 714 CSPSERSHCSPSERRHRSPSERRHHSPSEKSHHSPSERSHHSPSERRHSPLEERSHSL 773
 +P+E + +P+E +P+E ++P+E++ + P+E + ++P+E ++P E + ++ +
 Sbjct: 679 YAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPI 738

Query: 774 ERSRSPSERRSHRSFERS-HRRISERSHSPSEKSHLSPLERSRCSPPSERRGHSSSGKTC 832
 E + P+E ++ E + + E ++P+E++ P + +P+E ++ + +T
 Sbjct: 739 EETTYGPTTEETTYAPTEATTYAPTEETTYAPTEETTYEPTGETTYAPTEETTYAPTEETT 798

Query: 833 HSPSERSHRSPSGMRQGRTERSRRSSCERTRHSPSEMRPGRPSGRNHCSPPSERSRRSPL 892
 ++P+E + +P T E + + E T ++P+E P P+ +P+E + +P
 Sbjct: 799 YAPTEETTYAP-----TEETPYEPT-EETTYAPTEETPYEPTTEETTYTPTEETTYAPT 850

Query: 893 KEGLKYSFPGERPSHS 908
 +E Y+ P E+ +++
 Sbjct: 851 EE-TTYA-PTEKTTYA 864

Score = 437 (65.6 bits), Expect = 3.3e-37, P = 3.3e-37
 Identities = 85/417 (20%), Positives = 223/417 (53%)

Query: 502 ERTPRGPSETRHNPSWRNHRSPSERSQRSSLERRHHSQSRSHCSPPSRKNHSSPERSSW 561
 E TP P+E T + P+ +P+E + + E+ ++P++ + +P+ + P+E +
 Sbjct: 419 EETPYEPTTEETTYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTTEETT 478

Query: 562 RSPSQRNHCSPPERSCHLSERGLHSPSQRSHRGPSQRRHHSPPSERSHRSPSERSHRSPS 621
 +P++ +P E + ++ +E ++P++ + P++ + P+E + +P+E + +P+
 Sbjct: 479 YAPTEKTTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPT 538

Query: 622 ERRHRSPSQRSHRGPSERSHCSPSERRHRSPSQRSHRGPSERRHHSPSKRSHRSPARRSH 681
 E +P++ + P+E + +P+E P++ + P+E ++P++ + +P +
 Sbjct: 539 EETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIETT 598

Query: 682 RSPSERSHHSPSERSHHSPSERRHHSPSERSHHSPSERSHHSPSERRHRSPSERRHHSPS 741
 +P+E + ++P+E + + P+E ++P+E + +P+E + +P+E ++P+
 Sbjct: 599 YAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPA 658

Query: 742 EKSHHSPSERSHHSPSERRHSPLEERSHSLERSHRSPSERRSHRSFERS-HRRISERS 800
 E++ + P+E + ++P+E ++P E + ++ E + +P+E ++ E + + E +
 Sbjct: 659 EETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETT 718

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQRTSERSHRSSC 860
 ++P+E++ +P E + +P E + + +T ++P+E + +P+ +E +
 Sbjct: 719 YAPTEETTYAPTEETMYAPIEETTYGPTTEETTYAPTEATTYAPTEETPYAPTEETTYEPT 778

Query: 861 ERTRHSPSEMRPGRPSGRNHCSPSERSRRSPLKEGLKYSFPGERPSHLSRDFKNQTT 918
 T ++P+E P+ +P+E + +P+E Y P E +++ + + + T
 Sbjct: 779 GETTYAPTEETTYAPTEETTYAPTEETTYAPTEE-TPYE-PTEETTYAPTEETPYEPT 834

Score = 428 (64.2 bits), Expect = 3.1e-36, P = 3.1e-36
 Identities = 89/440 (20%), Positives = 228/440 (51%)

Query: 473 PGSPVKRTWHRHLKDKLTHKEHNHPSFYR-ERTPRGPSETRHNPSWRNHRSPSERSQRS 531
 P P + T + K+ T+ ++ E T P+E T + P+ P+E + +
 Sbjct: 470 PYEPTTEETTYAPTKE-TYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYA 528

Query: 532 SLERRHHSQSRSHCSPSRKNHSSPSERSWRSPSQRNHCSPPERSCHLSERGLHSPSQR 591
 E ++P++ + +P+ + +P+E + +P++ P E + ++ +E ++P++
 Sbjct: 529 PTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEE 588

Query: 592 SHRGPSQRRHHSPSERSHRSPSERSHRSPSERRHRSQRSRHRGPSESRSHCSPSERRHRS 651
 + P + ++P+E + +P+E + P+E +P++ + P+E + + +E +
 Sbjct: 589 TMYAPIEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYASTEETTYA 648

Query: 652 PSQSRHRGPSERRHHSPSKRSHRSPARRSHRSPSERSHHSPSERSHHSPSERRHHSPSER 711
 P++ + P+E + P++ + +P + +P+E + ++P+E + ++P+E ++P+E
 Sbjct: 649 PTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAE 708

Query: 712 SHCSPSERSHCSPSERRHRSPSERRHHSPEKSHHSPSERSHHSPSERRHHSPLERSRHS 771
 + P+E + +P+E +P+E ++P E++ + P+E + ++P+E ++P E + ++
 Sbjct: 709 TPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYGPTTEETTYAPTEATTYAPTEETPYA 768

Query: 772 LLSHRSPSERRSHRSFERS-HRRISERSHSPSEKSHLSPLERSRCSPSERRGHSSSGK 830
 E + P+ ++ E + + E ++P+E++ +P E + P+E ++ + +
 Sbjct: 769 PTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEETTYAPTEE 828

Query: 831 TCHSPSERSHRSPSGMRQRTSERSHRSSCERTRHSPSEMRPGRPSGRNHCSPSERSRRS 890
 T + P+E + +P+ +E + + E+T ++P+E P+ P+E + +
 Sbjct: 829 TPYEPTTEETTYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTTEETTYA 888

Query: 891 PLKEGLKYSFPGERPSHLSRD 912
 P KE Y+ P E +++ + +
 Sbjct: 889 PTKE-TTYA-PTEETTYASTEE 908

Score = 427 (64.1 bits), Expect = 4.0e-36, P = 4.0e-36
 Identities = 81/394 (20%), Positives = 213/394 (54%)

Query: 502 ERTPRGPSETRHNPSWRNHRSPSERSQSSSLERRHHSQSRSHCSPSRKNHSSPSERSW 561
 E T GP+E T + P+ +P+E + + E + P+ + +P+ + +P+E +
 Sbjct: 739 EETTYGPTTEETTYAPTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETT 798

Query: 562 RSPSQRNHCSPPERSCHLSERGLHSPSQSRHRGPQRHHSPSERSHRSPSERSHRSPS 621
 +P++ +P E + + +E ++P++ + P++ ++P+E + +P+E + +P+
 Sbjct: 799 YAPTEETTYAPTEETPYEPTTEETTYAPTEETPYEPTTEETTYTPTEETTYAPTEETTYAPT 858

Query: 622 ERRHRSQSRSHRGPSERSHCSPSERRHRSQSRSHRGPSERRHHSPSKRSHRSPARRSH 681
 E+ +P++ + P+E + P+E +P++ + P+E ++ ++ + +P +
 Sbjct: 859 EKTYYAPTEETTYAPTEETPYEPTTEETTYAPTKEETTYAPTEETTYASTEETTYAPTEETT 918

Query: 682 RSPSERSHHSPSERSHHSPSERRHHSPSERSHCSPSERSHCSPSERRHRSPSERRHHS 741
 +P+E + + P+E + ++P+E ++P+E + +P+E +P+E + P+
 Sbjct: 919 YAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPT 978

Query: 742 EKSHHSPSERSHHSPSERRHHSPLERSRHSLLERSHRSPSERRSHRSFERS-HRRISERS 800
 E++ ++P+E + ++P+E ++P+E + ++ E + +P+E + E + + E +
 Sbjct: 979 EETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETT 1038

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQRTSERSHRSSC 860
 ++P+E++ + E + +P+E ++ + +T + P+E + +P+ +E + +
 Sbjct: 1039 YAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPT 1098

Query: 861 ERTRHSPSEMRPGRPSGRNHCSPSERSRRSPLKE 894
 E T ++P+E P+ P+E + +P+E
 Sbjct: 1099 EETTYAPTEETTYAPAEETPYEPTTEETTYAPTEE 1132

Score = 424 (63.6 bits), Expect = 8.5e-36, P = 8.5e-36
 Identities = 81/394 (20%), Positives = 210/394 (53%)

Query: 502 ERTPRGPSETRHNPSWRNHRSPSERSQSSSLERRHHSQSRSHCSPSRKNHSSPSERSW 561
 E T P+E T + P+ +P+E + + E + P++ + +P+ + +P+E +
 Sbjct: 939 EETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETM 998

Query: 562 RSPSQRNHCSPERSCHLSERGLHSPSQSRHSGPSQRRHSPSERSHRSPSERSHRSPS 621
 +P + +P E + ++ +E + P++ + P++ ++P+E + + +E + +P+
 Sbjct: 999 YAPIEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYASTEETTYAPT 1058

Query: 622 ERRHRSPSQSRHSGPSERSHCSPSERRHRSPSQSRHSGPSERRHSPSKRSHRSPARRSH 681
 E +P+++ + P+E + +P+E +P++ + P+E ++P+++ + +PA +
 Sbjct: 1059 EETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETP 1118

Query: 682 RSPSERSHHSPSERSHHSPSERRHSPSERSHCSPSERSHCSPSERRHRSPSERRHHSPS 741
 P+E + ++P+E + ++P+E ++P E + P+E + +P+E +P+E ++P+
 Sbjct: 1119 YEPTEETTYAPTEETTYAPTEETMYAPIEETTYGTEETTYAPTEATTYAPTEETPYAPT 1178

Query: 742 EKSHHSPSERSHHSPSERRRHSPLERSRHSLLERSHRSPSERRSHRSFERS-HRRISERS 800
 E++ + P+ + ++P+E ++P E + ++ E + +P+E + E + + E +
 Sbjct: 1179 EETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEETTYAPTEETT 1238

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQGRTERSRRSSC 860
 + P+E++ +P E + +P+E ++ + +T ++P + + P+ +E + +
 Sbjct: 1239 YEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETYYGTEETTYAPTEATTYAPT 1298

Query: 861 ERTRHSPSEMRPGRPSGRNHCSPSERSRRSPLKE 894
 E T ++P+E P+G +P+E + +P +E
 Sbjct: 1299 EETPYAPTEETTYEPTGETTYAPTEETTYAPTEE 1332

Score = 422 (63.3 bits), Expect = 1.4e-35, P = 1.4e-35
 Identities = 84/407 (20%), Positives = 216/407 (53%)

Query: 502 ERTPRGSPSERTRHNPSWRNHRSPSERSQSSLERRHSPSQSRHCSPSRKNHSSPSERSW 561
 E T P+E T + P+ P+E + + E + P++ + +P+ + +P+E +
 Sbjct: 795 EETTYAPTEETTYAPTEETPYEPTTEETTYAPTEETPYEPTTEETTYPTTEETTYAPTEETT 854

Query: 562 RSPSQRNHCSPERSCHLSERGLHSPSQSRHSGPSQRRHSPSERSHRSPSERSHRSPS 621
 +P+++ +P E + ++ +E + P++ + P++ ++P+E + + +E + +P+
 Sbjct: 855 YAPTEKTTYAPTEETTYAPTEETPYEPTTEETTYAPTKETTYAPTEETTYASTEETTYAPT 914

Query: 622 ERRHRSPSQSRHSGPSERSHCSPSERRHRSPSQSRHSGPSERRHSPSKRSHRSPARRSH 681
 E +P+++ + P+E + +P+E +P++ + P+E ++P+++ + +PA +
 Sbjct: 915 EETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETP 974

Query: 682 RSPSERSHHSPSERSHHSPSERRHSPSERSHCSPSERSHCSPSERRHRSPSERRHHSPS 741
 P+E + ++P+E + ++P+E ++P E + +P+E + +P+E P+E ++P+
 Sbjct: 975 YEPTEETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPTTEETTYAPT 1034

Query: 742 EKSHHSPSERSHHSPSERRRHSPLERSRHSLLERSHRSPSERRSHRSFERS-HRRISERS 800
 E++ ++P+E + ++ +E ++P E + ++ E + P+E ++ E + + E +
 Sbjct: 1035 EETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETT 1094

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQGRTERSRRSSC 860
 ++P+E++ +P E + +P+E + + +T ++P+E + +P+ E +
 Sbjct: 1095 YAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYGPT 1154

Query: 861 ERTRHSPSEMRPGRPSGRNHCSPSERSRRSPLKEGLKYSPFGERPSHS 908
 E T ++P+E P+ +P+E + P E Y+ P E +++
 Sbjct: 1155 EETTYAPTEATTYAPTEETPYAPTEETTYEPTGE-TTYA-PTEETTYA 1200

Score = 421 (63.2 bits), Expect = 1.8e-35, P = 1.8e-35
 Identities = 86/418 (20%), Positives = 219/418 (52%)

Query: 491 HKEHNHPSFYRERTPRGSPSERTRHNPSWRNHRSPSERSQSSLERRHSPSQSRHCSPSR 550
 H H E T P+E T + P+ +P+E + + E + P++ + +P+
 Sbjct: 376 HYAHIEKPCDTEVTMYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEETTYPTPE 435

Query: 551 KNHSSPSERSWRSPSQRNHCSPERSCHLSERGLHSPSQSRHSGPSQRRHSPSERSHR 610
 + +P+E + +P+++ +P E + ++ +E + P++ + P++ ++P+E +
 Sbjct: 436 ETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTTEETTYAPTKETTYAPTEETTY 495

Query: 611 SPERSHRSPSERRHRSPSQSRHSGPSERSHCSPSERRHRSPSQSRHSGPSERRHSPSK 670
 + +E + +P+E +P++ + P+E + +P+E +P++ + P+E ++P++
 Sbjct: 496 ASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTE 555

Query: 671 RSHRSPARRSHRSPSERSHHSPSERSHHSPSERRHSPSERSHCSPSERSHCSPSERRHR 730
 + +PA + P+E + ++P+E + ++P+E ++P E + +P+E + +P+E
 Sbjct: 556 ETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEETPY 615

Query: 731 SPERRHSPSEKSHHSPSERSHHSPSERRRHSPLERSRHSLLERSHRSPSERRSHRSFE 790
 P+E ++P+E++ ++P+E + ++ +E ++P E + ++ E + P+E ++ E
 Sbjct: 616 EPTTEETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTE 675

Query: 791 RS-HRRISERSHSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQ 849
 + + E +++P+E++ +P E + +P+E + + +T ++P+E + +P+

Sbjct: 676 ETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMY 735

Query: 850 RTSERSHRSSCERTRHSPSEMRPGRPSGRNHCSPSERSRRSPLKEGLKYSFPGERPSSH 908
 E + E T ++P+E P+ +P+E + P E Y+ P E +++

Sbjct: 736 APIEETTYGPTTEETTYAPTEETTYAPTEETTYAPTEETTYEPTGE-TTYA-PTEETTYA 792

Score = 420 (63.0 bits), Expect = 2.3e-35, P = 2.3e-35
 Identities = 82/393 (20%), Positives = 206/393 (52%)

Query: 502 ERTPRGPSETRHNPSWRNHRSPSERSQRSSLERRHHSQSRSHCSPSRKNHSSPSERSW 561
 E TP P+E T + P+ +P+E + + +E ++P++ + +P+ + P+E +

Sbjct: 971 EETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPTTEET 1030

Query: 562 RSPSQRNHCSPERSCHSLSERGLHSPSQSRHSGPSQRRHHSERSHRSPERSHRSPS 621
 +P++ +P E + ++ +E ++P++ + P++ + P+E + +P+E + +P+

Sbjct: 1031 YAPTEETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPT 1090

Query: 622 ERRHRSPSQSRHSGPSERSHCSPSERRHRSPSQSRHSGPSERRHHSKRSRHRSPARRSH 681
 E +P++ + P+E + +P+E P++ + P+E ++P++ + +P +

Sbjct: 1091 EETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEET 1150

Query: 682 RSPSERSHHSPERSHHSPERRHSPERSHCSPSERSHCSPSERRHRSPERSRRHSPS 741
 P+E + ++P+E + ++P+E ++P+E + P+ + +P+E +P+E ++P+

Sbjct: 1151 YGPTTEETTYAPTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPT 1210

Query: 742 EKSHHSPERSHHSPERRHSPERSRHSLLERSHRSPERRSHRSFERS-HRRISERS 800
 E++ ++P+E + + P+E ++P E + + E + +P+E ++ E + + E

Sbjct: 1211 EETTYAPTEETPYEPTTEETTYAPTEETTYEPTTEETTYAPTEETTYAPTEETTYAPTEETM 1270

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQGRTERSERSHRSSC 860
 ++P +++ P E + +P+E ++ +T ++P+E + P+G +E + +

Sbjct: 1271 YAPIDETTYGPTTEETTYAPTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPT 1330

Query: 861 ERTHRSPSEMRPGRP-----SGRNHCSPSE 885
 E T ++P E P P S C+ E

Sbjct: 1331 EETTYAPMEETPYEPAEESTSTVSTEKPCNTEE 1363

Score = 419 (62.9 bits), Expect = 3.0e-35, P = 3.0e-35
 Identities = 83/411 (20%), Positives = 215/411 (52%)

Query: 502 ERTPRGPSETRHNPSWRNHRSPSERSQRSSLERRHHSQSRSHCSPSRKNHSSPSERSW 561
 E T P+E T + P+ +P+E + E ++P++ + +P+ + P E +

Sbjct: 947 EETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETT 1006

Query: 562 RSPSQRNHCSPERSCHSLSERGLHSPSQSRHSGPSQRRHHSERSHRSPERSHRSPS 621
 +P++ +P E + + +E ++P++ + P++ ++ +E + +P+E + +P+

Sbjct: 1007 YAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPA 1066

Query: 622 ERRHRSPSQSRHSGPSERSHCSPSERRHRSPSQSRHSGPSERRHHSKRSRHRSPARRSH 681
 E P++ + P+E + +P+E +P++ + P+E ++P++ + P +

Sbjct: 1067 EETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEET 1126

Query: 682 RSPSERSHHSPERSHHSPERRHSPERSHCSPSERSHCSPSERRHRSPERSRRHSPS 741
 +P+E + ++P+E + ++P E + P+E + +P+E + +P+E +P+E + P+

Sbjct: 1127 YAPTEETTYAPTEETMYAPIEETTYGPTTEETTYAPTEATTYAPTEETPYAPTEETTYEPT 1186

Query: 742 EKSHHSPERSHHSPERRHSPERSRHSLLERSHRSPERRSHRSFERS-HRRISERS 800
 ++ ++P+E + ++P+E ++P E + ++ E + P+E ++ E + + E

Sbjct: 1187 GETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEETTYAPTEETTYEPTTEETT 1246

Query: 801 HSPSEKSHLSPLERSRCSPSERRGHSSSGKTCHSPSERSHRSPSGMRQGRTERSERSHRSSC 860
 ++P+E++ +P E + +P+E ++ +T + P+E + +P+ +E + +

Sbjct: 1247 YAPTEETTYAPTEETTYAPTEETMYAPIDETYYGPTTEETTYAPTEATTYAPTEETPYAPT 1306

Query: 861 ERTHRSPSEMRPGRPSGRNHCSPSERSRRSPLKEGLKYSFPGERPSSHLSRD 912
 E T + P+ P+ +P+E + +P++ E Y P E + ++S +

Sbjct: 1307 EETTYEPTGETTYAPTEETTYAPTEETTYAPMEE-TPYE-PAEESTSTVSTE 1356

Score = 415 (62.3 bits), Expect = 8.0e-35, P = 8.0e-35
 Identities = 84/423 (19%), Positives = 218/423 (51%)

Query: 473 PGSPVKRTWHRHLKDKLTHKEHNHPSFYR-ERTPRGPSETRHNPSWRNHRSPSERSQRS 531
 P P + T + K+ T+ ++ E T P+E T + P+ P+E + +

Sbjct: 878 PYEPTTEETTYAPTKET-TYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYA 936

Query: 532 SLERRHHSQSRSHCSPSRKNHSSPSERSWRSPSQRNHCSPERSCHSLSERGLHSPSQSR 591
 E ++P++ + +P+ + +P+E + +P++ P E + ++ +E ++P++

Sbjct: 937 PTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEE 996

Query: 592 SHRGPSQRRHHSERSHRSPERSHRSPERRHRSPSQSRHSGPSERSHCSPSERRHRS 651
 + P + ++P+E + +P+E + P+E +P++ + P+E + + +E +

Sbjct: 997 TMYAPIEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYASTEETTYA 1056

Query: 652 PSQRSHRGPSERRHHSPSKRSHRSPARRSHRSPERSHHSPERSHHSPERRHHSRSPER 711
P++ + P+E + P++ + +P + +P+E + ++P+E + ++P+E ++P+E

Sbjct: 1057 PTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAE 1116

Query: 712 SHCSPSERSHCSPEERRHRSPEERRHHSPEKSHHSPERSHHSPERRHHSPLERSRHS 771
+ P+E + +P+E +P+E ++P E++ + P+E + ++P+E ++P E + ++

Sbjct: 1117 TPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYGPTTEETTYAPTEATTYAPTEETPYA 1176

Query: 772 LLSHRSPSERRSHRSFERS-HRRISERSHSPSEKSHLSPLERSRCSPEERRGHSSSGK 830
E + P+ ++ E + + E +++P+E++ +P E + P+E ++ + +

Sbjct: 1177 PTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEETTYAPTEE 1236

Query: 831 TCHSPSERSHRSPSGMRQGRTERSRRSSCERTRHSPSEMRPGRPSGRNHCSPEERSRRS 890
T + P+E + +P+ +E + + E T ++P + P+ +P+E + +

Sbjct: 1237 TTYEPTTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETYYGPTTEETTYAPTEATTYA 1296

Query: 891 PLKE 894
P +E

Sbjct: 1297 PTEE 1300

Score = 403 (60.5 bits), Expect = 1.6e-33, P = 1.6e-33
Identities = 84/394 (21%), Positives = 213/394 (54%)

Query: 501 RERTPRGPSETRHNPWRNHRSPSERSQRSSLERRHHSQSRSHCSPSRKNHSSPSERS 560
RE T PSE T + P +P+E+ +E + + ++ +P++ ++P+ER

Sbjct: 319 REETAAPSEDITYAPREVTPYAPTEKPY--DVEETTYVTEESTY-APTKSETNAPTERM 375

Query: 561 WRSPSQNRHCSPPERSCHLSERGLHSPSQSRHSGPSQRRHHSPEERSHRSPERSHRSP 620
+ ++ C E + ++ +E ++P++ + P++ ++P+E + P+E + +P

Sbjct: 376 HYAHIEKP-CDT-EVTMYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEETTYTP 433

Query: 621 SERRHRSPSQSRHSGPSERSHCSPEERRHRSQSRHSGPSERRHHSPSKRSHRSPARRS 680
+E +P++ + P+E++ +P+E +P++ + P+E ++P+K + +P +

Sbjct: 434 TEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTTEETTYAPTKEETTYAPTEET 493

Query: 681 HRSPSERSHHSPERSHHSPERRHHSPEERSHCSPEERSHCSPEERRHRSPEERRHSP 740
+ E + ++P+E + ++P+E + P+E + +P+E + +P+E +P+E ++P

Sbjct: 494 TYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAP 553

Query: 741 SEKSHHSPERSHHSPERRHHSPLERSRHSLLERSHRSPERRSHRSFERS-HRRISER 799
+E++ ++P+E + + P+E ++P E + ++ E + +P E ++ E + + E

Sbjct: 554 TEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYAPTEETTYAPAEET 613

Query: 800 SHSPSEKSHLSPLERSRCSPEERRGHSSSGKTCHSPSERSHRSPSGMRQGRTERSRRSS 859
+ P+E++ +P E + +P+E ++S+ +T ++P+E + +P+ +E + +

Sbjct: 614 PYEPTTEETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTTEETTYAP 673

Query: 860 CERTRHSPSEMRPGRPSGRNHCSPEERSRRSPLE 894
E T ++P+E P+ +P+E + +P +E

Sbjct: 674 TEETTYAPTEETTYAPTEETTYAPTEETTYAPAE 708

Score = 398 (59.7 bits), Expect = 5.5e-33, P = 5.5e-33
Identities = 84/402 (20%), Positives = 209/402 (51%)

Query: 475 SPVKRTWHRHLKOKLTHKEHNHPSFY-RERTPRGPSETRHNPWRNHRSPSERSQRSSL 533
+P + T + +++ T+ ++ E TP P+E T + P+ +P+E + +S

Sbjct: 992 APTEETMYAPIEET-TYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAST 1050

Query: 534 ERRHHSQSRSHCSPSRKNHSSPSERSWRSPQNRHCSPPERSCHLSERGLHSPSQSRH 593
E ++P++ + +P+ + P+E + +P++ +P E + ++ +E ++P++ +

Sbjct: 1051 EETTYAPTEETTYAPAEETPYEPTTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEET 1110

Query: 594 RGPSQRRHHSPEERSHRSPERSHRSPERRHRSQSRHSGPSERSHCSPEERRHRS 653
P++ + P+E + +P+E + +P+E +P + + GP+E + +P+E +P+

Sbjct: 1111 YAPAEETPYEPTTEETTYAPTEETTYAPTEETMYAPIEETTYGPTTEETTYAPTEATTYAPT 1170

Query: 654 QSRHSGPSERRHHSPSKRSHRSPARRSHRSPERSHHSPERSHHSPERRHHSPEERSH 713
+ + P+E + P+ + +P + +P+E + ++P+E + ++P+E + P+E +

Sbjct: 1171 EETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTTEET 1230

Query: 714 CSPSERSHCSPEERRHRSPEERRHHSPEKSHHSPERSHHSPERRHHSPLERSRHSLL 773
+P+E + P+E +P+E ++P+E++ ++P+E + ++P + +P E + ++

Sbjct: 1231 YAPTEETTYEPTTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETYYGPTTEETTYAPT 1290

Query: 774 ERSRSPSERRSHRSFERSHRRISERSHSPSEKSHLSPLERSRCSPEERRGHSSSGKTCH 833
E + +P+E + E E ++ P+ ++ +P E + +P+E ++ +T +

Sbjct: 1291 EATTYAPTEETPYAPTE-----ETTYEPTGETTYAPTEETTYAPTEETTYAPMEETPY 1343

Query: 834 SPERSHRSPSGMRQGRTERSRRSSCERTRHSPSEMRPGRPS 876

P+E S + S + T E + + E T PS+ P+
 Sbjct: 1344 EPAEESTSTVSTKPCNTEETDEPTDEPT-DEPSDEPTDEPT 1385

Score = 368 (55.2 bits), Expect = 9.5e-30, P = 9.5e-30
 Identities = 79/386 (20%), Positives = 211/386 (54%)

Query: 524 PSERSQRSSLERHHSPSQRSHCSPSRKNHSSPSERSWRSPQRNHCSPPERSCHSLSER 583
 PS+ ++ + E + P + + + PS +P E + +P+++ + E + + ++E
 Sbjct: 303 PSDETEAPT-EGTTYVPREETTAAPSEDTTYAPREVTPYAPTEKPY--DVEETTY-VTEE 358

Query: 584 GLHSPSQSRSHRGPSQRRHHSPSER-----SHRSPSERSHRSPSERRHRSQSRSHRGPS 637
 ++P++ P++R H++ E+ + +P+E + +P+E +P++ + P+
 Sbjct: 359 STYAPTKSETNAPTERMHYAHIEKPCDTEVTMYAPTEETTYAPTEETTYAPTEETTYAPT 418

Query: 638 ERSHCSPSERRHRSQSRSHRGPSERRHHSPSKRSHRSPARRSHRSPERSHHSPERSH 697
 E + P+E +P++ + P+E ++P++++ +P + +P+E + +P+E +
 Sbjct: 419 EETPYEPTETTYTPTETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTETT 478

Query: 698 HSPSERRHHSPSERSHCSPSERSHCSPSERRHRSPSERRHHSPSEKSHHSPERSHHSPS 757
 ++P++ ++P+E + + +E + +P+E +P+E +P+E++ ++P+E + ++P+
 Sbjct: 479 YAPTKETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPT 538

Query: 758 ERRRHSPLESRHSLERSHRSPERRSHRSFERS-HRRISERSHSPSEKSHLSPLERSR 816
 E ++P E + ++ E + +P+E + E + + E +++P+E++ +P+E +
 Sbjct: 539 EETTYAPTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETMYAPIEETT 598

Query: 817 CSPSERRGHSSSGKTCHSPSERSHRSPSGMRQGRTERSRRSCERTRHSPSEMRGRPS 876
 +P+E ++ + +T P +P+E + +P+ +E + +S E T ++P+E P+
 Sbjct: 599 YAPTEETTYAPAEETPYEPTETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPA 658

Query: 877 GRNHCSPSERSRRSPLKEGLKYSFPGERPSHS 908
 P+E + +P +E Y+ P E +++
 Sbjct: 659 EETPYEPTETTYAPTEE-TTYA-PTEETTYA 688

Score = 337 (50.6 bits), Expect = 2.1e-26, P = 2.1e-26
 Identities = 66/328 (20%), Positives = 170/328 (51%)

Query: 502 ERTPRGSPERTRHNPSWRNHRSPSERSQRSSLERHHSPSQRSHCSPSRKNHSSPSERSW 561
 E T P+E T + P+ +P+E + + E ++P++ + +P+ + +P+E +
 Sbjct: 1059 EETTYAPAEETPYEPTETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETP 1118

Query: 562 RSPSQRNHCSPERSCHSLSERGLHSPSQSRSHRGPSQRRHHSPSERSHRSPSERSHRSPS 621
 P++ +P E + ++ +E +++P + + GP++ ++P+E + +P+E + +P+
 Sbjct: 1119 YEPTETTYAPTEETTYAPTEETMYAPIEETTYGPTETTYAPTEATTYAPTEETPYAPT 1178

Query: 622 ERRHRSQSRSHRGPSERSHCSPSERRHRSQSRSHRGPSERRHHSPSKRSHRSPARRSH 681
 E P+ + P+E + +P+E +P++ + P+E + P++ + +P +
 Sbjct: 1179 EETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTETTYAPTEETT 1238

Query: 682 RSPSERSHHSPSERSHHSPSERRHHSPSERSHCSPSERSHCSPSERRHRSPSERRHHSPS 741
 P+E + ++P+E + ++P+E ++P+E + +P + + P+E +P+E ++P+
 Sbjct: 1239 YEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETYYGPTETTYAPTEATTYAPT 1298

Query: 742 EKSHHSPSERSHHSPSERRHRSPLERSRHSLLERSHRSPSERRSHRSFERSHRRIS---- 797
 E++ ++P+E + + P+ ++P+E + ++ E + +P E + E S +S
 Sbjct: 1299 EETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPMEETPYEPAEESTSTVSTK 1358

Query: 798 -----ERSHSPSEKSHLSPLERSRCSPSE 821
 E + P+++ P + P++
 Sbjct: 1359 CNTEETFTDEPTDEPTDEPSDEPTDEPTD 1386

Score = 333 (50.0 bits), Expect = 5.7e-26, P = 5.7e-26
 Identities = 63/320 (19%), Positives = 166/320 (51%)

Query: 502 ERTPRGSPERTRHNPSWRNHRSPSERSQRSSLERHHSPSQRSHCSPSRKNHSSPSERSW 561
 E T P+E T + P+ +P+E + + E ++P++ + P+ + +P+E +
 Sbjct: 1075 EETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTETTYAPTEETT 1134

Query: 562 RSPSQRNHCSPERSCHSLSERGLHSPSQSRSHRGPSQRRHHSPSERSHRSPSERSHRSPS 621
 +P++ +P E + + +E ++P++ + P++ ++P+E + P+ + +P+
 Sbjct: 1135 YAPTEETMYAPIEETTYGPTETTYAPTEATTYAPTEETPYAPTEETTYEPTGETTYAPT 1194

Query: 622 ERRHRSQSRSHRGPSERSHCSPSERRHRSQSRSHRGPSERRHHSPSKRSHRSPARRSH 681
 E +P++ + P+E + +P+E P++ + P+E + P++ + +P +
 Sbjct: 1195 EETTYAPTEETTYAPTEETTYAPTEETPYEPTETTYAPTEETTYEPTETTYAPTEETT 1254

Query: 682 RSPSERSHHSPSERSHHSPSERRHHSPSERSHCSPSERSHCSPSERRHRSPSERRHHSPS 741
 +P+E + ++P+E + ++P + + P+E + +P+E + +P+E +P+E + P+
 Sbjct: 1255 YAPTEETTYAPTEETMYAPIDETYYGPTETTYAPTEATTYAPTEETPYAPTEETTYEPT 1314

Query: 742 EKSHHSPSERSHHSPSERRHRSPLERSRHSLLERSHRSPSERRSHRSFERSHRRISERSH 801

Prosites for DKFZphtes3 8g11.2

(No Pfam data available for DKFZphtes3 8g11.2)

DKFZphtes3_8g5

group: testes derived

DKFZphtes3_8g5 encodes a novel 544 amino acid protein nearly identical to human KIAA087 protein.

The novel protein is a new splice variant of KIAA087.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

KIAA087, alternative spliced

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: unknown

Insert length: 2762 bp

No poly A stretch found, no polyadenylation signal found

```
1 CCGACATCGG CCGTGTCTCC AGCACCTGCC GCGGGCTGCG CGAGCTGTGC
51 CAGAGCAGCG GGAAGGTGTG GAAGGAGCAG TTCCGGGTGA GGTGACCTTC
101 CCTTATGAAA CACTACAGCC CCACCGACTA CGTCAATTGG TTGGAAGAGT
151 ATAAAGTTTCG GCAAAAAGCT GGGTTAGAAG CGCGGAAGAT TGTAGCCTCG
201 TTCTCAAAGA GGTCTTTTTC AGAGCACGTT CCTTGTAATG GCTTCAGTGA
251 CATTGAGAAC CTTGAAGGAC CAGAGATTTT TTTTGAGGAT GAACTGGTGT
301 GTATCCTTAAA TATGGAAGGA AGAAAAGCTT TGACCTGGAA ATACTACGCA
351 AAAAAAATTC TTTACTACCT GCGGCAACAG AAGATCTTAA ATAATCTTAA
401 GGCCTTTTCTT CAGCAGCCAG ATGACTATGA GTCGTATCTT GAAGGTGCTG
451 TATATATTGA CCAGTACTGC AATCCTCTCT CCGACATCAG CCTCAAAGAC
501 ATCCAGGCCC AAATTGACAG CATCGTGGAG CTTGTTTGCA AAACCCCTTCG
551 GGGCATAAAC AGTCGCCACC CCAGCTTGGC CTTCAAGGCA GGTGAATCAT
601 CCATGATAAT GGAATAGAA CTCCAGAGCC AGGTGCTGGA TGCCATGAAC
651 TATGTCTTTT ACGACCAACT GAAGTTCAAG GGGAAATCGAA TGGATTACTA
701 TAATGCCCTC AACTTATATA TGCATCAGGT TTTGATTTCG AGAACAGGAA
751 TCCCAATCAG CATGTCTCTG CTCTATTTGA CAATTGCTCG GCAGTTGGGA
801 GTCCCACTGG AGCCTGTCAA CTTCCTCAAG CACTTCTTAT TAAGGTGGTG
851 CCAAGGCCGA GAAGGGGCGA CCCTGGACAT CTTTGACTAC ATCTACATAG
901 ATGCTTTTGG GAAAGGCAAG CAGCTGACAG TGAAAGAATG CGAGTACTTG
951 ATCGGCCAGC ACGTGACTGC AGCACTGTAT GGGGTGGTCA ATGTCAAGAA
1001 GGTGTTACAG AGAATGGTGG GAAACCTGTT AAGCCTGGGG AAGCGGGAAG
1051 GCATCGACCA GTCATACCAG CTCCTGAGAG ACTCGCTGGA TCTCTATCTG
1101 GCAATGTACC CGGACCAGGT GCAGCTTCTC CTCTCCAAAG CCAGGCTTTA
1151 CTTCCACCTG GGAATCTGGC CAGAGAAGTC TTTCTGTCTT GTTTTGAAGG
1201 TGCTTGACAT CCTCCAGCAC ATCCAAACCC TAGACCCGGG GCAGCACGGG
1251 GCGGTGGGCT ACCTGGTGCA GCACACTCTA GAGCACATTG AGCGCAAAAA
1301 GGAGGAGGTG GCGCTAGAGG TGAAGCTGCG CTCCGATGAG AAGCACAGAG
1351 ATGTCTGTGA CTCCATCGGG CTCATTATGA AGCATAAGAG GTATGGCTAT
1401 AACTGTGTGA TCTACGGCTG GGACCCACC TGCAATGATG GACACGAGTG
1451 GATCCCGAAC ATGAACGTCC ACAGCCTGCC GCACGGCCAC CACCAAGCCT
1501 TCTATAAGCT GGTGGTGGAG GACGGCTCCT GTCGATACGC AGCCCAAGAA
1551 AACTTGGAAT ATAACGTGGA GCCTCAAGAA ATCTCACACC CTGACGTGGG
1601 ACGCTATTTC TCAGAGTTTA CTGGCACTCA CTACATCCCA AACGCAGAGC
1651 TGAGATCCG GTATCCAGAA GATCTGGAGT TTGTCTATGA AACGGTGCAG
1701 AATATTTTACA GTGCAAGAA AGAGAACATA GATGAGTAAA GTCTAGAGAG
1751 GACATTGCAC CTTTGTCTGT GCTGCTATCT TCCAAGAGAA CGGGACTCCG
1801 GAAGAAGACG TCTCCACGGA GCCCTCGGGA CCTGCTGCAC CAGGAAAGCC
1851 ACTCCACCAG TAGTGCTGGT TGCCTCCTAC TAAGTTTAAA TACCGTGTGC
1901 TCTTCCGAGC ATGCAAGAC AATGTTGCTC TCCGCTTACA CTAGTGAATT
1951 AATCTGAAAG GCACTGTGTC AGTGGCATGG CTTGTATGCT TGTCTGTGG
2001 TGACAGTTTG TGACATTCTG TCTTCATGAG GTCTCACAGT CGACGCTCCT
2051 GTAATCATTT TTTGTATTCA CTCCATTCCC CTGCTGTGCT GCATTTGTCT
2101 CAGAACATTT CCTTGGCTGG ACAGATGGGG TTATGCATTT GCAATAATTT
2151 CCTTCTGATT TCTCTGTGGA ACGTGTTCCG TCCCGAGTGA GGAAGTGTG
2201 TCTTTTACC CTGAAGTAG TTGCATATTC AGAGGTAAGG TTTGTGCTTA
2251 TCTTGGCAGC ATCTTAGAGA TGGAGACATT AACAAGCTAA TGGAATTAG
2301 AATCATTTGA ATTTATTTT TTCTAATATG TGAACACAG ATTTCAAGTG
2351 TTTTATCTTT TTTTATTTT AATTTAAATG GGAATATAAC ACGTTTTTC
2401 CTTCATATT CCTCTCTTGA GTTTATGCAC ATCTCTATAA ATCATTAGTT
2451 TTCTATTTTA TTACATAAAA TTCTTTTAGA AAATGCAAT AGTGAAGTT
2501 TGGAATGGAT TTTTCCATAC TCATCTACAA TTCTTCCATT TTAATGACT
2551 ACTTTTATTT TTTAATTTAA AAAATCTACT TCAGTATCAT GAGTAGGTCT
2601 TACATCAGTG ATGGGTTCCT TTTGTAGTGA GACATACAAA TCTGATGTTA
```


2651 ATGTTTGCTC TTAGAAGTCA TACTCCATGG TCTTCAAAGA CCAAAAAATG
 2701 AGGTTTGTCT TTTGTAATCA GGAAAAAATA AATTAATGAA CCTTAAAAA
 2751 AAAAAAAAAA GG

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 105 bp to 1736 bp; peptide length: 544
 Category: known protein
 Classification: unclassified

1 MKHYSPTDYV NWLEEKVRQ KAGLEARKIV ASFSKRFFSE HVPCNGFSDI
 51 ENLEGPEIFF EDELVCILNM EGRKALTWKY YAKKILYYLR QOKILNNLKA
 101 FLQPPDDYES YLEGAVYIDQ YCNPLSDISL KDIQAQIDSI VELVCKTLRG
 151 INSRHPSLAF KAGESSMIME IELQSQVLDA MNYVLYDQLK FKGNRMDYYN
 201 ALNLYMHQVL IRRGTIPISM SLLYLTIRQ LGVPLEPVNF PSHFLLRWCO
 251 GAEATLDIF DYIYIDAFGK GKQLTVKECE YLIGQHVTAAL YGVVNVKKV
 301 LQRMVGNLLS LGKREGIDQS YQLLRDSL DL LAMYPDQVQ LLLQARLYF
 351 HLGWPEKSF CLVLKVL DIL QHQTLDPGQ HGAVGYLVQH TLEHIERKKE
 401 EVGVEVKLRS DEKHRDVCYS IGLIMKHKRY GYNCVIYGWD PTCMMGHEWI
 451 RNMNVHSLPH GHQPFYNVL VEDGSCRYAA QENLEYNVEP QEISHPOVGR
 501 YFSEFTGTHY IPNAELEIRY PEDLEFVYET VQNIYSAKKE NIDE

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_8g5, frame 3

TREMBLNEW:AB020682_1 gene: "KIAA0875"; product: "KIAA0875 protein";
 Homo sapiens mRNA for KIAA0875 protein, partial cds., N = 1, Score =
 2832, P = 5.5e-295

>TREMBLNEW:AB020682_1 gene: "KIAA0875"; product: "KIAA0875 protein"; Homo
 sapiens mRNA for KIAA0875 protein, partial cds.
 Length = 621

HSPs:

Score = 2832 (424.9 bits), Expect = 5.5e-295, P = 5.5e-295
 Identities = 537/544 (98%), Positives = 537/544 (98%)

Query: 1 MKHYSPTDYVNWLEEKVRQKAGLEARKIVASFSKRFFSEHVPCNGFSDIENLEGPEIFF 60
 MKHYSPTDYVNWLEEKVRQKAGLEARKIVASFSKRFFSEHVPCNGFSDIENLEGPEIFF
 Sbjct: 85 MKHYSPTDYVNWLEEKVRQKAGLEARKIVASFSKRFFSEHVPCNGFSDIENLEGPEIFF 144

Query: 61 EDELVCILNMEGRKALTWKYYAKKILYYLRQOKILNNLKAFLQPPDDYESYLEGAVYIDQ 120
 EDELVCILNMEGRKALTWKYYAKKILYYLRQOKILNNLKAFLQPPDDYESYLEGAVYIDQ
 Sbjct: 145 EDELVCILNMEGRKALTWKYYAKKILYYLRQOKILNNLKAFLQPPDDYESYLEGAVYIDQ 204

Query: 121 YCNPLSDISLKDIQAQIDSIVELVCKTLRGINSRHPSLAFKAGESSMIMEIELQSQVLDA 180
 YCNPLSDISLKDIQAQIDSIVELVCKTLRGINSRHPSLAFKAGESSMIMEIELQSQVLDA
 Sbjct: 205 YCNPLSDISLKDIQAQIDSIVELVCKTLRGINSRHPSLAFKAGESSMIMEIELQSQVLDA 264

Query: 181 MNYVLYDQLKFKGNRMDYYNALNLYMHQVLIRRTGIPISMSLLYLTIRQLGVPLEPVNF 240
 MNYVLYDQLKFKGNRMDYYNALNLYMHQVLIRRTGIPISMSLLYLTIRQLGVPLEPVNF
 Sbjct: 265 MNYVLYDQLKFKGNRMDYYNALNLYMHQVLIRRTGIPISMSLLYLTIRQLGVPLEPVNF 324

Query: 241 PSHFLLRWCOGAEATLDIFDYIYIDAFGKGKQLTVKECEYLIGQHVTAALYGVVNVKKV 300
 PSHFLLRWCOGAEATLDIFDYIYIDAFGKGKQLTVKECEYLIGQHVTAALYGVVNVKKV
 Sbjct: 325 PSHFLLRWCOGAEATLDIFDYIYIDAFGKGKQLTVKECEYLIGQHVTAALYGVVNVKKV 384

Query: 301 LQRMVGNLLSLGKREGIDQSYQLLRDSL DLYLAMYPDQVQQLLLQARLYFHLGIWPEKSF 360
 LQRMVGNLLSLGKREGIDQSYQLLRDSL DLYLAMYPDQVQQLLLQARLYFHLGIWPEK

Pedant information for DKFZphtes3_8g5, frame 3

Report for DKFZphtes3 8q5.3

```
[LENGTH]          544
[MW]               63307.22
[pI]              5.82
[HOMOL]           TREMBL:AB020682_1 gene: "KIAA0875"; product: "KIAA0875 protein"; Homo sapiens
mRNA for KIAA0875 protein, partial cds. 0.0
[KW]              Alpha_Beta
[KW]              LOW COMPLEXITY          1.84 %
```

[illegible]

(No Prosite data available for DKFZphtes3_8g5.3)

(No Pfam data available for DKFZphtes3_8g5.3)

DKFZphtes3_8ml0

group: nucleic acid management

DKFZphtes3_8ml0 encodes a novel 221 amino acid protein with strong similarity to polyadenylate-binding proteins.

The poly(A)-binding protein (PABP) binds to the messenger (mRNA) 3'-poly(A) tail found on most eukaryotic mRNAs and together with the poly(A) tail has been implicated in governing the stability and the translation of mRNA.

The new protein can find application in modulation of mRNA translation and processing/stability.

strong similarity to polyadenylate-binding protein

frame shift at Bp 707-710

Sequenced by MediGenomix

Locus: unknown

Insert length: 2107 bp

Poly A stretch at pos. 2052, polyadenylation signal at pos. 2033

```
1 CGGAAAGGTC GCGGCTTGTG TGCCTGCGGG CAGCCGTGCC GAGAATGAAC
51 CCCAGCACCC CCAGCTACCC AACGGCCTCG CTCTACGTGG GGGACCTCCA
101 CCCCAGCGTG ACTGAGGCGA TGCTCTACGA GAAGTTCAGC CCGGCAGGGC
151 CCATCCTCTC CATCCGGATC TGCAGGGACT TGATCACCAG CGGCTCCTCC
201 AACTACGCGT ATGTGAACTT CCAGCATACG AAGGACGCGG AGCATGCTCT
251 GGACACCATG AATTTTGATG TTATAAAGGG CAAGCCAGTA CGCATCATGT
301 GGTCTCAGCG TGATCCATCA CTTCGAAAAA GTGGAGTGGG CAACATATTC
351 GTTAAAAATC TGGATAAGTC CATTAATAAT AAAGCACTGT ATGATACAGT
401 TTCTGCTTTT GGTAAACATCC TTTCGTGTAA CGTGGTTTGT GATGAAAATG
451 GTTCCAAGGG TTATGGATTT GTACACTTTG AGACACACGA AGCAGCTGAA
501 AGAGCTATTA AAAAAATGAA CGGAATGCTC CTAAATGGTC GCAAAAGTATT
551 TGTTGGACAA TTAAAGTCTC GTAAAGAACG AGAAGCTGAA CTGGAGCTA
601 GGGCAAAAGA GTTCCCAAT GTTTACATCA AGAATTTTGG AGAAGACATG
651 GATGATGAGC GCCTTAAGGA TCTCTTTGGC AAGTTCGGGC CCGCCTTAAG
701 TGTGAATTAA TGACCGATGA AAGTGGAAAA TCCAAAGGAT TTGGATTGTG
751 AAGCTTTGAA AGGCATGAAG ATGCACAGAA AGCTGTAGAT GAGATGAATG
801 GAAAGGAGCT CAATGGAAAA CAAATTTACG TTGGTTCGAGC TCAGAAAAAA
851 GTGGAACGCG AGACGGAAC TAAGCGCACA TTGAACAGA TGAAGCAAGA
901 TAGGATCACC AGATACCAGG TTGTTAATCT TTATGTGAAA AATCTTGATG
951 ATGGTATTGA TGATGAACGT CTCCGGAAAG CGTTTCTCC ATTTGGTACA
1001 ATCACTAGTG CAAAGGTTAT GATGGAAGGT GGTCCGAGCA AAGGGTTTGG
1051 TTTTGTATGT TTCTCCTCCC CAGAAGAAGC CACTAAAGCA GTTACAGAAA
1101 TGAACGGTAG AATTGTGGCC ACAAAGCCAT TGTATGTAGC TTTAGCTCAG
1151 CGCAAAGAAG AGCGCCAGGC TTACCTCACT AACGAGTATA TGCAGAGAAT
1201 GGCAAGTGTA CGAGCTGTGC CCAACCAGCG AGCACCTCCT TCAGGTTACT
1251 TCATGACAGC TGTCCCACAG ACTCAGAACG ATGCTGCATA CTATCCTCCT
1301 AGCCAAATTTG CTCGACTAAG ACCAAGTCCT CGCTGGACTG CTCAGGGTGC
1351 CAGACCTCAT CCATTCCAAA ATAAGCCCAG TGCTATCCGC CCAGGTGCTC
1401 CTAGAGTACC ATTTAGTACT ATGAGACCAG CTCTTTCACA GGTTCACGA
1451 GTCATGTCAA CGCAGCGTGT TGCTAACACA TCAACACAGA CAGTGGGTCC
1501 ACGTCTGCA GCTGCTGCTG CTGCTGCAGC TACCCCTGCT GTGCGCACGG
1551 TTCCACGGTA TAAATATGCT GCGGGAGTTC GCAATCCTCA GCAACATCGT
1601 AATGCACAGC CACAAGTTAC AATGCAACAG CTGCTGTTC ATGTACAAGG
1651 TCAGGAAACT TTGACTGCCT CCAGGTGGGC ATCTGCCCT CCTCAAAAGC
1701 AAAAGCAAAT GTTAGGTGAA CGGCTCTTTC CTCTTATCA AGCCATGCAC
1751 CCTACTCTTG CTGGGAAAAT CACTGGCATG TTGTTGGAGA TTGATAATTC
1801 AGAACTTCTT TATATGCTCG AGTCTCCAGA GTCACTCCGT TCTAAGGTTG
1851 ATGAAGCTGT AGCTGTACTA CAAGCCCACC AAGCTAAAGA GGCTACCCAG
1901 AAAGCAGTGA ACAGTGCTAC CGGTGTTCCA ACTGTTTAAA ATTGATCAGA
1951 GACCACGAAA AGAAATTTGT GCTTCACCGA AGAAAAATAT CTAACATCG
2001 AGAACTATG GGAATAAAAA TTGCAAAATC TAAAAATAAA AATGCAAAAT
2051 CTAAAAATAA AAAAAATAAA AAAAAATAAA AAAAAATAAA AAAAAATAAA
2101 AAAAAGG
```

BLAST Results

Entry HSPOLYAB from database EMBL:
Human mRNA for polyA binding protein
Score = 5420, P = 0.0e+00, identities = 1162/1243

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 707 bp to 1936 bp; peptide length: 410
 Category: strong similarity to known protein
 Classification: unset
 Prosite motifs: RNP_1 (10-18)
 RNP_1 (112-120)

```

1 LMTDESGKSK GFGFVSFERH EDAQKAVDEM NGKELNGKQI YVGRAQKKVE
51 RQTELKRTFE QMKQDRITRY QVVNLYVKNL DDGIDDERLR KAFSPFGTIT
101 SAKVMEGGR SKGFGFVCFS SPEEATKAVT EMNGRIVATK PLYVALAQRK
151 EERQAYLTNE YMQRMASVRA VPNQRAPPSG YFMTAVPQTQ NHAAYPPSQ
201 IARLRPSRW TAQGARPHPF QNKPSAIRPG APRVPFSTMR PASSQVPRVM
251 STQRVANTST QTVGPRPAAA AAAAATPAVR TVPRYKYAAG VRNPQQHRNA
301 QPQVTMQQLA VHVQGQETLT ASRLASAPPQ KQKQMLGERL FPLIQAMHPT
351 LAGKITGMLL EIDNSELlym LESPELRSK VDEAVVLQA HQAKEATQKA
401 VNSATGVPTV

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_8m10, frame 2

PIR:DNHUPA polyadenylate-binding protein - human, N = 1, Score = 1931,
 P = 1.7e-199

PIR:I48718 poly(A) binding protein - mouse, N = 1, Score = 1928, P =
 3.6e-199

>PIR:DNHUPA polyadenylate-binding protein - human
 Length = 633

HSPs:

Score = 1931 (289.7 bits), Expect = 1.7e-199, P = 1.7e-199
 Identities = 384/415 (92%), Positives = 394/415 (94%)

```

Query:      1 LMTDESGKSKGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRTFE 60
            +MTDESGKSKGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKR FE
Sbjct:    219 VMTDESGKSKGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRKF 278

Query:      61 QMKQDRITRYQVVNLYVKNLDDGIDDERLRKAFSPFGTITSAKVMEGGRSKGFGFVCFS 120
            QMKQDRITRYQ VNLVYKNLDDGIDDERLRK FSPFGTITSAKVMEGGRSKGFGFVCFS
Sbjct:    279 QMKQDRITRYQGVNLYVKNLDDGIDDERLRKEFSPFGTITSAKVMEGGRSKGFGFVCFS 338

Query:     121 SPEEATKAVTEMNGRIVATKPLYVALAQRKEERQAYLTNEYMQRMASVRAVPN-----Q 174
            SPEEATKAVTEMNGRIVATKPLYVALAQRKEERQA+LTN+YMQRMASVRAVPN      Q
Sbjct:    339 SPEEATKAVTEMNGRIVATKPLYVALAQRKEERQAHLTNQYMQRMASVRAVPNPVINPYQ 398

Query:     175 RAPPSSGYFMTAVPQTQNHAAAYPPSQIARLRPSRWTAQGARPHPFQNKPSAIRPGAPRV 234
            APPSSGYFM A+PQTQN AAYPPSQ+A+LRPSRWTAQGARPHPFQN P AIRP APR
Sbjct:    399 RAPPSSGYFMAAIPQTQNRAAYPPSQVQALRPSRWTAQGARPHPFQNMPGAIRPAAPRP 458

Query:     235 PFSTMRPASSQVPRVMSTQRVANTSTQTVGPRPAAAAAATPAVRTVPYKYAAGVRNP 294
            PFSTMRPASSQVPRVMSTQRVANTSTQTVGPRPAAAAAATPAVRTVPYKYAAGVRNP
Sbjct:    459 PFSTMRPASSQVPRVMSTQRVANTSTQTMGPRPAAAAAATPAVRTVPYKYAAGVRNP 517

Query:     295 QQHRNAQPQVTMQQLAVHVQGQETLTASRLASAPPQKQKQMLGERLFPLIQAMHPTLAGK 354
            QQH NAQPQVTMQQ AVHVQGQE LTAS LASAPPQ+QKQMLGERLFPLIQAMHPTLAGK
Sbjct:    518 QQHLNAQPQVTMQQPAVHVQGQEPLTASMLASAPPQEQKQMLGERLFPLIQAMHPTLAGK 577

Query:     355 ITGMLLEIDNSELlymLESPELRSKVD EAVAVLQA HQAKEATQKAVNSATGVPTV 410
            ITGMLLEIDNSELL+MLESPELRSKVD EAVAVLQA HQAKEA QKAVNSATGVPTV
Sbjct:    578 ITGMLLEIDNSELHMLLESPELRSKVD EAVAVLQA HQAKEAAQKAVNSATGVPTV 633

```

Score = 315 (47.3 bits), Expect = 1.9e-27, P = 1.9e-27

Identities = 71/163 (43%), Positives = 102/163 (62%)

Query: 1 LMTDESGKSGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRTFE 60
 ++ DE+G SKG+GFV FE E A++A++MNG LN ++++VGR + + ER+ EL +
 Sbjct: 130 VVCDENG-SKGYGFVHFETQEAAERAIEKMNGMLLNDRKVFVGRFKSRKEREAEELGARAK 188

Query: 61 QMKQDRITRYQVNNLYVKNLDDGIDDERLRKAFSPFGTITSAKVMM-EGGRSKGFGFVCF 119
 + N+Y+KN + +DDERL+ F P S KVM E G+SKGFGFV F
 Sbjct: 189 EF-----TNVYIKNFGEDMDDERLKDLPFGP---ALSVKVMTDESGKSGFGFVSF 235

Query: 120 SSPEEATKAVTEMNGRIVATKPLYVALAQRKEERQAYLTNEYMQ 163
 E+A KAV EMNG+ + K +YV AQ+K ERQ L ++ Q
 Sbjct: 236 ERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRKFEQ 279

Score = 214 (32.1 bits), Expect = 1.9e-14, P = 1.9e-14
 Identities = 50/150 (33%), Positives = 87/150 (58%)

Query: 8 KSKGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRTFEQMKQDRI 67
 +S G+ +V+F++ DA++A+D MN + GK + + +Q R L+++
 Sbjct: 50 RSLGYAYVNFQPPADAERALDTMNFVIGKPKVRIMWSQ-----RDP SLRKS----- 96

Query: 68 TRYQVNNLYVKNLDDGIDDERLRKAFSPFGTITSAKVMMEGGRSKGFGFVCFSSPEEATK 127
 V N+++KNLD ID++ L FS FG I S KV+ + SKG+GFV F + E A +
 Sbjct: 97 ---GVGNIFIKNLDKSIDNKALYDTFSAFGNLSCKVVCDENGSKGYGFVHFETQEAAER 153

Query: 128 AVTEMNGRIVATKPLYVALAQRKEERQAYL 157
 A+ +MNG ++ + ++V + ++ER+A L
 Sbjct: 154 AIEKMNGMLLNDRKVFVGRFKSRKEREAEEL 183

Score = 120 (18.0 bits), Expect = 4.8e-04, P = 4.8e-04
 Identities = 30/99 (30%), Positives = 54/99 (54%)

Query: 70 YQVNNLYVKNLDDGIDDERLRKAFSPFGTITSAKVM--MEGGRSKGFGFVCFSSPEEATK 127
 Y + +LYV +L + + L + FSP G I S +V M RS G+ +V F P +A +
 Sbjct: 8 YPMASLYVGDLPDVTEAMLYEKFSPAGPILSIRVCRDMITRRSLGYAYVNFQPPADAER 67

Query: 128 AVTEMNGRIVATKPLYVALAQRKEE-RQAYLTNEYMQRM 165
 A+ MN ++ KP+ + +QR R++ + N +++ +
 Sbjct: 68 ALDTMNFVIGKPKVRIMWSQORDPSLRKSGVGNIFIKNL 106

Peptide information for frame 3

ORF from 45 bp to 707 bp; peptide length: 221
 Category: strong similarity to known protein
 Classification: unset
 Prosite motifs: RNP_1 (138-146)

1 MNPSTPSYPT ASLYVVDLHP DVTEAMLYEK FSPAGPILSI RICRDLITSG
 51 SSNYAYVNFQ HTKDAEHALD TMNFDVIK GK PVRIMWSQRD PSLRSGVGN
 101 IFVKNLDSI NNKALYDTVS AFGNLS CNV VCDENGSKGY GFVHFETHEA
 151 AERAIKKMNG MLLNGRKVFV GQFKSRKERE AELGARAKEF PNVYIKNFGE
 201 DMDDERLKD L FGKFGPALSV N

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_8m10, frame 3

SWISSPROT:PAB1 HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING
 PROTEIN 1) (PABP 1)., N = 1, Score = 1039, P = 5.7e-105

PIR:I48718 poly(A) binding protein - mouse, N = 1, Score = 1031, P =
 4e-104

PIR:DNHUPA polyadenylate-binding protein - human, N = 1, Score = 1009,
 P = 8.7e-102

>SWISSPROT:PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING
 PROTEIN 1) (PABP 1).
 Length = 636

HSPs:

Score = 1039 (155.9 bits), Expect = 5.7e-105, P = 5.7e-105
Identities = 199/220 (90%), Positives = 205/220 (93%)

Query: 1 MNPSTPSYPTASLYVGDLPDVTEAMLYEKFSPAGPILSIRICRDLITSGSSNYAYVNFQ 60
MNPS PSYP ASLYVGDLPDVTEAMLYEKFSPAGPILSIR+CRD+IT S YAYVNFQ
Sbjct: 1 MNPSAPSYPMASLYVGDLPDVTEAMLYEKFSPAGPILSIRVCRDMITRSLGYAYVNFQ 60

Query: 61 HTKDAEHALDTMNFVDVIKGPVRIMWSQRDPSLRKSGVGNIFVKNLDKSINNKAlyDTVS 120
DAE ALDTMNFVDVIKGPVRIMWSQRDPSLRKSGVGNIF+KNLDKSI+NKAlyDT S
Sbjct: 61 QPADAERALDTMNFVDVIKGPVRIMWSQRDPSLRKSGVGNIFIKNLDKSIDNKAlyDTFS 120

Query: 121 AFGNILSCNVVCDENGSKGYGFVHFETHEAAERAIAKKMNGMLLNGRKVFVGQFKSRKERE 180
AFGNILSC VVCDENGSKGYGFVHFET EAAERAI+KMNGMLLN RKVFVG+FKSRKERE
Sbjct: 121 AFGNILSCKVVCDENGSKGYGFVHFETQEAERAIEKMNGMLLNDRKVFVGRFKSRKERE 180

Query: 181 AELGARAKEFPNVYIKNFGEDMDDERLKD LFGKFGPALSV 220
AELGARAKEF NVYIKNFGEDMDDERLKD LFGKFGPALSV
Sbjct: 181 AELGARAKEFTNVYIKNFGEDMDDERLKD LFGKFGPALSV 220

Score = 275 (41.3 bits), Expect = 4.1e-23, P = 4.1e-23
Identities = 71/233 (30%), Positives = 120/233 (51%)

Query: 2 NPSTPSYPTASLYVGDLPDVTEAMLYEKFSPAGPILSIRICRDLITSGSSNYAYVNFQ 61
+PS +++++L + LY+ FS G ILS ++ D S + + Q
Sbjct: 90 DPSLRKSGVGNIFIKNLDKSIDNKAlyDTFS AFGNILSCKVVCDENGSKGYGFVHFETQE 149

Query: 62 TKD-AEHALDTMNFVDVIKGPVRIMW-SQRDPSL--RKSGVGNIFVKNLDKSINNKAlyD 117
+ A ++ M + K R +R+ L R N++++KN + +++++L D
Sbjct: 150 AAERAIEKMNGMLLNDRKVFVGRFKSRKERE AELGARAKEFTNVYIKNFGEDMDDERLKD 209

Query: 118 TVSAFGNILSCNVVCDENG-SKGYGFVHFETHEAAERAIAKKMNGMLLNGRKVFVGQFKSR 176
FG LS V+ DE+G SKG+GFV FE HE A++A+ +MNG LNG++++VG+ + +
Sbjct: 210 LFGKFGPALSVKVMTDES GSKSGFGFVS FERHEDAQKAVDEMNGKELNGKQIYVGRAQK 269

Query: 177 KEREAEALGARAKEFP-----NVYIKNFGEDMDDERLKD LFGKFGPALSV 219
ER+ EL + ++ N+Y+KN + +DDERL+ F FG S
Sbjct: 270 VERQTELKRKFEQMKQDRITRYQGVNLYVKNLDDGIDDERLRKEFSPFGTITS 322

Score = 227 (34.1 bits), Expect = 6.3e-18, P = 6.3e-18
Identities = 57/187 (30%), Positives = 101/187 (54%)

Query: 12 SLVYVGDLPDVTEAMLYEKFSPAGPILSIRICRDLITSGSSNYAYVNFQHTKDAEHALDT 71
++Y+ + D+ + L + F GP LS+++ D + S + +V+F+ +DA+ A+D
Sbjct: 192 NVYIKNFGEDMDDERLKD LFGKFGPALSVKVMTDE-SGKSGFGFVS FERHEDAQKAVDE 250

Query: 72 MNFVDVIKGPVRIMWSQR-----DPSLRKSGVGNIFVKNLDKSINNKA 114
MN + GK + + +Q+ D R GV N++VKNLD I+++
Sbjct: 251 MNGKELNGKQIYVGRAQKQKVERQTELKRKFEQMKQDRITRYQGV-NLYVKNLDDGIDDER 309

Query: 115 LYDTVSAFGNILSCNVVCDENGSKGYGFVHFETHEAAERAIAKKMNGMLLNGRKVFVGQFK 174
L S FG I S V+ + SKG+GFV F + E A +A+ +MNG ++ + +V +
Sbjct: 310 LRKEFSPFGTITSAKVMMEGGRSGKGFVCFSSPEEATKAVTEMNGRIVATKPLYVALAQ 369

Query: 175 SRKEREAEAL 183
++ER+A L
Sbjct: 370 RKEERQAHL 378

Score = 100 (15.0 bits), Expect = 2.3e-02, P = 2.3e-02
Identities = 26/99 (26%), Positives = 53/99 (53%)

Query: 8 YPTASLYVGDLPDVTEAMLYEKFSPAGPILSIRICRDLITSG-SSNYAYVNFQHTKDAE 66
Y +LYV+L + + L ++FSP G I S ++ ++ G S + +V F ++A
Sbjct: 291 YQGVNLYVKNLDDGIDDERLRKEFSPFGTITSAKV---MMEGGRSGKGFVCFSSPEEAT 347

Query: 67 HALDTMNFVDVIKGPVRIMWSQRDPSLRKSGVGNIFVKNL 106
A+ MN ++ KP+ + +QR R++ + N +++ +
Sbjct: 348 KAVTEMNGRIVATKPLYVALAQKKEE-RQAHLTNQYMORM 386

Pedant information for DKFZphtes3_8ml0, frame 2

Report for DKFZphtes3_8ml0.2

[LENGTH] 409
[MW] 45235.68
[pI] 10.08
[HOMOL] SWISSPROT:PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN
1) (PABP 1). 0.0

[FUNCAT] 04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S. cerevisiae, YER165w] 1e-54

[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YER165w] 1e-54

[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YER165w] 1e-54

[FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YER165w] 1e-54

[FUNCAT] 04.05.99 other mrna-transcription activities [S. cerevisiae, YNL016w] 1e-15

[FUNCAT] 11.01 stress response [S. cerevisiae, YGR159c] 1e-12

[FUNCAT] 04.01.04 rna processing [S. cerevisiae, YGR159c] 1e-12

[FUNCAT] 04.99 other transcription activities [S. cerevisiae, YNL175c] 4e-09

[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YPR112c] 5e-08

[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YHR086w] 3e-07

[FUNCAT] 03.13 meiosis [S. cerevisiae, YHR086w] 3e-07

[FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YHR086w] 3e-07

[FUNCAT] 04.07 rna transport [S. cerevisiae, YOL123w HRP1 - CF Ib] 9e-07

[FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YCL011c] 3e-06

[FUNCAT] 99 unclassified proteins [S. cerevisiae, YGR250c] 8e-06

[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YDR432w] 2e-05

[FUNCAT] 08.01 nuclear transport [S. cerevisiae, YDR432w] 2e-05

[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YFR023w] 3e-05

[FUNCAT] 03.01 cell growth [S. cerevisiae, YBR212w] 3e-04

[BLOCKS] BL00030B Eukaryotic RNA-binding region RNP-1 proteins

[SCOP] dlsxl_4.34.7.1.3 Sex-lethal protein [(Drosophila melanogaster) 1e-17

[PIRKW] nucleus 0.0

[PIRKW] duplication 0.0

[PIRKW] RNA binding 0.0

[PIRKW] nucleolus 2e-09

[PIRKW] tandem repeat 2e-09

[PIRKW] single-stranded DNA binding 3e-06

[PIRKW] DNA binding 5e-13

[PIRKW] phosphoprotein 6e-10

[PIRKW] ribosome 3e-08

[PIRKW] mitochondrion 3e-08

[PIRKW] alternative splicing 9e-11

[PIRKW] chloroplast 2e-19

[PIRKW] transcription regulation 2e-07

[PIRKW] protein biosynthesis 3e-08

[SUPFAM] nucleolin 6e-10

[SUPFAM] glycine-rich RNA-binding protein 2e-07

[SUPFAM] unassigned ribonucleoprotein repeat-containing proteins 2e-19

[SUPFAM] polyadenylate-binding protein 0.0

[SUPFAM] ribonucleoprotein repeat homology 0.0

[PROSITE] RNP_1 2

[PFAM] RNA recognition motif. (aka RRM, RBD, or RNP domain)

[KW] Irregular

[KW] 3D

[KW] LOW_COMPLEXITY 5.62 %

SEQ MTDESGKSKGFGFVSFERHEDAQKAVDEMNGKELNGKQIYVGRAQKKVERQTELKRTFEQ

SEG

lsxl-

SEQ MKQDRITRYQVNVLYVKNLDDGIDDERLRKAFSPFGTITSAKVMMEGGRSKGFGFVCFSS

SEG

lsxl-CEECECCCTTTTHHHHHHHHTTTTCCCCCEECTTTCTTEEEECTTT

SEQ PEEATKAVTEMNGRIVATKPLYVALAQRKEERQAYLTNEYMQRMASVRAVPNQRAPPSGY

SEG

lsxl- HHHHHHHHHHTTTTCCCCCBBCCBCC.....

SEQ FMTAVPQTQNHAAAYPPSQIARLRPSRPTAQGARPHFPQNKPSAIRPGAPRVPFSTMRP

SEG

lsxl-

SEQ ASSQVPRVMSTQRVANTSTQTVGPRPAAAAAATPAVRTVPKYAAGVRNPQQHRNAQ

SEGxxxxxxxxxxxxxxxxxxxxxxxx.....

lsxl-

SEQ PQVTMQQLAVHVQGQETLTASRLASAPPQKQKQMLGERLFPLIQAMHPTLAGKITGMLE

SEG

lsxl-

SEQ IDNSELLYMLESPELSRSKVDEAVAVLQAHQAKEATQKAVNSATGVPTV

SEG

lsxl-

Prosites for DKFZphtes3_8m10.2

PS00030	9->17	RNP_1	PDOC00030
PS00030	111->119	RNP_1	PDOC00030

Pfam for DKFZphtes3_8m10.2

HMM_NAME	RNA recognition motif. (aka RRM, RBD, or RNP domain)		
HMM	*IYVGNLPWDtTEEDLrDlFsQFGpIvsIrMMrDReTGRSRGF AFVEFED		
	+YV+NL+ +++E LR +FS+FG I+S+++M+ E GRS+GF+FV F +		
Query	74	LYVKNLDDGIDDERLRKAFSPFGTITSAKVM--EGGRSKGFGFVCFSS	120
HMM	EEDAekAideMNGmeFmGRrIRV*		
	+E+A+KA+ EMNG+++ ++++V		
Query	121	PEEATKAVTEMNGRIVATKPLYV	143

Pedant information for DKFZphtes3_8m10, frame 3

Report for DKFZphtes3_8m10.3

```

[LENGTH]      235
[MW]           26308.08
[pI]           8.95
[HOMOL]       SWISSPROT:PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN
1) (PABP 1). 1e-113
[FUNCAT]      04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation) [S.
cerevisiae, YER165w] 1e-64
[FUNCAT]      30.03 organization of cytoplasm [S. cerevisiae, YER165w] 1e-64
[FUNCAT]      05.04 translation (initiation, elongation and termination) [S. cerevisiae,
YER165w] 1e-64
[FUNCAT]      30.10 nuclear organization [S. cerevisiae, YER165w] 1e-64
[FUNCAT]      03.19 recombination and dna repair [S. cerevisiae, YFR023w] 1e-24
[FUNCAT]      11.04 dna repair (direct repair, base excision repair and nucleotide excision
repair) [S. cerevisiae, YFR023w] 1e-24
[FUNCAT]      04.05.99 other mrna-transcription activities [S. cerevisiae, YNL016w]
2e-19
[FUNCAT]      04.05.03 mrna processing (splicing) [S. cerevisiae, YOR319w] 2e-14
[FUNCAT]      04.01.04 rna processing [S. cerevisiae, YGR159c] 1e-11
[FUNCAT]      11.01 stress response [S. cerevisiae, YGR159c] 1e-11
[FUNCAT]      99 unclassified proteins [S. cerevisiae, YGR250c] 1e-09
[FUNCAT]      04.07 rna transport [S. cerevisiae, YOL123w HRP1 - CF Ib] 1e-09
[FUNCAT]      30.13 organization of chromosome structure [S. cerevisiae, YCL011c] 8e-09
[FUNCAT]      98 classification not yet clear-cut [S. cerevisiae, YPR112c] 2e-08
[FUNCAT]      03.13 meiosis [S. cerevisiae, YHR086w] 2e-08
[FUNCAT]      04.99 other transcription activities [S. cerevisiae, YBR212w] 3e-08
[FUNCAT]      03.01 cell growth [S. cerevisiae, YBR212w] 3e-08
[FUNCAT]      06.04 protein targeting, sorting and translocation [S. cerevisiae, YDR432w]
3e-04
[FUNCAT]      08.01 nuclear transport [S. cerevisiae, YDR432w] 3e-04
[BLOCKS]      BL00030B Eukaryotic RNA-binding region RNP-1 proteins
[BLOCKS]      BL00900D Bacteriophage-type RNA polymerase family proteins signatur
[SCOP]         d1sx1_ 4.34.7.1.3 Sex-lethal protein [(Drosophila melanogaster) 9e-23
[SCOP]         d2ula_ 4.34.7.1.2 U1A protein [human (Homo sapiens) 6e-24
[SCOP]         dlup1_2 4.34.7.1.1 Nuclear ribonucleoprotein A1, RNP A1, UP 1e-13
[PIRKW]        nucleus 1e-110
[PIRKW]        duplication 1e-110
[PIRKW]        RNA binding 1e-110
[PIRKW]        nucleolus 4e-10
[PIRKW]        tandem repeat 4e-10
[PIRKW]        single-stranded DNA binding 1e-06
[PIRKW]        DNA binding 9e-12
[PIRKW]        phosphoprotein 4e-10
[PIRKW]        mitochondrion 6e-07
[PIRKW]        heterotrimer 4e-06
[PIRKW]        alternative splicing 1e-15
[PIRKW]        chloroplast 5e-11
[PIRKW]        transcription regulation 3e-09
[PIRKW]        GTP binding 2e-06
[SUPFAM]       helix-destabilizing protein 1e-07
[SUPFAM]       nucleolin 4e-10
[SUPFAM]       glycine-rich RNA-binding protein 2e-07
[SUPFAM]       yeast HRP1 protein 2e-08

```


[SUPFAM] unassigned ribonucleoprotein repeat-containing proteins 3e-25
 [SUPFAM] polyadenylate-binding protein 1e-112
 [SUPFAM] ribonucleoprotein repeat homology 1e-112
 [PROSITE] RNP_1 1
 [PFAM] RNA recognition motif. (aka RRM, RBD, or RNP domain)
 [KW] All_Beta
 [KW] 3D

SEQ ERSRLVCLRAAVPRMNPSTPSYPTASLYVGDLHPDVTEAMLYEKFSPAGPILSIRICRDL
 lhal-EEEEETTTTCHHHHHHHHGGGCCCEEEEEEEETT
 SEQ ITSGSSNYAYVNFQHTKDAEHALDTMNFVDVIKGPVRIMWSQRDPSPSLRKSQGVGNIFVKNL
 lhal- TTTCEEEEEEEECCHHHHHHHHTTEEE-TT---EEEEEECTTTTCCCCCEEEEECC
 SEQ DKSINNKAlyDTVSAFGNILSCNVVCDENGSKGYGFVHFETHEAAERAIAKKMNGMLNLR
 lhal- TTTTCHHHHHHHHGGGCCCEEEEEETTTTCEEEEEEEECCHHHHHHHH.....
 SEQ KVFGVQFKSRKEREAEELGARAKEFPNVYIKNFGEDMDDERLKDILFGKFGPALSVN
 lhal-

Prosites for DKFZphtes3_8m10.3

PS00030 152->160 RNP_1 PDOC00030

Pfam for DKFZphtes3_8m10.3

HMM_NAME RNA recognition motif. (aka RRM, RBD, or RNP domain)
 HMM *IYVGNLPWDtTEEDLrDlFsQFGpIvsIrMMrDRetGRSRGF AFVEFED
 +YVG+L +D+TE +L + FS+ GPI+SIR+ RD T S +A+V+F+
 Query 27 LYVGDLHPDVTEAMLYEKFSPAGPILSIRICRDLITSGSSNYAYVNFQH 75
 HMM EEDAekAIdemNGmeFmGRrIRV*
 DAE A+D+MN ++ G+++R+
 Query 76 TKDAEHALDTMNFVDVIKGPVRI 98
 HMM *IYVGNLPWDtTEEDLrDlFsQFGpIvsIrMMrDRetGRSRGF AFVEFED
 I+V+NL+ +++ L D S FG I+S++++ D + S+G++FV FE+
 Query 115 IFVKNL DKSINNKAlyDTVSAFGNILSCNVVCD--ENGSKGYGFVHFET 161
 HMM EEDAekAIdemNGmeFmGRrIRV*
 +E+AE+AI +MNGM+++GR++ V
 Query 162 HEAAERAIAKKMNGMLNLRKVFV 184

DKF2phtes3_8p7

group: testes derived

DKF2phtes3_8p7 encodes a novel 412 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

2 EST hits (both from testis librarys)

Sequenced by MediGenomix

Locus: unknown

Insert length: 2899 bp

Poly A stretch at pos. 2870, polyadenylation signal at pos. 2852

```
1 CCGACCCGCC CTGGGGTGCT GCGTGCGCTG CCTGCTCCCG CCTGAGGAAA
51 ACACCTGCCA TGGCGCAAGG CCGGGAGCGC GACGAAGGCC CCCACTCCGC
101 CGGCGGCGCG TCCTTGTCCTG TGAGATGGGT GCAAGGATTC CCTAAGCAGA
151 ATGTTTCAAT GTCAACGACA ACACCATTTG CTACCCCTGT GGGAATTATG
201 TAATATTTAT TAATATTGAA ACCAAGAAAA AGACTGTACT GCAGTGTAGT
251 AATGGAAATTG TGGGCGTCAT GGCAACTAAC ATCCCCCTGTG AAGTTGTGGC
301 TTTTCTGAC CGGAAGCTAA AACCTCTCAT CTACGTATAC AGCTTTCAG
351 GATTGACCAG AAGGACCAAA TTGAAAGGCA ACATTCTCCT GGACTACACT
401 TTAATTTTCT TCAGTTACTG TGGCACCTAC CTGGCTAGTT ACTCCTCTCT
451 CCCAGAATTT GAACCTGGCC TTTGGAAGTG GGAATCGAGT ATCATTTTGT
501 GTAAGAAATC ACAGCCTGGA ATGGATGTGA ACCAAATGTC TTTTAACCCC
551 ATGAAGTGGC GCCAGCTGTG CTTATCAAGT CCAAGTACAG TGAGCGTGTG
601 GACCAATTGAA AGAAGTAACC AGGAGCATTT TTTGAGAGCA AGGTCGGTGA
651 AATTACCTCT AGAAGATGGG TCATTTTSTA ATGAAACGGA TGTCGTTTTC
701 CCCCAGTCGT TGCCGAAAGA TCTCATCTAT GGTCCCGTGC TGCCACTGTC
751 AGCCATTGCC GGGCTGGTAG GCAAAGAGGC AGAGACTTTC CGGCCGAAAG
801 ATGATCTATA TCCTTTGCTT CACCCGACTA TGCATTGCTG GACTCCAACA
851 AGTGACTTGT ACATTGGCTG TGAAGAGGGT CATCTTTTAA TGATTAATGG
901 AGACACCTTG CAAGTGACTG TACTTAATAA GATAGAAGAG GAATCGCCAT
951 TGGAAAGACAG AAGAAATTTT ATCAGTCCAG TAACCTTGGT ATATCAGAAG
1001 GAGGCGGTGC TGGCTTCTGG AATTGATGGC TTTGTGTATT CTTTATTAT
1051 TAAAGATAGA AGTTACATGA TCGAGGATTT TCTTGAGATT GAAAGACCTG
1101 TAGAACATAT GACATTTTCT CCCAATTATA CAGTGTGCTG GATTCAAACA
1151 GACAAGGGAT CTGTTTATAT CTACACTTTT GGTAAGGAGC CAACCTTAAA
1201 TAAAGTCCTA GATGCTTGTG ATGGGAAATT TCAGGCAATT GACTTTATCA
1251 CACCTGGAAC CCAATACTTC ATGACACTTA CATATTGAGG GGAAATTTGT
1301 GTTTGGTGGC TGGAGGATTG TGCTTGTGTA AGCAAGATTT ATCTGAATAC
1351 CCTAGCAACG GTTCTGGCTT GCTGTCCATC CTCCCTCTCT GCAGCCGTGG
1401 CCACGGAGGA TGGCTCGGTC TACTTCATCA GCGTATATGA TAAGGAATCC
1451 CCTCAGGTGC TGCACAAGGC CTTTCTCTCG GAATCGTCCG TGCAAGCAGT
1501 CGTGTAAGTC CTTTCTGCCT CCAGGAGCGG CTCCGTGTCA CACCCGTCTG
1551 TTGAAAATTC TAGTGAAGCC ATCCTTTCTT TTAATTTTAA GTTTTACGTG
1601 TTTTCAATTT TTTGAATGTT AATATATTCA CACAGTTCAA CACTCAAAG
1651 GTACAGAGGG CTGTGTAGTA AAGTACCCCG CATACCCAGG TCTGTCTTGT
1701 CAGGCAGCCT GGTACCAATT TCTCATGTCT CTCTGAGATT GTTTTATCCA
1751 TGAACAAGCA AAACATAATA AGCACTTCTT TTTACTTGTA TCAATGGCCA
1801 TCATGTGTGT ATAGTGTGCC AGGCATTTCT GCTGTATTAA CTCCATGAGG
1851 TAAACACTCT TGTGTCTCTT ATTTGACAGG TGAGGAAGAT AAGGCACAAG
1901 GATTTTAAAT AACTTGCTCA ATAGTACACA GATAGTGAAT GGCAAAATGT
1951 GGGATTTGAA CCCAGGTAGT TGGGCTGCAG AGTCACTGCC TTTGCTCTTA
2001 AAAGGAGAAA ACTATGTACA ATGCCTCATT TCTTTTTTCA CTTAATCGTA
2051 TATCTTGGAG AATGTTTAT ATCCACACAT AAAGACCAGC CTGATTATTT
2101 GTATAGCCAC ATAGTATTC ATTATATGAA TATACTATCA TTTTTTAAAA
2151 ACGGTATATT AATGAACATT TAGAGTATTT CAAAACCTTT GAAGCAATAC
2201 TTTTAAAGAT ATAATATAGA GACATTAGAT TTGGACTTGT AGGTGCTATC
2251 ATTATTACTG TTTCTTTTAT ATTTATTATA TTATTAGTAA TTAATAAGAA
2301 CAGACATTTG TATTTGCTT TACAGCTTGA GATCACTGTA GCTTGTGGCA
2351 TGTGATCCTC AAAACACCAG TCAGAAAGGT GTTATTCTTA TCCCTATTAG
2401 ACAATTAGG GAATTCAGGG TTAGAGAGGT GAGGAAAAGC ATTGTCCAAG
2451 ATTACACATT ACACAGCTAG CACACTGAGG AGCTGGCCCT GCCACTGTGG
2501 ACTGCCCAGC TCCACCACCC TAGCTCAGTG GGGAAAGGAT GATAACCTCC
2551 TTCCATTTAC CCCCTGCCTT TCTGCACTGT CATTTTTTGT TGCCTTTCCT
2601 TTCTCAGATC CTCTTATTCT AATTACATC TTCCCACTTT TTCTAATTTG
2651 ATAAAGTTGT AGACATGTTT CACTACATTC TTCTCCAC TGCCAGGTAC
2701 CAGACACAGG GTAATGAAAT GTCACACCCA CCACTAATTT GAGAATTGCT
```

BLAST Results

Medline entries

Peptide information for frame 2

```

1  MATNIPCEVV  AFSDRKLKPL  IYVYSFPGLT  RRTKLKGNIL  LDYTLLSFSY
51 CGTLYSTASYSS  LPEFELALWN  WESSIILCKP  SQPGMDVNQM  SFNPMNWRQL
101 CLSSPSTVSV  WTIERSNQKE  CFRARSLVCK  LQDGSDFNFT  DVVFPQSLPK
151 DLIYGPVLPL  SAIAGLVQHE  AETFRPKDDL  YPLLHPTMHC  WTPTSOLYIG
201 CEEGHLMLIN  KDTLQVTYLN  KIEEERPLD  RNRNFSVPTL  VYQKEGVLAS
251 GIDGFVYSYF  IGDRSYVMED  FLEIESRPVEH  MTFSPNVTVL  LIQTDKGSVY
301 IYTFGKEPTL  NKVLDACDGK  FQAIIDFITP  QYFMTLTYS  GEICVWVLED
351 CACVSKIYLN  TLATVLACCP  SSLSAAVGTE  DGSVYFISVY  DKESPQVHHK
401 AFLSESSVOH  VV

```

Alert BLASTP hits for DKFZphtes3_8p7, frame 2

Pedant information for DKFZphtes3_8p7, frame 2

Report for DKFZphtes3_8p7.2

(No Prosite data available for DKFZphtes3_8p7.2)
(No Pfam data available for DKFZphtes3_8p7.2)

DKFZphtes3_9e22

group: testes derived

DKFZphtes3_9e22 encodes a novel 227 amino acid protein with weak partial similarity to Ring-finger proteins.

For the novel protein, Pfam, but not Prosite predicts a C3HC4 type RING finger motife. No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to zinc finger proteins

Sequenced by DKFZ

Locus: unknown

Insert length: 1318 bp

Poly A stretch at pos. 1308, no polyadenylation signal found

```
1 GCTCCCCCGG CTTTCGGAGC CCGGGGGCGG CCTGTGGCGC GCGGAGCCCG
51 CGCCGGACTG CGCCTCTTTG GACCTTGAGG GGAAACATGC GTTGGCCTTG
101 GATCGTTTGA AATTCTAAGT TTGGGATCCC CGCCCCGCCC CCTGCCTCTT
151 CCGCCCGCGG GGTTCCTTCC TTTTTCCTT TTGCTTTTTC TCCTTTTCTC
201 CCTCCGGGTC TCCTTTTGA CTCCCTCCC CTTATGCTC GCCCAGCCCT
251 CCCCCTGCTG CTGAGAAGTG GGGGAGGGTC TCGGCCTCCA GGTTCGCGCC
301 CCACCGGGGC CCGGGCGAGC ATGGGGGGCA AGCAGAGCAC GCGCGCCCGC
351 TCCCGGGGCC CTTCCCGGG GGTCTCCACC GATGACAGCG CCGTGCCGCC
401 GCGGGGAGGG GCGCCCCATT TCGGGCACTA CCGGACGGGC GCGGGGGCCA
451 TGGGGCTGCG CAGCCGCTCG GTCAGCTCGG TGGCAGGCAT GGGCATGGAC
501 CCCAGCACGG CCGGGGGGGT GCCCTTTGGC CTCTACACC CCGCCTCCCG
551 GGGCACCGGC GACTCCGAGA GGGCGCCCGG CGGCGGAGGG TCTGCGTCCG
601 ACTCCACCTA TGCCCATGGC AATGGTTACC AGGAGACGGG CGGCGGTAC
651 CATAGAGACG GGATGCTGTA CCTGGGCTCC CGAGCCTCGC TGGCGGATGC
701 TCTACCTCTG CACATCGCAC CCAGGTGGTT CAGCTCGCAT AGTGGTTTCA
751 AGTGCCCCAT TTGCTCCAAG TCTGTGGCTT CTGACGAGAT GGAAATGCAC
801 TTTATAATGT GTTTGAGCAA ACCTCGCCTC TCCTACAACG ATGATGTGCT
851 GACTAAAGAC GCGGGTGAGT GTGTGATCTG CCTGGAGGAG CTGCTGCAGG
901 GGGACACGAT AGCCAGGCTG CCCTGCCTGT GCATCTATCA CAAAAGCTGC
951 ATAGACTCGT GGTTCGAAGT GAACAGATCT TGTCCGGAAC ACCCTGCGGA
1001 CTGACTGCGG GGCTTGCTTG CTGACTCCTC TCAAAGGGAC AGAGCGCCCC
1051 TGCTCCAGGG AGGAGGCTCA CCGGACCCTG GGGCAGAGCT GAGCTTGCGA
1101 CACCAGCGGG AACAGGCAC CCCTTCTGCA CTGACTTCCA GATCATGGTT
1151 CTCCCTTCCT CCCTGAGGAC ACCAAATTGG ATGAGAGCAA GTTTGAGAGA
1201 AGAATGAATC AACTGCTATC CTTCCCTCA CCCCTCAGCC CAGGAGGGAA
1251 AGGGCATTTC CTTTTTCATC TTTGAAAGGC ATTGTGGGTC TGTCTTTAAA
1301 GTGTTTACAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 321 bp to 1001 bp; peptide length: 227
Category: similarity to known protein
Classification: unclassified

```
1 MGGKQSTAAR SRGFPFGVST DDSAVPPPGG APHFGHYRTG GGAMGLRSRS
51 VSSVAGMGMD PSTAGGVFPF LYTPASRGTG DSERAPGGGG SASDSTYAHG
101 NGYQETGGGH HRDGMPLYLGS RASLADALPL HIAPRWFSH SGFKCPICSK
151 SVASDEMETH FIMCLSKPRL SYNDVLTGD AGEVCICLEE LLQGDITARL
```

201 PCLCIYHKSC IDSWFEVNRSCPEHPAD

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_9e22, frame 3

TREMBL:AF078823_1 product: "RING-H2 finger protein RHA2b"; Arabidopsis thaliana RING-H2 finger protein RHA2b mRNA, complete cds., N = 1, Score = 111, P = 2.8e-06

TREMBL:AF078822_1 product: "RING-H2 finger protein RHA2a"; Arabidopsis thaliana RING-H2 finger protein RHA2a mRNA, complete cds., N = 1, Score = 112, P = 6.6e-06

TREMBL:AC004138_14 gene: "T17M13.17"; Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence., N = 2, Score = 123, P = 1.4e-05

PIR:T02286 hypothetical protein T13D8.23 - Arabidopsis thaliana, N = 1, Score = 142, P = 8.8e-08

>PIR:T02286 hypothetical protein T13D8.23 - Arabidopsis thaliana
Length = 327

HSPs:

Score = 142 (21.3 bits), Expect = 8.8e-08, P = 8.8e-08
Identities = 24/57 (42%), Positives = 30/57 (52%)

Query: 166 SKPRLSYNDVLT KDAGECVICLEELLQGD TIARLPCLCIYHKSCIDSWFEVNRSCP 222
S P + LT D +C +C+EE + G LPC IYHK CI W +N SCP
Sbjct: 206 SLPSVKITPQH LTNDMSQCTVCMEEFIVGGDATELPCKHIYHKDCIVPWLRLNNSCP 262

Pedant information for DKFZphtes3_9e22, frame 3

Report for DKFZphtes3_9e22.3

[LENGTH] 227
[MW] 23782.62
[pI] 6.18
[HOMOL] PIR:T02286 hypothetical protein T13D8.23 - Arabidopsis thaliana 2e-08
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YDR313c] 4e-06
[FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YOL013c]
0.001
[FUNCAT] 06.13 proteolysis [S. cerevisiae, YOL013c] 0.001
[PFAM] Zinc finger, C3HC4 type (RING finger)
[KW] Irregular

SEQ MGGKQSTAARSRGPFPGVSTDDSAVPPPGGAPHFGHYRTGGGAMGLRSRSVSSVAGMGMD
PRD ccc
SEQ PSTAGGVVPGFLYTPASRGTDGDSERAPGGGGSASDSTYAHGNGYQETGGGHHRDGMLYLGS
PRD ccc
SEQ RASLADALPLHIAPRWFSHSGFKCPIKSKSVASDEMEMHFIMCLSKPRLSYNDVLT KD
PRD hhhhhhhhceccccccccccccccccccccccccchhhhhhhhhhhcccccccccccccccc
SEQ AGEVCICLEELLQGD TIARLPCLCIYHKSCIDSWFEVNRSCPEHPAD
PRD cccccccccccccccccccccccccccccccccccccchhhhhhhhhcccccccc

(No Prosite data available for DKFZphtes3_9e22.3)

Pfam for DKFZphtes3_9e22.3

HMM_NAME Zinc finger, C3HC4 type (RING finger)
HMM *CPICFctFQlDyPWPfdePmMlPCgHsFCypCirrW.....CPmC*
C IC L+++ D++ LPC+ ++ ++CI +W CP+
Query 184 CVIC-----LEELLQGD TIARLPCLCIYHKSCIDSWFEVNRSCPEH 224

DKFZphtes3_9i20

group: testes derived

DKFZphtes3_9i20 encodes a novel 205 amino acid protein with similarity to human KIAA0336 gene.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by DKFZ

Locus: /map="44.1 cR from top of Chr17 linkage group"

Insert length: 2509 bp

Poly A stretch at pos. 2499, polyadenylation signal at pos. 2481

```
1 CTCGCCGAGA TGACCTGGGC ACCTCTGCGT TGAATCGGCA AATACTGATC
51 AAGCCGCGATT TATTCTGCTC TCAGGAACTC TAAGTCTAGC AGAGAAGATG
101 AGGCGGTAGA AGTTTCATCA TGGCTTGGCT GGAGGACAAG CAAATTGAGG
151 ACATTGGCAA CGGAGTGATC AAAATGATAG ATCATGAGGC CTAAAATGAA
201 TAAGGAAAGA AGAGAAGTGG CAGAGGCTGA GAACAGAAAG AGAGGGTGGG
251 GGGGCTGTAA ATCTTGAAGA TTAGGGTATA ATATGAGTAT ATGGGTAAGA
301 ATTGGAAGAA TTGTGTAGGA GGCAGTAGTC AAAAAGTAGA AGCAGTTTGG
351 AAGAGTAGTT ACAAATATCA AGAGCCAGGT GGCTAAAAGG TGGAGCTATA
401 GGTCAATTGAA GCTCAAGAAA CTGAGTCTCT AGGGCATTGG TTAAGTCATC
451 TGTCTAGACT TCAAAGTTGT CTAGGATGAT AATTCAGAAC ACTGATCTGT
501 GCCAAAGTCA CAGGTTTTC ACGACTGAAA ACAACATAGC AAAATAAGCC
551 AAGATGTCTG TGGATCCAAT GACCTACGAG GCCCAGTTCT TTGGCTTCAC
601 GCCACAAACG TGCATGCTTC GGATCTACAT TGCATTTCAA GACTACCTAT
651 TTGAAGTGAT GCAGGCCGTT GAACAGGTTA TTCTGAAGAA GCTGGATGGC
701 ATCCCAGACT GTGACATTAG CCCAGTGCAG ATTCGCAAT GCACAGAGAA
751 GTTTCCTTTC TTCATGAAAG GACATTTTGA TAACCTTTTT AGCAAAATGG
801 AGCAACTGTT TTTGCAGCTG ATTTTACGTA TTCCCTCAAA CATCTTGCTT
851 CCTGAAGATA AATGTAAGGA GACACCTTAT AGTGAGGAAG ATTTTCAGCA
901 TCTCCAGAAA GAAATGAAC AGTTACAGGA GAAGTACAAG ACTGAATTAT
951 GTACTAAGCA GGCCCTTCTT GCAGAATTAG AAGAGCAAAA AATTGTTTCA
1001 GCCAACTCA AACAGACGTT GACTTTCCTT GATGAGCTTC ATAATGTTGG
1051 CAGAGATCAT GGGACTAGTG ATTTTAGGGA GAGTTTAGTA TCCCTGGTTC
1101 AGAAGTCCAG AAAAAGTACG AACATTAGAG ACAATGTGGA AAAGGAATCG
1151 AAACGACTGA AAATATCTTA ATTGCTCAGT AGTCAAAAGG AGGAGCCTGT
1201 CAAAAAGTAG AATCATAAGG ACTGTTCAAA CCATAAGGAC TGTTCAAATC
1251 ATACCACTGA CTGTTCAAAC CAACCATACT TTTTATTAGA TTTGCTTTGT
1301 CAACTCTTTC TTGTATTCTG TGTTCCTCTC TTTTGTGGTC CACTTTGCTG
1351 AGGTATGAAG TGTACTACTT TGAAGTAGGC TGAAGCATCT GAGTCTTCTA
1401 ATAAGTGGGA AGGGATCCAA CAAAGAAGCC ATGACCAGTT AAAGATATTT
1451 GCAGAGTTAC ACCTTGGTCA TAAGTCCTTT GTGACCTTGA TTATTTTGGC
1501 TTAATCTTTG GATGAGACCA GACAAGAAAA GGATTAACG GGTGGCTCCT
1551 TTAATATTAT TATTATTGTT TTTGAGACAA GGTCCCTTTC TGTACCCAG
1601 GTTAGAGTAG ATTTTCAGTG CACAATCTTG GCTCACTGCA ACCTCTGTGT
1651 CCTGGGCTCA AGTGATCCTC CTGCCTCAGC CTCCCAAGTA GCTAGGACCA
1701 CAGGTGCGTG TCACCATGCT TGGCTAATTT TTTGTCAGAA ACGAGGCCCTC
1751 ACTATATTGT CCAGGCTGAG TGGCTCTTTT ATTAACCACT CATTACACTG
1801 CGGAACAGCC AACATAGAGT ACTTGCTCTC GTCCTGTGAA TTTCTTTTCA
1851 TGAGGGAGTC AATATGTAGT GGAAAGAAGC ATGTAGCAAA AAAGACAACC
1901 TTGATCTTTA ATAAAAAGA AGTTGGTTTA TTCCAAAAT AAATCCCTTG
1951 ACAAAAACCC TGGTGATGTT AAGCAATTGA CTGCTTTAGA GTCCAGCAGA
2001 AGACCTTAGA CAAAAAAGC AGAACCCACT GGAGTAGAAA AGGAAGCATG
2051 TAGCATATAC TCAGTAGTGA AATTTAATTT TACTGACTGT TAGGTATCTA
2101 TGCCAATTTG TTTTCATACT TCAGTTGGTT TTGGAATCTG CCTTATACCT
2151 AATATTTATT TATTCACACT CATAAGCATC AAATATTTAA TGCCCTCAGT
2201 GGGAAATTTG TGTTTAAACT CAATGGAATC TAATATTTCT TTATGTCGTT
2251 AGTCCCTGTA AAATGTTAGG TCACCAAGG AAAGGGGAGA AATAGCAATG
2301 GTTGTTCCTA AGGTATTGCT TGCCCTCCAT GTCTTCCTAA AGAGCAGAAC
2351 TTGGAGTTTC TCCTTTATGT AGAGAAGAAG TAACTTAGGG TGTATTTGCA
2401 ATGAAATATT CAGATATATT GAAAGCTTGT GTTTACATGA AATATGTTTA
2451 TTATCAAGAA GTCCTTTTTC CAATTCTGTA CATTAAATAT ATGTGTTTTA
2501 AAAAAAAA
```

BLAST Results

Entry AC004148 from database EMBL:
Homo sapiens chromosome 17, clone HCIT524C5, complete sequence.
Score = 5245, P = 0.0e+00, identities = 1049/1049
3 exons

Entry HS556361 from database EMBL:
human STS TIGR-A003N29.
Score = 1005, P = 1.3e-39, identities = 201/201

Entry HSG043 from database EMBL:
human STS SHGC-36031.
Score = 955, P = 2.8e-37, identities = 205/215

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 554 bp to 1168 bp; peptide length: 205
Category: putative protein
Classification: no clue

```

1 MSVDPMTYEA OFFGFTPOTC MLRIYIAFQD YLFEVMOAVE QVILKKLDGI
51 PDCDISPVQI RKCTEKFLCF MKGHFDNLFS KMEQLFLQLI LRIPSNILLP
101 EDKCKETPYS EEDFQHLQKE IEQLQEKYKT ELCTKQALLA ELEEQKIVQA
151 KLKQTLTFFD ELHNVGRDHG TSDFRESLVS LVQNSRKLN IRDNVEKESK
201 RLKIS

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_9i20, frame 2

TREMBLNEW:HSAB2334_1 gene: "KIAA0336"; Human mRNA for KIAA0336 gene,
complete cds., N = 1, Score = 107, P = 0.0081

>TREMBLNEW:HSAB2334_1 gene: "KIAA0336"; Human mRNA for KIAA0336 gene,
complete cds.
Length = 1,583

HSPs:

Score = 107 (16.1 bits), Expect = 8.2e-03, P = 8.1e-03
Identities = 42/140 (30%), Positives = 76/140 (54%)

```

Query:    65 EKFLCFMKGHFDNLFSKMEQLFLQLILRIPSNILLPEDKCKETPYSEED----FQHLQKE 120
          EK CF+K H +NL +EQ +L R ILL +D ++P + D + L+++
Sbjct:   796 EKEKCFIKEH-ENLKPLLEQK--ELDRRAELILL-KDSLAKSPSVKNDPLSSVKELEEK 851

Query:   121 IEQLQE--KYKTELCTKQALLAELEEQKIVQAKLKQTLTFFDELHNVGRDHGTSDFRESL 178
          IE L++ K K E K L+A ++ +K + + K+T T +EL ++ + S+
Sbjct:   852 IENLEKECKEKEEKINKIKLVA-VKAKKELDSSRKETQTVKEELESRLSEK--DQLSASM 908

Query:   179 VSLVQNSRKLNIRDNVEKESKRLKI 204
          L+Q + +N+ EK+S++L +
Sbjct:   909 RDLIQGAESYKNLLLEYEQSEQLDV 934

```

Pedant information for DKFZphtes3_9i20, frame 2

Report for DKFZphtes3_9i20.2

```

[LENGTH]    205
[MW]         24140.13
[pI]         5.51
[KW]         All Alpha
[KW]         COILED_COIL      18.05 %

```

(No Pfam data available for DKFZphtes3 9i20.2)

DKFZphtes3_9k22

group: testes derived

DKFZphtes3_9k22 encodes a novel 304 amino acid protein with partial similarity to X. leavis katanin p80.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

similarity to C-terminus of katanin p80

Sequenced by DKFZ

Locus: unknown

Insert length: 2676 bp

Poly A stretch at pos. 2665, no polyadenylation signal found

```
1 CTCTCTAGGC TGCCGGGCGC TGGTCGTCAG CGCCGAGGCT GGGCTGAGGC
51 GCCGCGGTAC CATGAGGCGC CGGTACTTAA GAGATTATGG CATCAGAAAC
101 CCACAATGTT AAAAAACGGA ACTTTGTAA TAAGATTGAG GATCATTTC
151 TTGATCTTCC TAGAAAAAG ATCTCTAATT TCACTAATAA GAACATGAAG
201 GAGGTTAAGA AATCTCCAAA ACAGTTGGCT GCTTACATAA ATAGAACAGT
251 TGGACAAACT GTGAAAAGCC CAGATAAACT TCGTAAAGTG ATCTATCGCA
301 GAAAGAAAGT TCATCATCCC TTTCCAAATC CTTGTTACAG AAAAAACAG
351 TCCCCTGGAA GTGGGGGCTG TGACATGGCA AATAAGAAA ATGAAGTGGC
401 TTGTGCAGGC CACCTGCCTG AAAAATTACA CCATGATAGT CGAACATATT
451 TGGTTAACTC CAGTGATTCT GGTCTTCAC AGACAGAAAG CCCATCATCA
501 AAATATAGTG GGTTTTTTTC TGAGGTTTCT CAGGACCATG AAACAATGGC
551 CCAAGTTTTG TTCAGCAGGA ATATGAGATT GAATGTAGCT TTAACCTTCT
601 GGAGAAAGAG AAGTATAAGT GAACTGTAG CTTATTGTT GAGGATAGAA
651 GATCTTGGCG TTGTGGTAGA TTGCCTTCCT GTGCTCACCA ATTGTTTACA
701 GGAAGAAAAA CAATATATCT CACTTGGCTG CTGTGTTGAC TTGTGCTC
751 TAGTAAAGTC ACTACTTAAA AGCAAATTTG AAGAATATGT TATAGTTGGT
801 TTAAGCTGGC TTCAAGCAGT CATTAAAAGG TGGTGGTCAG AACTATCATC
851 CAAAACAGAA ATTATAAATG ATGGAATAT TCAAATTTTA AAACAACAAT
901 TAAGTGGATT ATGGGAACAG GAAAACCATC TTACTTTGGT TCCAGGATAT
951 ACTGGTAATA TAGCTAAGGA TGATAGTGCT TATTATTAC AGTTACATTG
1001 AGAGATTTC TCTACTAAG AGCATTGGT TTTTCAAAAC ATCCCTGAAC
1051 TGTATAATTT ACAAAAAAAA AAGTCTCGTC TGAGAAGTGT GAACTGTGGA
1101 AGAAATCAAA ACTATTTTTT CTTTAAAAA GCCACGTAAT GAAACCACTA
1151 ATGAATCCC AGCAATCTGC TTCACATTGA AGTGGAAGAA TATCCAAAAG
1201 GAGCAGCTTC AATTTTCATT AGGTGAAAGT GCACTATGAA GATTGTTTAC
1251 CTTTGTCTGA TTTGGGAGTT ATATGTTTAT TTGGTAACAT TAAGAAGTAC
1301 TGGATTTTAA TGCAATCCTG CATAAAAAA TAATTATAC TATGTGAAAA
1351 AATAAGACAG GACTTACCAC TAGGAACAC CAAGACCAAT CATCATTAAC
1401 TTTTTTAAGA TTGTGTTTTA TTAAAAAA AAAACACTTA AATGTGTGCA
1451 GCTATTTTCT TATGTTGAAA AGACTGAAAG TTTAAACAT GAAAAAATC
1501 AATATTAAC ATTTTGTGTT CACACTGAGA TACTGTGTAT GTAAATGCC
1551 TTAATTATTA ATAAGCCAAT GTGTTATGAT ACCAATATCT GTTTTAAAAA
1601 ACTAAAACCA ACCATGCTTC TGGCATGATA AAATCATGGA ATTAATCAG
1651 GGGTTTACAT TCTGTAGAG TGTTCTTGAA ACACCTCTCTG CACCATTTTT
1701 AAAACTTGAG AATAGTTTTA GTATCTCTGA TATTTTTTGC CAGAATCATC
1751 ATGTCATGTA TGAATGTGTT ATCCCTATCT AAGGAAAAAG GTGAATATGT
1801 TTTTGTATGA ATGTTTAACT GGAAATGTCC ATGGACTTGG CTAATTTATA
1851 TTTACTTTTT ATTGTACATA GATTCTAAT ATTTTTCATT CCTGTATCAT
1901 TTAAGCTTCC TTCATTTGAG TAAATTCAC AAATATTTCT ATTTTTTTGC
1951 TTTTGTAAAT TCTGATTTTA TATGAATTCT AATTCTTTTT CACTACATAT
2001 GTTTTAAAGA GTTACATACA GTGATTTAGA ATGGTTTACA GTTAATGCTG
2051 ATCTTGTATT TTAAATTCAC ACACTTGTG TCACTACCTC CTCTAATGGT
2101 TAGTATGATA TTGATAGCAG CTGTATGAGG TCTTTTTTTA AAATACCACT
2151 TTTAGTGTCA GTGAACCAAA TTCTGGAATG TCTTAACAGC TCTAAATCTT
2201 ACTTGTCTTG AAAATGATTG GGGTTTAATA CCACTGCTGG TGGTTCACAC
2251 ATCATCCCAT CCTTAATATG CCTGACAGGC ATCTGAGCAA AGGTTTTTAG
2301 TAATTGAATT TCTCTGCAGT AGTCCTTCAA GCACTTGAAT GTAAACCTTT
2351 AGCATTTTAT CGTTTAATGA CTACTGATAC GAATCTCAAG CAGATTTCTT
2401 GCTCTTAAAA ACTGAGTTCT ACTGAGTTCT GGTTTTGTGT AGCTATATTT
2451 TATATAGCTA GATATTCCTC ACAGTGAACA TGAATTGTAA TAATTGGTTA
2501 TTTCTTAAAG TCTTTAGATT ATAATAATTT CAGATTATTG CACGTCTGTG
2551 ATTTGACAGG TGAGTTATTT AAGAGGCCAG TTTTCAGGAC ATCGGAATTT
2601 GAATTGTAAC CCTGTATCT CTGTGAAACT TTTAATATGA TAAATATAA
2651 CTTTCTTTTG TGCTTAAAAA AAAAAA
```

BLAST Results

Entry HS541354 from database EMBL:
human STS WI-11840.
Score = 1267, P = 7.1e-50, identities = 271/281

Medline entries

98227670:
Katanin, a microtubule-severing protein, is a novel AAA ATPase
that targets to the centrosome using a WD40-containing subunit.

Peptide information for frame 3

ORF from 87 bp to 998 bp; peptide length: 304
Category: similarity to known protein
Classification: unclassified

```

1 MASETHNVKK RNFCKIEDH FIDLPRKKIS NFTNKNMKEV KKSPKQLAAY
51 INRTVGQTVK SPDKLRKVIY RRRKKVHPPF NPCYRKKQSP GSGGCDMANK
101 ENELACAGHL PEKLHDSRT YLVNSSDSGS QTESPSSKY SGFFSEVSQD
151 HETMAQVLF S RNMRLNVALT FWRKRSISEL VAYLLRIEDL GVVVDCLPVL
201 TNCLQEEKQY ISLGCCVDLL PLVKSLLKSK FEEYVIVGLN WLQAVIKRWW
251 SELSSKTEII NDGNIQILKQ QLSGLWEQEN HLTLPVGYTG NIAKDVDAYL
301 LQLH

```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3_9k22, frame 3

TREMBL:AF056021_1 product: "p80 katanin"; Xenopus laevis p80 katanin
mRNA, partial cds., N = 1, Score = 146, P = 1.2e-07

TREMBL:AF052432_1 product: "katanin p80 subunit"; Homo sapiens katanin
p80 subunit mRNA, complete cds., N = 1, Score = 150, P = 1.2e-07

TREMBL:AF052433_1 product: "katanin p80 subunit"; Strongylocentrotus
purpuratus katanin p80 subunit mRNA, complete cds., N = 2, Score = 146,
P = 4.2e-07

>TREMBL:AF052432_1 product: "katanin p80 subunit"; Homo sapiens katanin p80
subunit mRNA, complete cds.
Length = 655

HSPs:

Score = 150 (22.5 bits), Expect = 1.2e-07, P = 1.2e-07
Identities = 35/105 (33%), Positives = 55/105 (52%)

```

Query: 145 SEVSQDHETMAQVLF SRNMRLNVALT FWRKRSISEL VAYLLRIEDL GVVVDCLPVL TNCL 204
      S++ + H+TM VL SR+ L+ W I V + I DL VVVD L N +
Sbjct: 489 SQIRKGHDTMCVVLT SRHKNLDTVRVWMTGDIKTSVDSAVAINDL SVVVDLL----NIV 544

Query: 205 QEEKQYISLGCCVDLL PLVKSLLKSK FEEYVIVGLN WLQAVIKRW 249
      ++ L C +LP ++ LL+SK+E YV G L+ +++R+
Sbjct: 545 NQKASLWKLDLCTTVLPQIEKLLQSKYESYVQTGCTSLKLILQRF 589

```

Pedant information for DKFZphtes3_9k22, frame 3

Report for DKFZphtes3_9k22.3

```

[LENGTH]      304
[MW]           34767.24
[pI]           9.18
[KW]           All_Alpha

```

[KW] LOW_COMPLEXITY 3.95 %

```
SEQ  MASETHNVKRRNFCNKIEDHFIDLPRKKISNFTNKNMKEVKKSPKQLAAYINRTVGQTVK
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
SEQ  SPDKLRKVIYRRKKVHHPFPNFCYRKKQSPGSGGCDMANKENELACAGHLPEKLHDSRT
SEG  .....
PRD  ccchhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccc
SEQ  YLVNSSDSGSSQTESPSSKYSGFFSEVSQDHETMAQVLF SRNMRLNVALTFWRKRSISEL
SEG  .....
PRD  eeeeeeeeeeeeeeeeeeeeecccccccccccccccccccccccccccccccccccccccc
SEQ  VAYLLRIEDLGVVVDCLPVLTNCLQEKKQYISLGCCVDLLPLVKSLLKSKFEEYVIVGLN
SEG  .....
PRD  hhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccc
SEQ  WLQAVIKRWSELSSKTEIINDGNIQILKQQLSGLWEQENHLLVPGYTGNIAKDVDAYL
SEG  .....
PRD  hhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccc
SEQ  LQLH
SEG  ....
PRD  hccc
```

(No Prosite data available for DKFZphtes3_9k22.3)

(No Pfam data available for DKFZphtes3_9k22.3)

Localization of expressed proteins

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
DKF2p434B0435	AL117496	6248	48	5366	1773	transport and traffic	similar to: kinesin like proteins	512.1 cR from top of Chr10 linkage group	"secre pathway"	None
DKF2p434N0535	AL117518	4055	126	4025	1300	differentiation & development	similar to: Drosophila chromatin protein		"no predict"	None
DKF2p564A0122	AL110209	2722	65	1300	412	signaling & communication	similar to: acyltransferase	16	"mitochondri a"	Mitochondria
DKF2p564A022	AL136620	1376	132	632	167	unknown	unknown	4	"no predict"	Endoplasmic Reticulum
DKF2p564A032	AL50267	2214	76	1953	626	differentiation & development	similar to: MG21 contains three conserved protein motifs present in GTP- binding proteins, but these are not conserved in 2_2a3.1	238.7 cR from top of Chr20 linkage group	"no predict"	Nucleus
DKF2p564A0723	AL80116	2524	42	2177	712	cell cycle	similar to: origin recognition complex	6q14.3-16.1	"nucleus"	Cytosol + Nucleus
DKF2p564A202	AL80056	707	33	620	196	metabolism	similar to: protein involved in energy metabolism	10	"mitochondri a"	Endoplasmic Reticulum
DKF2p564B0482	AL110243	2092	317	1579	421	signaling & communication	Unknown, contains 2 WD- 40 repeats, which are typical for the beta- transducin subunit of G-proteins		"no predict"	Cytosol + Nucleus
DKF2p564B1023	AL136611	2905	157	1896	580	nucleic acid management	similar to: RNA helicase		"nucleus / nuclear envelope"	Nucleus

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
DKFZp564B1162	AL136646	4593	661	2625	655	signaling & communication	unknown	4	"no predict"	Cytoskeleton
DKFZp564B122	AL049972	1842	70	1536	488	unknown	unknown		"no predict"	Cytosol
DKFZp564B1471	AL136667	1484	78	323	82	membrane protein	unknown		"no predict"	Endoplasmic Reticulum
DKFZp564B162	AL136621	1914	246	1631	462	nucleic acid management	similar to: Zinc finger protein	13q12	"no predict"	other/unknc
DKFZp564B163	AL50268	1208	191	577	129	transport and traffic	similar to: GTP binding protein		"secr pathway"	Cytosol + Nucleus
DKFZp564B212	AL136623	1915	218	1348	377	protein management	similar to: protein involved in posttranslational modification	22q12.1	"secr pathway"	Endoplasmic Reticulum
DKFZp564B2123	AL136612	3300	121	699	193	signaling & communication	similar to: Neurocalcin is a Ca(2+)-binding protein with 3 EF-hands. Homology with recoverin indicates involvement in Ca2+ dependent activation of guanylate cyclase.	574.6 cR from top of Chr8 linkage group	"no predict"	Cytosol + Nucleus
DKFZp564B246	AL136664	2054	73	1074	334	metabolism	similar to: dTDP-6-deoxy-L-mannose-dehydrogenase	5	"nucleus or cytosol"	Nucleus
DKFZp564C0362	AL80076	1731	60	1142	361	nucleic acid management	similar to: ssDNA binding protein		"no predict"	other/unknown
DKFZp564C0469	AL050298	899	86	898	270	unknown	unknown		"nucleus"	Cytosol + Nucleus
DKFZp564C1362	AL136647	837	137	673	179	metabolism	similar to: molecular clock protein	16p12.3-p13.11	"mitochondria"	Other/unknown

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
DKFZp564C1616	AL136597	3928	240	1997	586	structure & motility	shares the features of mayven and kelch and therefore should be involved in the organisation of cyto skeleton binding to membrane proteins		"cytoskeleton / plasma membrane"	Nucleus
DKFZp564C162	AL136627	2305	155	625	157	membrane protein	unknown	86.2 cR from top of Chr1 linkage group	"no predict"	Endoplasmic Reticulum
DKFZp564C1664	AL136656	1866	180	1040	287	unknown	unknown	745_A_2; 756_F_2; 842_C_2	"no predict"	Cytosol
DKFZp564C182	AL136628	2835	272	1177	302	unknown	unknown		"no predict"	Golgi
DKFZp564C183	AL136639	1709	105	1448	448	nucleic acid management	similar to: DEAD-box helicase	87.50 cR from top of Chr16 linkage group	"nucleus / nuclear envelope"	Nuclear envelope
DKFZp564C196	AL050020	2266	366	966	200	signaling & communication	similar to: neuronal calcium sensor		"no predict"	Nucleus
DKFZp564D116	AL050022	2535	29	1849	607	signaling & communication	similar to: GTP-binding protein		"no predict"	Cytosol
DKFZp564D202	AL136631	1787	18	944	309	unknown	unknown		"no predict"	Cytosol
DKFZp564E0123	AL136613	2005	104	1000	299	unknown	unknown	16q13	"no predict"	Cytosol + Nucleus
DKFZp564E0482	AL136697	2923	163	1581	473	signaling & communication	similar to: calmodulin- related protein	200.5 cR from top of Chr3 linkage group	"membranes"	Cytosol + Nucleus

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
DKFZp564E1782	AL136696	1618	40	972	311	membrane protein	unknown	171.7 cR from top of Chr14 linkage group	"no predict"	Endoplasmic Reticulum
DKFZp564E2182	AL50261	2367	193	804	204	Cell Cycle	similar to: protein involved in cell cycle, DNA repair, maintenance of minichromosomes	6q22.1-22.33	"nucleus"	Nucleus
DKFZp564F0223	AL136614	1016	68	613	182	unknown	unknown	12q24	"secre pathway / endosomes"	other/unknown
DKFZp564F052	AL049989	1649	34	1303	423	signaling & communication	similar to: sorting nexin 7		"membranes"	Cytosol
DKFZp564F0522	AL049943	2078	283	943	220	unknown	unknown	2	"no predict"	Nucleus
DKFZp564F1862	AL80081	1987	250	918	223	differentiation & development	similar to: DnaJ proteins, but lacks CRR domain of these proteins.	7q31	"no predict"	Endoplasmic Reticulum
DKFZp564F2116	AL136598	1512	115	738	208	membrane protein	unknown	15q25	"nucleus"	other/unknown
DKFZp564F2122	AL136604	1910	156	1856	567	unknown	unknown	311.4 cR from top of Chr14 linkage group	"no predict"	Cytoskeleton (microtubules)
DKFZp564F2162	AL136648	1549	95	730	212	unknown	unknown	209.8 cR from top of Chr20 linkage group	"peroxisomes"	Peroxisomes
DKFZp564G0222	AL80115	1165	157	933	259	nucleic acid management	unknown		"no predict"	Endoplasmic Reticulum

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
DKFZp564G083	AL136641	1027	37	570	178	protein management	similar to: yeast, ARD1 and NAT1, are required for the expression of an N-terminal protein acetyltransferase 1.	20	"no predict"	Cytosol + Nucleus
DKFZp564G182	AL136632	2444	539	1225	229	unknown	unknown	6p22.1-22	"no predict"	Cytosol + Nucleus
DKFZp564H012	AL136633	957	93	632	180	unknown	unknown		"no predict"	Mitochondrion
DKFZp564H1122	AL136605	1734	159	1133	325	membrane protein	unknown	11q14	"no predict"	Nucleus
DKFZp564H1322	AL136606	2292	270	1829	520	membrane protein	unknown	19q13.2 from BCKDHA-D19S217	"no predict"	Cytosol + Nucleus
DKFZp564H1562	AL136649	2014	75	971	299	structure & motility	similar to: Cell cell interaction protein	1	"plasma membrane"	Plasma membrane + cell contact sites
DKFZp564I0123	AL136615	1467	126	1064	313	signaling & communication	similar to: protein activator of the interferon-induced protein kinase		"cytosol or nucleus"	Cytosol
DKFZp564I0422	AL136607	4748	511	1194	228	signaling & communication	unknown		"no predict"	Golgi + Plasma membrane
DKFZp564I1216	AL136600	1548	81	635	185	membrane protein	unknown	873.3-875.1 CR from top of Chr1 linkage group	"no predict"	Endoplasmic Reticulum
DKFZp564I1782	AL136699	1741	168	410	81	signaling & communication	similar to: phospholemman protein,	11q23	"secretory pathway"	Golgi + Plasma

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
							a membrane substrate for the cAMP-dependent protein kinase; seems to serve as chloride channels or as chloride-channel regulators. Transmembrane Protein			membrane
DKF2p564J206	AL136665	1122	34	921	296	unknown	unknown	377.5 cR from top of Chr8 linkage group	"mitochondria"	Mitochondria
DKF2p564J2423	AL136616	1713	58	882	275	metabolism	similar to: protein involved in amino acid metabolism	8p11.2	"cytosol"	Cytosol + Nucleus
DKF2p564J2482	AL136700	1860	10	1650	547	nucleic acid management	similar to: Dead-box helicase	175.5 cR from topFT of Chr7 linkage group	"nucleus / nuclear envelope"	Nucleus
DKF2p564J1022	AL110301	1409	5	1021	290	nucleic acid management	Unknown, contains a Leucine zipper	12	"cytosol or nucleus"	Cytosol + Nucleus
DKF2p564J1516	AL136601	2868	352	1839	496	structure & motility	similar to: RNA binding, Tubulin binding	20, 12.10 cR from GCT10F11	"cytosol"	Cytosol
DKF2p564J1864	AL136660	690	109	648	180	transport and traffic	similar to: canin and chicken microsomal signal peptidase 23 kd subunit.		"endoplasmic reticulum"	Endoplasmic Reticulum
DKF2p564J2222	AL136608	1858	154	1440	429	structure & motility	similar to: actin-related protein		"plasma membrane / cytoskeleton"	Plasma membrane
DKF2p564K0322	AL136609	2775	779	2392	538	unknown	unknown		"no"	Plasma

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
									"predict"	membrane
DKFZp564K0822	AL136610	2789	10	525	172	unknown	unknown	7	"no predict"	Golgi
DKFZp564K1216	AL49933	1938	357	1418	354	signaling & communication	similar to: GTP-binding regulatory protein	7	"membranes"	Golgi + Plasma membrane
DKFZp564K192	AL136637	1931	107	1015	303	unknown	unknown	6p22.1-22.3	"no predict"	Other/unknown
DKFZp564K1964	AL1117619	1560	207	884	226	unknown	unknown	17	"no predict"	Endoplasmic Reticulum
DKFZp564K2216	AL136602	2088	832	1155	108	unknown	unknown		"no predict"	Mitochondria
DKFZp564L023	AL136643	2978	279	2045	589	protein management	Unknown, Pfam prediction: ubiquitin family	9	"cytosol"	Cytosol + Nucleus
DKFZp564L1216	AL136603	2042	73	873	267	membrane protein	unknown		"secr pathway"	Golgi + plasma membrane
DKFZp564L2423	AL136617	2416	29	1072	348	transport and traffic	Unknown, a lectin character is predicted	2	"endoplasmic reticulum"	Endoplasmic Reticulum
DKFZp564M082	AL80071	902	227	589	121	unknown	Unknown, contains osteopontin motive		"no predict"	Cytosol + Nucleus
DKFZp564M112	AL80070	2686	14	595	194	signaling & communication	unknown	956.7 cR from top of Chr2 linkage group	"no predict"	Golgi
DKFZp564M173	AL136644	636	26	400	125	unknown	similar to: janus proteins		"no predict"	Cytosol + Nucleus
DKFZp564M1863	AL117602	1192	125	1027	301	signaling &	similar to: phospho- ducin-like protein, G-protein	9	"cytosol"	Cytosol

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
						communication	modulator			
DKFZp564M1982	AL390217	2707	302	1150	286	unknown	unknown		"no predict"	Cytosol
DKFZp564M2423	AL80119	2201	86	1246	387	unknown	unknown	72.60 cR from top of Chr3 linkage group	"cytosol"	Cytosol
DKFZp564N0582	AL50264	1646	75	506	144	cell cycle	similar to: DRR1 gene	3p21.1	"cytoskeleton / plasma membrane"	Cytoskeleton (focal adhesion sites) + nucleus
DKFZp564N1623	AL136618	2936	172	1047	292	signaling & communication	Unknown, contains a WW domain which binds proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes		"no predict"	Cytosol + Nucleus
DKFZp564O043	AL050390	2515	186	1509	441	structure & motility	similar to: ankyrin	7	"no predict"	Cytosol + Nucleus
DKFZp564O0523	AL136619	1736	24	1103	360	unknown	unknown	7q21-q22	"no predict"	Nucleus
DKFZp564O123	AL80122	1985	234	872	213	unknown	unknown		"no predict"	Cytosol + Nucleus
DKFZp564O1762	AL136652	1260	56	901	282	signaling & communication	similar to: low-density lipoprotein (LDL) receptors are the major		"secretory pathway"	Golgi

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
							cholesterol-carrying lipoproteins of plasma. The novel protein contains an additional leucine zipper suitable for protein-protein interaction.			
DKFZp556401923	AL050295	2091	237	2090	617	metabolism	similar to: dTDP-6-deoxy-L-mannose-dehydrogenase		"secre pathway"	Cytosol
DKFZp556402423	AL390214	3564	656	1072	139	unknown	Unknown, contains CAAX box (prenyl group binding site); found in :Ras proteins, and ras-like proteins such as Rho, Rab, Rac, Ral, and Rap; nuclear lamins A and B; Some G protein alpha subunits, G protein gamma subunits; some dnaJ-like proteins		"no predict"	Cytosol + Nucleus
DKFZp55640243	AL050015	1074	23	834	270	unknown	unknown	3	"no predict"	Endoplasmic Reticulum
DKFZp55611024	AL050037	1783	5	970	322	unknown	similar to: hypothetical protein Rv0712 - Mycobacterium tuberculosis		"no predict"	Cytosol
DKFZp556J2046	AL136720	1706	16	678	221	metabolism	similar to: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase.	16	"no predict"	Mitochondria
DKFZp556K144	AL136727	3084	456	1079	208	transport and traffic	similar to: Rab protein		"secre pathway"	Golgi
DKFZp556D0919	AL050100	2777	48	494	148	unknown	unknown	12	"no"	Golgi

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
									predict"	
DKFZp586E1124	AL136942	2005	184	861	226	transport and traffic	similar to: golgi transmembrane spanning transporter	8	"Golgi"	Golgi + plasma membrane
DKFZp586E1123	AL136936	1854	367	954	196	protein management	similar to: heat shock protein	578.9 cR from top of Chr12 linkage group	"cytosol or nucleus"	Cytosol + Nucleus
DKFZp586E11519	AL050101	2140	82	1680	559	unknown	similar to: A.thaliana A_IG002N01		"no predict"	Cytosol
DKFZp586F1918	AL050091	3489	184	594	137	unknown	unknown		"no predict"	Cytosol + Nucleus
DKFZp586F1919	AL136915	2024	134	745	204	membrane protein	unknown	14.8 cR from top of Chr20 linkage group	"secr pathway"	Golgi + plasma membrane
DKFZp586H2219	AL50282	1971	199	1623	475	unknown	unknown	22q11.2-qter	"no predict"	Cytosol
DKFZp586I0418	AL136912	1568	163	822	220	unknown	unknown	7q31	"no predict"	Cytosol + Nucleus
DKFZp586I1520	AL050149	2439	11	1711	566	transport and traffic	similar to: nuclear RanGTP binding protein		"nucleus"	Nucleus
DKFZp586J1023	AL136938	1048	72	749	236	protein management	similar to: glutathione S-transferase / posttranslational modification		"no predict"	Cytosol + Nucleus
DKFZp586J1119	AL136919	2343	28	2151	708	signaling & communication	unknown		"membranes"	Endoplasmic Reticulum
DKFZp586J1923	AL050220	745	49	588	179	differentiation &	similar to: serine protease	19	"secr pathway"	Endoplasmic Reticulum

CloneID	AccNo	Contig (bp)	ORFStart (bp)	ORFStop (bp)	ORFSize (aa)	ProteinGroup	Similarity	ChromLocation STS	Localization Predicted	Localization
						development				
DKFZp586K0919	AL50283	1782	204	1316	371	unknown	unknown		"no predict"	Cytosol + Nucleus
DKFZp586L0118	AL136913	1076	45	596	184	protein management	similar to: mitochondrial Ribosomal S40 protein		"nucleus"	Nucleus
DKFZp586M2420	AL136927	1986	23	1855	611	transport and traffic	similar to: mannosyltransferase	11	"secr pathway"	Endoplasmic Reticulum
DKFZp727E151	AL390215	1957	340	1701	454	membrane protein	similar to: transporter proteins (contains 9 transmembrane domains)		"no predict"	Endoplasmic Reticulum
DKFZp727M111	AL117479	2275	79	1899	633	unknown	unknown		"no predict"	Cytosol
DKFZp727M231	AL117480	2428	56	1681	542	unknown	unknown		"no predict"	Cytosol
DKFZp761G05121	AL118986	4592	107	3613	1169	protein management	similar to: SH3 BINDING PROTEIN		"cytosol"	Cytosol
DKFZp761G18121	AL136548	4117	107	1438	444	signaling & communication	similar to: ALLOGRAFT INFLAMMATORY FACTOR		"nucleus"	Nucleus
DKFZp761I112121	AL136549	4130	139	3894	1252	cell cycle	similar to: p53 inducible protein	5q34	"no predict"	Cytosol
DKFZp761M02121	AL136551	3328	178	2163	662	cell cycle	similar to: p53 regulated PA26-r2 nuclear protein		"nucleus"	Cytosol
DKFZp761O15121	AL136552	4293	112	2421	770	signaling & communication	similar to: semaphorin W	328.8 cR from top of Chr2 linkage group	"secr pathway"	Endoplasmic Reticulum

Table of cDNA clones and related data

Group: cell cycle

CloneID	Homology	Function	Group
hfb2_16g18	Similarity to KIAA0797 and yeast Smt4p	Novel protein with similarities to S. pombe SPAC17A5.07c and the S. cerevisiae Smt4p suppressor of Mif2 gene.; involved in centromer organisation	Cell cycle
hfb2_2k14	Strong similarity to human N33 tumour suppressor gene	New tumour suppressor gene	Cell cycle
htes3_35b4	Human M-phase phosphoprotein-1	The novel protein is C-terminal identical to human M-phase phosphoprotein-1, which is expressed and phosphorylated in the metaphase. Therefore the novel protein seems to be involved in the mitotic spindle during cell division.	Cell cycle
htes3_35p22	Strong similarity to oncogene 1 (tre-2 locus)	Oncogene	Cell cycle
htes3_7j3	Related to the C-TAK1 Cdc25C associated protein kinase	Cdc25C is a protein kinase that controls entry into mitosis by dephosphorylation of Cdc2. Cdc25C function is regulated by phosphorylation, too. Serine 216 phosphorylation of Cdc25C mediates the binding of 14-3-3 protein to Cdc25C. C-TAK1 (Cdc twenty-five	Cell cycle
htes3_7p10	Strong similarity to XPMC2 protein	XPMC2 of xenopus rescues several different yeast mitotic catastrophe mutants defective in Wee1/Mik1 kinase function.	Cell cycle
hute1_20m11	Similarity to suppressor protein sds22	Suppressor regulator of protein phosphatase-1	Cell cycle

Group cell structure and motility

CloneID DKV 99	Homology	Function	Group
hfbr2_16c16	Similarity to Drosophila kelch	Shares the features of mayven and kelch and therefore should be involved in the organisation of cyto skeleton binding to membrane proteins	Structure and motility
hfbr2_2b5	Similarity to collagen proteins	New collagen alpha chain	Structure and motility
htes3_15i5	Strong similarity to "radial spokehead" proteins	Part of sperm motor	Structure and motility
htes3_18l7	Similarity to ankyrins	Putative ankyrin	Structure and motility
htes3_1k11	Strong similarity to mouse ENC-1	Nuclear matrix protein	Structure and motility
htes3_72k15	Strong similarity to Rattus norvegicus actin-filament binding protein Frabin.	FGD1-related F-actin-binding protein (Farbin/FGD1) is a novel F-actin binding protein. Modulation of cell structure and motility as well as modulation of the JNK/SAPK pathway.	Structure and motility
htes3_7b22	Similarity to paramyosins	Protein involved in motility	Structure and motility
hutel_19g22	Strong similarity to tuftelin/enamelin	New connective tissue protein	Structure and motility
hutel_24j6	Strong similarity Rattus norvegicus cell adhesion regulator (CAR1) mRNA	Cell adhesion regulator (signal transduction molecule influencing cell adhesion to collagen)	Structure and motility

Group Differentiation/Development

Clone ID DEP2	Homology	Function	Group
hfbr2_2d15	Mus musculus testis-specific Y-encoded-like protein (Tspy11).	TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y-chromosome	Differentiation/Development
htes3_35e21	Similarity to interleukin-7 precursor	New interleukin	Differentiation/Development
hutel_2h3	Strong similarity to mouse E25 and gallus E3-16	Homolog is marker for chondro-osteogenic differentiation	Differentiation/Development

Group kidney derived

CloneID DEF2P	Homology	Function	Group
hfkd2_1j9	Strong similarity to XLCL2 protein, African clawed frog	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived
hfkd2_24e23	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived
hfkd2_46a6	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived
hfkd2_46b10	Similarity to C.elegans F25B5.3	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived
hfkd2_46d13	Weak similarity to KE03 protein	Contains a RGD site; No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived
hfkd2_4b6	Similarity to Homo sapiens clone 25003 partial CDS.	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived
hfkd2_4c8	Similarity to KIAA0549 and HAP1 (Huntingtin-associated protein-1)	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Kidney derived

Group mammary carcinoma derived

CloneID DFP2	Homology	Function	Group
hmcfl_1c23	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Mammary Carcinoma derived
hmcfl_lgl3	Similarity to KIAA0766; very weak similarity to transposases	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Mammary Carcinoma derived

Group Nucleic acid management

CloneID	Homology	Function	Group
hfbr2_23b10	Similarity to rat RNA helicase HEL117	RNA helicase	Nucleic Acid Management
hfbr2_3cl8	Strong similarity to RNA helicase and RNA-dependent ATPase from the DEAD box family	DEAD-box	Nucleic Acid Management
hfbr2_64a15	Similarity to inorganic pyrophosphatases (unspliced)	Inorganic pyrophosphatase	Nucleic Acid Management
hfbr2_6017	Strong similar to RNA helicases	RNA helicases	Nucleic Acid Management
hfbr2_72b18	Similarity to DNA damage induced genes	Similar to dinP of <i>E. coli</i> , yqjH of <i>B. subtilis</i> , dinP of <i>M. tuberculosis</i> and T19K24.15 of <i>A. thaliana</i> . The dinB/P pathway is a second SOS-pathway in <i>E. coli</i>	Nucleic Acid Management
hfbr2_72l12	Similarity to YDR126w	DNA binding protein	Nucleic acid management
hfbr2_82i24	Strong similarity to DEAD-box subfamily ATP-dependent helicase	Dead-box helicase	Nucleic Acid Management
htes3_14h21	Strong similarity to RNA helicases	RNA helicase	Nucleic Acid Management
htes3_15j3	Similarity to YGR276c, a ribonuclease H of <i>S. cerevisiae</i> .	Rnase H	Nucleic Acid Management
htes3_20m18	Similarity to the <i>S. cerevisiae</i> mitochondrial carrier protein RIM2.	The novel protein contains a leucine zipper and a Prosite mitochondrial energy transfer proteins signature. It is member of a family of substrate carrier proteins which are found in the inner mitochondrial membrane and are involved in energy transfer.	Nucleic Acid Management
htes3_22g2	KIAA0829 is shorter, nearly identical to rat TIP120	Involved in TATA box binding complex	Nucleic Acid Management
htes3_2m18	Nearly identical to mouse Dhml	Multifunctional nuclease/exoribonuclease	Nucleic acid management
htes3_7p9	Similarity to nuclear domain 10 protein NDP52	Transcription control	Nucleic Acid Management
htes3_8m10	Strong similarity to polyadenylate-binding proteins.	The poly(A)-binding protein (PABP) binds to the messenger (mRNA) 3'-poly(A) tail found on most eukaryotic mRNAs and together with the poly(A) tail has been implicated in governing the stability and the translation of mRNA.	Nucleic Acid Management
htel1_18l1	Strong similarity to <i>S. cerevisiae</i> YHR148w	Mitochondrial Ribosomal S40 protein	Nucleic Acid Management

Group testis associated

CloneID ORF2	Homology	Function	Group
htes3_14g5	Strong similarity to cell growth regulating nucleolar protein LYAR, of mouse	Contains a ATP/GTP-binding site motif A (P-loop), but not the zinc finger motif and nuclear localization signals of lyar.	Testes associated
htes3_14p14	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_14p7	Weak similarity to kinesin associated protein KAP3	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_15a13	Similarity to S.cerevisiae Hop1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_15g14	Similarity to YOR243c	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_15h1	Weak similarity to Hsp70/Hsp90 organizing protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_15j18	Unknown	Unknown; no predictive prosite pfam or SCOP motive	Testes associated
htes3_17f10	T2387.2B PROTEIN	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_18f3	Similarity to TNF-inducible protein CG12-1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_19f19	Weak similarity to S. cerevisiae protein YFL046w.	The protein contains a RGD cell attachment site.	Testes associated
htes3_19j17	Partial similarity to C.elegans Y40B1A.2 protein.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Testes associated
htes3_20c21	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Testes associated
htes3_21n23	Strong similarity to rat 7acom protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_22c23	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_22n13	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_27o14	Similarity to C.elegans C55A6.1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_28d14	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_2a11	Similarity to mucin	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_2d15	Similarity to C.elegans F25H2.1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_2f14	Weak similarity to omega protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_2g7	Similarity to neurofilament proteins	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_2h15	Similarity to S.pombe cdc23	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_21i19	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Testes associated

CloneID DJ2p	Homology	Function	Group
htes3_2m20	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Testes associated
htes3_2n9	Very weak similarity to Homo sapiens PAC clone DJ0771P04 from 7q11.21-q11.23.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Testes associated
htes3_30f4	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Testes associated
htes3_35g6	Strong similarity to R27216_1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_35n24	Unknown	Contains an IG MHC pattern	Testes associated
htes3_35p17	Similarity to S.cerevisiae VAC8 and beta-Catenin, but contains no amadillo motifs	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_4b4	Rattus norvegicus late gestation lung protein 1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_4f17	Similarity to KIAA0333 Methyl-CpG binding protein; does not contain such a motive.	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_4o19	Similarity to mucin	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_50j4	Unknown, prolin rich protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_50n23	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_50n6	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_6b21	Similarity to KIAA0256	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_6d16	WUGSC:H DJ1185107.2, differences to genmodel	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_72k11	Similarity to S.pombe hypothetical repeat-containing protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_7d17	Similarity to KIAA0454	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_7j8	WUGSC:H DJ1159004.1 similarity to YBL104p	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_8g11	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_8g5	KIAA087, alternative spliced	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_8p7	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_9e22	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_9i20	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated
htes3_9k22	Similarity to C-terminus of katanin p80	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Testes associated

Group transmembrane proteins

CloneID DCT29	Homology	Function	Group
hfb2_16112	Similarity to Fugu rubripes PUT2	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane protein
hfb2_16112	Similarity to gallus putative transmembrane protein E3-16	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfb2_22h13	Similarity to Drosophila melanogaster EG:39E1.3.	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfb2_2b17	Similarity to Drosophila hypothetical 30K protein	3 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfb2_2d17	Unknown	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfb2_64k24	Similarity to several proteins	5 transmembrane regions. No informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane protein
hfb2_82c20	Similarity to C.elegans D1007.5	7 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfb2_82e17	Similarity to C.elegans "R01B10.5"	6 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfb2_82g14	Unknown proline rich protein	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfk2_24a15	Similarity to C. elegans R07G3.8	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfk2_3i13	Similarity to A.thaliana YUP8H12.2	3 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hfk2_4m11	Weak similarity to YMR034c	4 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hmc1_1a11	Similarity to YDR255c and SPBC29A3.03c	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hmc1_1e15	Similarity to D-XYLOSE TRANSPORTER	Transporter; 9 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
htes3_15c6	Unknown	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
htes3_20l3	Partial similarity to the IL-17 receptor.	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
htes3_27k4	Strong similarity to C.elegans R07H8.2/ZK185.2	Contains a leucine zipper 10 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive;	Transmembrane protein
htes3_2h1	Similarity to C.elegans C13F10.5	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
htes3_35k24	Unknown	5 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hutel_19f19	Similarity to mouse P24 protein	2 transmembrane domains No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein
hutel_24c19	Unknown	1 transmembrane domain No informative BLAST results; No predictive prosite, pfam or SCOP motive	Transmembrane protein

Group Brain derived

CloneID	Homology	Function	Group
hbr2_16f21	Strong similarity to zinc finger protein 216 has no zn finger, is only similar	PROSITE: Contains no Zinc finger; No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_16k22	Weak similarity to thioredoxin	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_22f21	Weak similarity to C.elegans C18C4.5	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_22i4	Similarity to Human P52rIPK N-terminus	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_22k3	Weak homology with : EXTENSIN (PROLINE-RICH GLYCOPROTEIN)	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_22k8	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_23f2	Similarity to Vps29p; saccharomyces cerevisiae (baker's yeast) pep11 protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_23o24	Similarity to CAAX-box protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_23o5	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2a2	Similarity to 52X autoantigen Ro/SS-A - human	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2c1	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2c18	Weak similarity to cyclin-dependent kinase p130-PITSLRE	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2d20	Similarity to Synechocystis sp. (PCC 6803)	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2g18	J30M3.2 extension of genmodel	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2h1	Similarity to C.elegans D2007.4 protein	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2h10	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_2k19	Similarity to KIAA0378	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_3f16	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hbr2_3l2	Weak similarity to ubiquitin-like protein DSK2 yeast	Pfam: ubiquitin family; No informative BLAST results; No predictive prosite or SCOP motive	Brain derived
hbr2_62n10	Similarity to reticulocyte-binding protein	Contains a Leucine zipper; No informative BLAST results; No predictive pfam or SCOP motive	Brain derived
hbr2_64a11	Similarity to Drosophila irregular chiasm C-rough precursor (frame shift)	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived

CloneID	Homology	Function	Group
hfr2_64c16	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_64c4	Similarity to A. thaliana T08113.5	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_64h6	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_64i20	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_64o16	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_6a17	Weak similarity to finger protein zFOC1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_6i20	Similarity to ribosomal protein L15 precursor, mitochondrial	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_7lo20	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_72d13	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_72m16	Similarity to C.elegans H14A12.3	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_72n12	Strong similarity to rat Ganglioside expression factor (GEF-2) but even higher identity with C.elegans putative protein identities = 91/116 (78%)	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_78d13	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_78n23	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_7a24	DXF2phfr2_7a24.1 similarity to C-terminus of TGF-beta-activated kinase	Only c-terminus homolog; contains no kinase domain; No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_7e22	Similarity to cytochrome b561	No heme domain but a c may helix loop helix signature	Brain derived
hfr2_7j4	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived
hfr2_82m16	Very weak similarity to A.thaliana F28A23.140	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Brain derived

Group Intracellular Transport and Trafficking

CloneID	Homology	Function	Group
hbr2_23124	Strong similarity to human GP36b glycoprotein and canine VIP 36	A lectin character is predicted. Due to the intracellular localisation of the homologue proteins, it should be involved in cell trafficking	Transport and traffic
hbr2_2117	Strong similarity to rab1	GTP binding	Transport and traffic
hbr2_41m15	Strong similarity to ras-related GTP-binding protein Rab17	GTP-binding, signal transduction	Transport and traffic
hbr2_62f10	Strong similarity to zinc transporter proteins	Zinc transporter protein	Transport and traffic
hbr2_62l19	2 nearly identical to dog GTP-binding protein rab10	GTP binding	Transport and traffic
hbr2_64j18	Strong similarity to dog signal peptidase (EC 3.4.99.-)	Identical to canin and chicken microsomal signal peptidase 23 kd subunit.	Transport and traffic
hkd2_24n20	Strong similarity to eps8 binding protein e3B1	Contains an Src homology domain 3 and is similar to human eps8 SH3 domain binding protein 1 (e3B1) and spectrins. The new protein seems to be part of the signalling pathway between tyrosine kinases and the membrane/cyto skeleton	Transport and traffic
hkd2_24p5	Human ankyrin G (ANK-3) new splice variant	New ankyrin protein	Transport and traffic
hkd2_4k14	Strong similarity to Rab6	New Rab protein	Transport and traffic
htes3_1gl13	Similarity to 256 kD golgin, strong similarity to rat "cp151"	New golgin protein	Transport and traffic
htes3_17n18	TonB-dependent receptor protein signature 1	Involved in receptor-mediated uptake	Transport and traffic
htes3_21l16	Identical to rat ribosome attached membrane protein 4	Responsible for transport of proteins into ER	Transport and traffic
htes3_23l11	Nearly identical to mouse ADP-ribosylation-like factor homolog 6 (Arl6).	Protein secretion through the endoplasmic reticulum and the Golgi vesicular trafficking system is initiated by the binding of ADP-ribosylation factors	Transport and traffic
htes3_26g22	Similarity to kinesins.	The novel protein contains a ATP/GTP-binding site motif A (P-loop) and a kinesin motor domain signature. Kinesin is a microtubule-associated force-producing protein that play a role in organelle transport.	Transport and traffic
htes3_4h6	Strong similarity to Kinesin light chain	New kinesin light chain	Transport and traffic
htes3_72p16	Strong similarity to mouse MEM3 and yeast VPS35	New vacuolar protein sorting-associated protein	Transport and traffic
hute1_19h17	Strong similarity to C.elegans ZK1086.1	Steroid turnover in cells	Transport and traffic
hute1_20h13	Strong similarity to alpha-adaptins	New adaptin chain (clathrin assembly protein complex 2 alpha-a large chain)	Transport and traffic
hute1_24e11	Similarity to golgi 4-transmembrane spanning transporter mtp	New golgi transmembrane spanning transporter	Transport and traffic

Group signal transduction

CloneID DRZP	Homology	Function	Group
hfbr2_23b21	Nearly identical to bovine neurocalcin	Neurocalcin is a Ca(2+)-binding protein with 3 EF-hands. Homology with recoverin indicates involvement in Ca2+ dependent activation of guanylate cyclase.	Signal transduction
hfbr2_23n16	Similarity to putative phosphatidylinositol-4-phosphate 5-kinase	Contains a WW domain which binds proteins with particular proline- motifs, [AP]-P- [AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes	Signal transduction
hfbr2_2c17	(similarity to YMR131c and retinoblastoma-binding protein RBp46)	The protein contains 1 WD-40 repeat, which is typical for the beta-transducin subunit of G-proteins.	signal transduction
hfbr2_62b11	Putative GTPase-activating protein, related to human chimaerins	The new protein is expected to activate p21rac-related small GTPases	Signal transduction
hfbr2_78c24	Strong similarity to guanylate-binding proteins (GBPs)	Modulating/blocking the response of cells to interferons.	Signal transduction
hfbr2_82e4	Strong similarity to rat calmodulin-binding protein	Involved in calmodulin-related pathway	Signal transduction
hfbr2_82i17	Similarity to plasma membrane substrate for cAMP-dependent protein kinase	Transmembrane protein with strong similarity to the phospholemmann protein, a membrane substrate for the cAMP-dependent protein kinase; seems to serve as chloride channels or as chloride-channel regulators. Transmembrane Protein	Signal Transduction
hfbr2_82m6	Strong similarity to mouse "sphingosine kinase	Sphingosine kinase	Signal transduction
hfkd2_46m4	Nearly identical to mouse GTP-binding protein	GTP-binding protein	Signal transduction
htes3_15k11	KIAA0781, 5' extension	Heart development/signal transduction	Signal transduction
htes3_1c1	Similarity to GTPase-activating proteins	GTPase-activating proteins	Signal transduction
htes3_1n3	Similarity to Tup1p	Beta-transducin subunit of G-proteins	Signal transduction
htes3_20k2	Strong similarity to rat vanilloid receptor subtype 1.	VR1 seems to play an important role in the activation and sensitization of nociceptors. It is the receptor for e.g. capsaicin, a selective activator of nociceptors, a natural product of capsicum peppers. The novel protein is the human orthologue of rat VR1.	Signal transduction
htes3_21d4	Similarity to RCC1-like G exchanging factor RLG	RCC1 is a eukaryotic protein which binds to chromatin and interacts with ran, a nuclear GTP-binding protein.	Signal transduction
htes3_23n19	Similarity to rat protein kinase C-interacting RBCC protein 1	Protein kinase C-interacting protein	Signal transduction
htes3_4f5	Similarity to S.pombe "beta-transducin"	Contains 3 WD-40 repeats, which are typical for the beta-transducin subunit of G-proteins; in addition, a Cytochrome C family heme-binding site signature is present.	Signal Transduction
htes3_6c11	Strong similarity to YNL132w	Could be a steroid receptor	Signal transduction
htes3_8e24	Related to yeast YGL099w and mouse MMR1 putative GTP-binding proteins.	a novel 658 amino acid putative GTP-binding protein	Signal Transduction
hute1_20g21	Ras inhibitor	Receptor tyrosine kinase (RTK)/RAS/MAP kinase signaling cascade	Signal transduction
hute1_22d2	Similarity to GTP-binding proteins	GTP-binding proteins	Signal transduction

hutel_22e12	Strong similarity to S.cerevisiae YGI054c and cornichon	The Drosophila cni and mammalian proteins cornicon are part of a signal transduction pathway involving hte EGF-receptor	Signal transduction
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Group Metabolism

Clone ID	Homology	Function	Group
hfr2_3g8	Similarity to N-terminal Acetyltransferase Complex ARD1 homolog	In yeast, ARD1 and NAT1, are required for the expression of an N-terminal protein acetyltransferase 1.	Metabolism
hfr2_62o17	Similarity to apolipoprotein E receptor	Low-density lipoprotein (LDL) receptors are the major cholesterol-carrying lipoproteins of plasma. The novel protein contains an additional leucine zipper suitable for protein-protein interaction.	Metabolism
hfr2_6b24	Similar to dTDP-6-deoxy-L-mannose-dehydrogenases	DTDP-6-deoxy-L-mannose-dehydrogenase	Metabolism
hfr2_78k24	Similarity to Mus musculus ubiquitin specific protease UBP43.	The novel protein contains a Prosite ubiquitin carboxyl-terminal hydrolases family 2 signature 2. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated protein	Metabolism
hfk2_24b15	Similarity to phosphomannomutases	Phosphoserine signature typical for Phosphoglucosyltransferase or Phosphomannomutase ; conversion of Hexose phosphates.	Metabolism
hfk2_3o17	Strong similarity NADH Oxidoreductase B22 subunit-	The new protein is the human ortholog of the bovine EC 1.6.5.3. chain CI-B22 and therefore part of the human respiratory chain.	Metabolism
hfk2_46j20	Strong similarity to 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	The new protein seems to be the human 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase.	Metabolism
htes3_15c24	Strong similarity to 2-hydroxyacid dehydrogenases	New human 2-hydroxyacid dehydrogenase	Metabolism
htes3_17l17	Strong similarity to transketolases	Transketolase testis specific	Metabolism
htes3_27d1	Similarity to ubiquitin-specific proteases	Protease	Metabolism
htes3_2a17	Similar to thiol-proteases	Putative thiol-protease	Metabolism
htes3_35b5	Strong similarity to bovine vacuolar ATPase (EC 3.6.1.1-) chain A	ATPase	Metabolism
htes3_35k16	Similarity to acyl-CoA synthetase	Acyl-CoA synthetase	Metabolism
htes3_35n12	Strong similarity to ADP/ATP carrier proteins	Involved in mitochondrial energy metabolism	Metabolism
htes3_35n9	Carboxylesterase, splice variant	Carboxylesterase	Metabolism
hutel_20b19	Similarity to sarcosine oxidases	Sarcosine oxidases	Metabolism
hutel_20m24	Strong similarity to S.cerevisiae Alg9p probable mannosyltransferase	Possible mannosyltransferase	Metabolism
hutel_23e13	Strong similarity to heat shock 27K proteins	Heat shock protein related new subtilase	Metabolism

Group transcription factors

CloneID	Homology	Function	Group
DKF2P			
hfkcd2_46k19	Strong similarity to pterin-4-alpha-carbinolamine dehydratase	Dcoh is a bifunctional protein, complexed with biopterin. It serves as dimerization cofactor of hepatocyte nuclear factor-1 and catalyzes the dehydration of the biopterin cofactor of phenylalanine hydroxylase	Transcription factor
hfkcd2_47a4	Similarity to zinc fingers	New putative transcription factor with one C2H2 zinc fingers.	Transcription factor
htes3_2e12	Similarity to finger proteins	Transcription factor with three C2H2 zinc fingers. Additionally, a cytochrome C family heme-binding site signature is present in the protein	Transcription factors
htes3_2l1j15	3 strong similarity to "NY-CO-33"	Transcription factor	Transcription factors
htes3_17n12	Nearly identical to mouse SOX-LZ	SOX-LZ, related to SRY and HMG-box-Proteins	Transcription factors
hutcl_18i19	Similarity to transcription factor SF3	The SREBP-2 protein is cleaved to release soluble NH2-terminal that enter the nucleus and activate genes encoding the low density lipoprotein receptor and enzymes of cholesterol synthesis; a lim domain; shows similarity to the common sunflower transcript1	Transcription factor
hutcl_1i2	Similarity to Dictostelium myosin heavy chain kinase	Zn-finger protein	Transcription factor

Group uterus associated

Cloned ID	Homology	Function	Group
hutel_17k7	Similarity to HPBRII-4 MRNA	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_18c12	Similarity to candidate tumor suppressor p33ING1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_18i4	Weak similarity to C.elegans D2085.2	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_19g19	Partial similarity to bovine elastin fragment	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_19j11	Strong similarity to KIAA0231, similarity to ras binding protein Sur8	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_22n2	Similar to F46F6.1	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_21d15	Unknown	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_22o2	Similarity to S.pombe SPBC3E7.03c	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated
hutel_23g11	Similarity to SPAC31G5.12c and Mafip	No informative BLAST results; No predictive prosite, pfam or SCOP motive	Uterus associated

Prosite Key

NAME: N-glycosylation site.
 CONSENSUS: N-{P}-[ST]-{P}.

NAME: Glycosaminoglycan attachment site.
 CONSENSUS: S-G-x-G.

NAME: Tyrosine sulfation site.

NAME: cAMP- and cGMP-dependent protein kinase phosphorylation site.
 CONSENSUS: [RK](2)-x-[ST].

NAME: Protein kinase C phosphorylation site.
 CONSENSUS: [ST]-x-[RK].

NAME: Casein kinase II phosphorylation site.
 CONSENSUS: [ST]-x(2)-[DE].

NAME: Tyrosine kinase phosphorylation site.
 CONSENSUS: [RK]-x(2,3)-[DE]-x(2,3)-Y.

NAME: N-myristoylation site.
 CONSENSUS: G-{EDRKHPFYW}-x(2)-[STAGCN]-{P}.

NAME: Amidation site.
 CONSENSUS: x-G-[RK]-[RK].

NAME: Aspartic acid and asparagine hydroxylation site.
 CONSENSUS: C-x-[DN]-x(4)-[FY]-x-C-x-C.

NAME: Vitamin K-dependent carboxylation domain.
 CONSENSUS: x(12)-E-x(3)-E-x-C-x(6)-[DEN]-x-[LIVMFY]-x(9)-[FYW].

NAME: Phosphopantetheine attachment site.
 CONSENSUS: [DEQGSTALMKRH]-[LIVMFYSTAC]-[GNQ]-[LIVMFYAG]-[DNEKHS]-S-[LIVMST]-
 CONSENSUS: {PCFY}-[STAGCPQLIVMF]-[LIVMATN]-[DENQGTAKRHLM]-[LIVMWSTA]-[LIVGSTACR]-
 CONSENSUS: x(2)-[LIVMFA].

NAME: Acyl carrier protein phosphopantetheine domain profile.

NAME: Prokaryotic membrane lipoprotein lipid attachment site.
 CONSENSUS: {DERK}(6)-[LIVMFWSTAG](2)-[LIVMFYSTAGCQ]-{AGS}-C.

NAME: Prokaryotic N-terminal methylation site.
 CONSENSUS: [KRHEQSTAG]-G-[FYLIVM]-[ST]-[LT]-[LIVP]-E-[LIVMFWSTAG](14).

NAME: Prenyl group binding site (CAAX box).
 CONSENSUS: C-{DENQ}-[LIVM]-x>.

NAME: Protein splicing signature.
 CONSENSUS: [DNEG]-x-[LIVFA]-[LIVMY]-[LVAST]-H-N-[STC].

NAME: Endoplasmic reticulum targeting sequence.
 CONSENSUS: [KRHQSA]-[DENQ]-E-L>.

NAME: Microbodies C-terminal targeting signal.
 CONSENSUS: [STAGCN]-[RKH]-[LIVMAFY]>.

NAME: Gram-positive cocci surface proteins 'anchoring' hexapeptide.
 CONSENSUS: L-P-x-T-G-[STGAVDE].

NAME: Bipartite nuclear targeting sequence.

NAME: Cell attachment sequence.
 CONSENSUS: R-G-D.

NAME: ATP/GTP-binding site motif A (P-loop).
 CONSENSUS: [AG]-x(4)-G-K-[ST].

NAME: Cyclic nucleotide-binding domain signature 1.
 CONSENSUS: [LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LIVMFY](4)-x(2)-G.

NAME: Cyclic nucleotide-binding domain signature 2.

CONSENSUS: [LIVMF]-G-E-x-[GAS]-[LIVM]-x(5,11)-R-[STAQ]-A-x-[LIVMA]-x-[STACV].

NAME: cAMP/cGMP binding motif.

NAME: EF-hand calcium-binding domain.

CONSENSUS: D-x-[DNS]-[ILVIFYW]-[DENSTG]-[DNQGHRK]-[GP]-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

NAME: Actinin-type actin-binding domain signature 1.

CONSENSUS: [EQ]-x(2)-[ATV]-[FY]-x(2)-W-x-N.

NAME: Actinin-type actin-binding domain signature 2.

CONSENSUS: [LIVM]-x-[SGN]-[LIVM]-[DAGHE]-[SAG]-x-[DNEAG]-[LIVM]-x-[DEAG]-x(4)-[LIVM]-x-[LM]-[SAG]-[LIVM]-[LIVMT]-W-x-[LIVM](2).

NAME: Anaphylatoxin domain signature.

CONSENSUS: [CSH]-C-x(2)-[GAP]-x(7,8)-[GASTDEQR]-C-[GASTDEQL]-x(3,9)-[GASTDEQN]-x(2)-[CE]-x(6,7)-C-C.

NAME: Anaphylatoxin domain profile.

NAME: Apple domain.

CONSENSUS: C-x(3)-[LIVMFY]-x(5)-[LIVMFY]-x(3)-[DENQ]-[LIVMFY]-x(10)-C-x(3)-C-T-

CONSENSUS: x(4)-C-x-[LIVMFY]-F-x-[FY]-x(13,14)-C-x-[LIVMFY]-[RK]-x-[ST]-x(14,15)-

CONSENSUS: S-G-x-[ST]-[LIVMFY]-x(2)-C.

NAME: Band 4.1 family domain signature 1.

CONSENSUS: W-[LIV]-x(3)-[KRQ]-x-[LIVM]-x(2)-[QH]-x(0,2)-[LIVMF]-x(6,8)-[LIVMF]-

CONSENSUS: x(3,5)-F-[FY]-x(2)-[DENS].

NAME: Band 4.1 family domain signature 2.

CONSENSUS: [HYW]-x(9)-[DENQSTV]-[SA]-x(3)-[FY]-[LIVM]-x(2)-[ACV]-x(2)-[LM]-x(2)-

CONSENSUS: [FY]-G-x-[DENQST]-[LIVMFYS].

NAME: Band 4.1 family domain profile.

NAME: Clq domain signature.

CONSENSUS: F-x(5)-[ND]-x(4)-[FYWL]-x(6)-F-x(5)-G-x-Y-x-F-x-[FY].

NAME: C-terminal cystine knot signature.

CONSENSUS: C-C-x(13)-C-x(2)-[GN]-x(12)-C-x-C-x(2,4)-C.

NAME: C-terminal cystine knot profile.

NAME: CUB domain profile.

NAME: Death domain profile.

NAME: EGF-like domain signature 1.

CONSENSUS: C-x-C-x(5)-G-x(2)-C.

NAME: EGF-like domain signature 2.

CONSENSUS: C-x-C-x(2)-[GP]-[FYW]-x(4,8)-C.

NAME: Calcium-binding EGF-like domain pattern signature.

CONSENSUS: [DEQN]-x-[DEQN](2)-C-x(3,14)-C-x(3,7)-C-x-[DN]-x(4)-[FY]-x-C.

NAME: Laminin-type EGF-like (LE) domain signature.

CONSENSUS: C-x(1,2)-C-x(5)-G-x(2)-C-x(2)-C-x(3,4)-[FYW]-x(3,15)-C.

NAME: Coagulation factors 5/8 type C domain (FA58C) signature 1.

CONSENSUS: [GAS]-W-x(7,15)-[FYW]-[LIV]-x-[LIVFA]-[GSTDEN]-x(6)-[LIVF]-x(2)-[IV]-x-

CONSENSUS: [LIVT]-[QKM]-G.

NAME: Coagulation factors 5/8 type C domain (FA58C) signature 2.

CONSENSUS: P-x(8,10)-[LM]-R-x-[GE]-[LIVP]-x-G-C.

NAME: Forkhead-associated (FHA) domain profile.

NAME: Fibrinogen beta and gamma chains C-terminal domain signature.

CONSENSUS: W-W-[LIVMFYW]-x(2)-C-x(2)-[GSA]-x(2)-N-G.

NAME: Type I fibronectin domain.

CONSENSUS: C-x(6,8)-[LFY]-x(5)-[FYW]-x-[RK]-x(8,10)-C-x-C-x(6,9)-C.

NAME: Type II fibronectin collagen-binding domain.

CONSENSUS: C-x(2)-P-F-x-[FYWI]-x(7)-C-x(8,10)-W-C-x(4)-[DNSR]-[FYW]-x(3,5)-[FYW]-x-[FYWI]-C.

NAME: Hemopexin domain signature.

CONSENSUS: [LIFAT]-x(3)-W-x(2,3)-[PE]-x(2)-[LIVMFY]-[DENQS]-[STA]-[AV]-[LIVMFY].

NAME: Kringle domain signature.

CONSENSUS: [FY]-C-R-N-P-[DNR].

NAME: Kringle domain profile.

NAME: LDL-receptor class A (LDLRA) domain signature.

CONSENSUS: C-[VILMA]-x(5)-C-[DNH]-x(3)-[DENQHT]-C-x(3,4)-[STADE]-[DEH]-[DE]-x(1,5)-C.

NAME: LDL-receptor class A (LDLRA) domain profile.

NAME: C-type lectin domain signature.

CONSENSUS: C-[LIVMFYATG]-x(5,12)-[WL]-x-[DNSR]-x(2)-C-x(5,6)-[FYWLIVSTA]-[LIVMSTA]-C.

NAME: C-type lectin domain profile.

NAME: Link domain signature.

CONSENSUS: C-x(15)-A-x(3,4)-G-x(3)-C-x(2)-G-x(8,9)-P-x(7)-C.

NAME: Osteonectin domain signature 1.

CONSENSUS: C-x-[DN]-x(2)-C-x(2)-G-[KRH]-x-C-x(6,7)-P-x-C-x-C-x(3,5)-C-P.

NAME: Osteonectin domain signature 2.

CONSENSUS: F-P-x-R-[IM]-x-D-W-L-x-[NQ].

NAME: Somatomedin B domain signature.

CONSENSUS: C-x-C-x(3)-C-x(5)-C-C-x-[DN]-[FY]-x(3)-C.

NAME: Thyroglobulin type-I repeat signature.

CONSENSUS: [FYWHP]-x-P-x-C-x(3,4)-G-x-[FYW]-x(3)-Q-C-x(4,10)-C-[FYW]-C-V-x(3,4)-[SG].

NAME: P-type 'Trefoil' domain signature.

CONSENSUS: R-x(2)-C-x-[FYPST]-x(3,4)-[ST]-x(3)-C-x(4)-C-C-[FYWH].

NAME: Cellulose-binding domain, bacterial type.

CONSENSUS: W-N-[STAGR]-[STDN]-[LIVM]-x(2)-[GST]-x-[GST]-x(2)-[LIVMFT]-[GA].

NAME: Cellulose-binding domain, fungal type.

CONSENSUS: C-G-G-x(4,7)-G-x(3)-C-x(5)-C-x(3,5)-[NHG]-x-[FYWM]-x(2)-Q-C.

NAME: Chitin recognition or binding domain signature.

CONSENSUS: C-x(4,5)-C-C-S-x(2)-G-x-C-G-x(4)-[FYW]-C.

NAME: Barwin domain signature 1.

CONSENSUS: C-G-[KR]-C-L-x-V-x-N.

NAME: Barwin domain signature 2.

CONSENSUS: V-[DN]-Y-[EQ]-F-V-[DN]-C.

NAME: BIR repeat.

CONSENSUS: [HKEPILVY]-x(2)-R-x(3,7)-[FYW]-x(11,14)-[STAN]-G-[LMF]-X-[FYHDA]-X(4)-[DESL]-X(2,3)-C-X(2)-C-X(6)-[WA]-X(9)-H-X(4)-[PRSD]-X-C-X(2)-[LIVMA].

NAME: WAP-type 'four-disulfide core' domain signature.

CONSENSUS: C-x-{C}-[IDN]-x(2)-C-x(5)-C-C.

NAME: Phorbol esters / diacylglycerol binding domain.

CONSENSUS: H-x-[LIVMFYW]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC]-x(5,10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5,9)-C.

NAME: C2 domain signature.

CONSENSUS: [ACG]-x(2)-L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[STAP]-D-[PA]-[FY].

NAME: C2-domain profile.

NAME: CAP-Gly domain signature.

CONSENSUS: G-x(8,10)-[FYW]-x-G-[LIVM]-x-[LIVMFY]-x(4)-G-K-[NH]-x-G-[STAR]-x(2)-G-
CONSENSUS: x(2)-[LY]-F.

NAME: Ly-6 / u-PAR domain signature.

CONSENSUS: [EQR]-C-[LIVMFYAH]-x-C-x(5,8)-C-x(3,8)-[EDNQSTV]-C-{C}-x(5)-C-
CONSENSUS: x(12,24)-C.

NAME: MAM domain signature.

CONSENSUS: G-x-[LIVMFY](2)-x(3)-[STA]-x(10,11)-[LV]-x(4)-[LIVMF]-x(6,7)-C-[LIVM]-x-
CONSENSUS: F-x-[LIVMFY]-x(3)-[GSC].

NAME: MAM domain profile.

NAME: PH domain profile.

NAME: Phosphotyrosine interaction domain (PID) profile.

NAME: Src homology 2 (SH2) domain profile.

NAME: Src homology 3 (SH3) domain profile.

NAME: VWFC domain signature.

CONSENSUS: C-x(2,3)-C-x-C-x(6,14)-C-x(3,4)-C-x(2,10)-C-x(9,16)-C-C-x(2,4)-C.

NAME: WW/rsp5/WWP domain signature.

CONSENSUS: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

NAME: WW/rsp5/WWP domain profile.

NAME: ZP domain signature.

CONSENSUS: [LIVMFYW]-x(7)-[STAPDNL]-x(3)-[LIVMFYW]-x-[LIVMFYW]-x-[LIVMFYW]-x(2)-C-
CONSENSUS: [LIVMFYW]-x-[ST]-[PSL]-x(2,4)-[DENS]-x-[STADNQLF]-x(6)-[LIVM](2)-x(3,4)-
CONSENSUS: C.

NAME: S-layer homology domain signature.

CONSENSUS: [LVFYT]-x-[DA]-x(2,5)-[DNGSATPHY]-[WYFPDA]-x(4)-[LIV]-x(2)-[GTALV]-
CONSENSUS: x(4,6)-[LIVFYC]-x(2)-G-x-[PGSTA]-x(2,3)-[MFYA]-x-[PGAV]-x(3,10)-[LIVMA]-
CONSENSUS: [STKR]-[RY]-x-[EQ]-x-[STALIVM].

NAME: 'Homeobox' domain signature.

CONSENSUS: [LIVMFYG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-
CONSENSUS: [LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

NAME: 'Homeobox' domain profile.

NAME: 'Homeobox' antennapedia-type protein signature.

CONSENSUS: [LIVMFE]-[FY]-P-W-M-[KRQTA].

NAME: 'Homeobox' engrailed-type protein signature.

CONSENSUS: L-M-A-Q-G-L-Y-N.

NAME: 'Paired box' domain signature.

CONSENSUS: R-P-C-x(11)-C-V-S.

NAME: 'POU' domain signature 1.

CONSENSUS: [RKQ]-R-[LIM]-x-[LF]-G-[LIVMFY]-x-Q-x-[DNQ]-V-G.

NAME: 'POU' domain signature 2.

CONSENSUS: S-Q-[ST]-[TA]-I-[SC]-R-F-E-x-[LSQ]-x-[LI]-[ST].

NAME: Zinc finger, C2H2 type, domain.

CONSENSUS: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H.

NAME: Zinc finger, C3HC4 type (RING finger), signature.

CONSENSUS: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].

NAME: Nuclear hormones receptors DNA-binding region signature.

CONSENSUS: C-x(2)-C-x-[DE]-x(5)-[HN]-[FY]-x(4)-C-x(2)-C-x(2)-F-F-x-R.

NAME: GATA-type zinc finger domain.

CONSENSUS: C-x-[DN]-C-x(4,5)-[ST]-x(2)-W-[HR]-[RK]-x(3)-[GN]-x(3,4)-C-N-[AS]-C.

NAME: Poly(ADP-ribose) polymerase zinc finger domain signature.

CONSENSUS: C-[KR]-x-C-x(3)-I-x-K-x(3)-[RG]-x(16,18)-W-[FYH]-H-x(2)-C.

NAME: Poly(ADP-ribose) polymerase zinc finger domain profile.

NAME: Fungal Zn(2)-Cys(6) binuclear cluster domain signature.

CONSENSUS: [GASTPV]-C-x(2)-C-[RKHSTACW]-x(2)-[RKHQ]-x(2)-C-x(5,12)-C-x(2)-C-x(6,8)-

CONSENSUS: C.

NAME: Fungal Zn(2)-Cys(6) binuclear cluster domain profile.

NAME: Prokaryotic dksA/traR C4-type zinc finger.

CONSENSUS: C-[DES]-x-C-x(3)-I-x(3)-R-x(4)-P-x(4)-C-x(2)-C.

NAME: Copper-fist domain signature.

CONSENSUS: M-[LIVMF](3)-x(3)-K-[MY]-A-C-x(2)-C-I-[KR]-x-H-[KR]-x(3)-C-x-H-x(8)-

CONSENSUS: [KR]-x-[KR]-G-R-P.

NAME: Copper fist DNA binding domain profile.

NAME: Leucine zipper pattern.

CONSENSUS: L-x(6)-L-x(6)-L-x(6)-L.

NAME: bZIP transcription factors basic domain signature.

CONSENSUS: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

NAME: Myb DNA-binding domain repeat signature 1.

CONSENSUS: W-[ST]-x(2)-E-[DE]-x(2)-[LIV].

NAME: Myb DNA-binding domain repeat signature 2.

CONSENSUS: W-x(2)-[LI]-[SAG]-x(4,5)-R-x(8)-[YW]-x(3)-[LIVM].

NAME: Myc-type, 'helix-loop-helix' dimerization domain signature.

CONSENSUS: [DENSTAP]-K-[LIVMWAGSN]-{FYWCPhKR}-[LIVT]-[LIV]-x(2)-[STAV]-[LIVMSTAC]-x-

CONSENSUS: [VMFYH]-[LIVMTA]-{P}-{P}-[LIVMSR].

NAME: p53 tumor antigen signature.

CONSENSUS: M-C-N-S-S-C-M-G-G-M-N-R-R.

NAME: CBF-A/NF- κ B subunit signature.

CONSENSUS: C-V-S-E-x-I-S-F-[LIVM]-T-[SG]-E-A-[SC]-[DE]-[KRQ]-C.

NAME: CBF-B/NF- κ B subunit signature.

CONSENSUS: Y-V-N-A-K-Q-Y-x-R-I-L-K-R-R-x-A-R-A-K-L-E.

NAME: 'Cold-shock' DNA-binding domain signature.

CONSENSUS: [FY]-G-F-I-x(6,7)-[DER]-[LIVM]-F-x-H-x-[STKR]-x-[LIVMFY].

NAME: CTF/NF-I signature.

CONSENSUS: R-K-R-K-Y-F-K-K-H-E-K-R.

NAME: Ets-domain signature 1.

CONSENSUS: L-[FYW]-[QEDH]-F-[LI]-[LVQK]-x-[LI]-L.

NAME: Ets-domain signature 2.

CONSENSUS: [RKH]-x(2)-M-x-Y-[DENQ]-x-[LIVM]-[STAG]-R-[STAG]-[LI]-R-x-Y.

NAME: Ets-domain profile.

NAME: Fork head domain signature 1.

CONSENSUS: [KR]-P-[PTQ]-[FYLVQH]-S-[FY]-x(2)-[LIVM]-x(3,4)-[AC]-[LIM].

NAME: Fork head domain signature 2.

CONSENSUS: W-[QKR]-[NS]-S-[LIV]-R-H.

NAME: Fork head domain profile.

NAME: HSF-type DNA-binding domain signature.

CONSENSUS: L-x(3)-[FY]-K-H-x-N-x-[STAN]-S-F-[LIVM]-R-Q-L-[NH]-x-Y-x-[FYW]-[RKH]-K-

CONSENSUS: [LIVM].

NAME: Tryptophan pentad repeat (IRF family) signature.

CONSENSUS: W-x-[DNH]-x(5)-[LIVF]-x-[IV]-P-W-x-H-x(9,10)-[DE]-x(2)-[LIVF]-F-[KRQ]-x-

CONSENSUS: [WR]-A.

NAME: LIM domain signature.

CONSENSUS: C-x(2)-C-x(15,21)-[FYWH]-H-x(2)-[CH]-x(2)-C-x(2)-C-x(3)-[LIVMF].

NAME: LIM domain profile.

NAME: NF-kappa-B/Rel/dorsal domain signature.

CONSENSUS: F-R-Y-x-C-E-G.

NAME: MADS-box domain signature.

CONSENSUS: R-x-[RK]-x(5)-I-x-[DN]-x(3)-[KR]-x(2)-T-[FY]-x-[RK](3)-x(2)-[LIVM]-x-

CONSENSUS: K(2)-A-x-E-[LIVM]-[ST]-x-L-x(4)-[LIVM]-x-[LIVM](3)-x(6)-[LIVMF]-x(2)-

CONSENSUS: [FY].

NAME: MADS-box domain profile.

NAME: T-box domain signature 1.

CONSENSUS: L-W-x(2)-[FC]-x(3,4)-[NT]-E-M-[LIV](2)-T-x(2)-G-[RG]-[KRQ].

NAME: T-box domain signature 2.

CONSENSUS: [LIVMYW]-H-[PADH]-[DEN]-[GS]-x(3)-G-x(2)-W-M-x(3)-[IVA]-x-F.

NAME: TEA domain signature.

CONSENSUS: G-R-N-E-L-I-x(2)-Y-I-x(3)-[TC]-x(3)-R-T-[RK](2)-Q-[LIVM]-S-S-H-[LIVM]-

CONSENSUS: Q-V.

NAME: Transcription factor TFIIB repeat signature.

CONSENSUS: G-[KR]-x(3)-[STAGN]-x-[LIVMYA]-[GSTA](2)-[CSAV]-[LIVM]-[LIVMFY]-[LIVMA]-

CONSENSUS: [GSA]-[STAC].

NAME: Transcription factor TFIID repeat signature.

CONSENSUS: Y-x-P-x(2)-[IF]-x(2)-[LIVM](2)-x-[KRH]-x(3)-P-[RKQ]-x(3)-L-[LIVM]-F-x-

CONSENSUS: [STN]-G-[KR]-[LIVM]-x(3)-G-[TAGL]-[KR]-x(7)-[AGC]-x(7)-[LIVM].

NAME: TFIIS zinc ribbon domain signature.

CONSENSUS: C-x(2)-C-x(9)-[LIVMQSAR]-[QH]-[STQL]-[RA]-[SACR]-x-[DE]-[DET]-[PGSEA]-

CONSENSUS: x(6)-C-x(2,5)-C-x(3)-[FW].

NAME: TSC-22 / dip / bun family signature.

CONSENSUS: M-D-L-V-K-x-H-L-x(2)-A-V-R-E-E-V-E.

NAME: Prokaryotic transcription elongation factors signature 1.

CONSENSUS: [ST]-x(2)-[GS]-x(3)-[LI]-x(2)-E-L-x(2)-L-x(3,4)-R-x(2)-[IV]-x(3)-[LIV]-

CONSENSUS: x(6)-G-D-x(2)-E-N-[GSA]-x-Y.

NAME: Prokaryotic transcription elongation factors signature 2.

CONSENSUS: S-x(2)-S-P-[LIVM]-[AG]-x-[SAG]-[LIVM]-[LIVMY]-x(4)-[DG]-[DE].

NAME: DEAD-box subfamily ATP-dependent helicases signature.

CONSENSUS: [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN].

NAME: DEAH-box subfamily ATP-dependent helicases signature.

CONSENSUS: [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

NAME: Eukaryotic putative RNA-binding region RNP-1 signature.

CONSENSUS: [RK]-G-[EDRKHPCG]-[AGSCI]-[FY]-[LIVA]-x-[FYLM].

NAME: Fibrillarin signature.

CONSENSUS: [GST]-[LIVMAP]-V-Y-A-[TV]-E-[FY]-[SA]-x-R-x(2)-R-[DE].

NAME: MCM family signature.

CONSENSUS: G-[IVT]-[LVAC](2)-[IVT]-D-[DE]-[FL]-[DNST].

NAME: MCM family domain.

NAME: XPA protein signature 1.

CONSENSUS: C-x-[DE]-C-x(3)-[LIVMF]-x(1,2)-D-x(2)-L-x(3)-F-x(4)-C-x(2)-C.

NAME: XPA protein signature 2.

CONSENSUS: [LIVM](2)-T-[KR]-T-E-x-K-x-[DE]-Y-[LIVMF](2)-x-D-x-[DE].

NAME: XPG protein signature 1.

CONSENSUS: [VI]-[KRE]-P-x-[FYIL]-V-F-D-G-x(2)-[PIL]-x-[LVC]-K.

NAME: XPG protein signature 2.

CONSENSUS: [GS]-[LIVM]-[PER]-[FYS]-[LIVM]-x-A-P-x-E-A-[DE]-[PAS]-[QS]-[CLM].

NAME: Bacterial regulatory proteins, araC family signature.

CONSENSUS: [KRQ]-[LIVMA]-x(2)-[GSTALIV]-{FYWPGDN}-x(2)-[LIVMSA]-x(4,9)-[LIVMF]-

CONSENSUS: x(2)-[LIVMSTA]-[GSTACIL]-x(3)-[GANQRF]-[LIVMFY]-x(4,5)-[LFY]-x(3)-

CONSENSUS: [FYIVA]-{FYWHCM}-x(3)-[GSADENQKR]-x-[NSTAPKL]-[PARL].

NAME: Bacterial regulatory proteins, araC family DNA-binding domain profile.

NAME: Bacterial regulatory proteins, arsR family signature.

CONSENSUS: C-x(2)-D-[LIVM]-x(6)-[ST]-x(4)-S-[HYR]-[HQ].

NAME: Bacterial regulatory proteins, asnC family signature.

CONSENSUS: [GSTAP]-x(2)-[DNEA]-[LIVM]-[GSA]-x(2)-[LIVMFY]-[GN]-[LIVMST]-[ST]-x(6)-R-

CONSENSUS: [LVT]-x(2)-[LIVM]-x(3)-G.

NAME: Bacterial regulatory proteins, crp family signature.

CONSENSUS: [LIVM]-[STAG]-[RHNW]-x(2)-[LIM]-[GA]-x-[LIVMFYA]-[LIVSC]-[GA]-x-[STACN]-

CONSENSUS: x(2)-[MST]-x-[GSTN]-R-x-[LIVMF]-x(2)-[LIVMF].

NAME: Bacterial regulatory proteins, deoR family signature.

CONSENSUS: R-x(3)-[LIVM]-x(3)-[LIVM]-x(16,17)-[STA]-x(2)-T-[LIVMA]-[RH]-[KRNA]-D-

CONSENSUS: [LIVMF].

NAME: Bacterial regulatory proteins, gntR family signature.

CONSENSUS: [LIVAPKR]-[PILV]-x-[EQTIVMR]-x(2)-[LIVM]-x(3)-[LIVMFYK]-x-[LIVFT]-

CONSENSUS: [DNGSTK]-[RGTLV]-x-[STAIVP]-[LIVA]-x(2)-[STAGV]-[LIVMFYH]-x(2)-[LMA].

NAME: Bacterial regulatory proteins, iclR family signature.

CONSENSUS: [GA]-x(3)-[DS]-x(2)-E-x(6)-[CSA]-[LIVM]-[GSA]-x(2)-[LIVM]-[FYH]-[DN].

NAME: Bacterial regulatory proteins, lacI family signature.

CONSENSUS: [LIVM]-x-[DE]-[LIVM]-A-x(2)-[STAGV]-x-V-[GSTP]-x(2)-[STAG]-[LIVMA]-x(2)-

CONSENSUS: [LIVMFYAN]-[LIVMC].

NAME: Bacterial regulatory proteins, luxR family signature.

CONSENSUS: [GDC]-x(2)-[NSTAVY]-x(2)-[IV]-[GSTA]-x(2)-[LIVMFYWCT]-x-[LIVMFYWCR]-x(3)-

CONSENSUS: [NST]-[LIVM]-x(5)-[NRHSA]-[LIVMSTA]-x(2)-[KR].

NAME: Bacterial regulatory proteins, lysR family signature.

CONSENSUS: [NQKRHSTAG]-[LIVMFYTA]-x(2)-[STAGLV]-[STAG]-x(4)-[LIVMYCTQR]-[PSTANLVER]-

CONSENSUS: x-[PSTAGQV]-[PSTAGNVMF]-[LIVMFA]-[STAGH]-x(2)-[LIVMF]-x(2)-[LIVMFW]-

CONSENSUS: [RKEAV]-x(2)-[LIVMFYNTAE]-x(3)-[LIMVT].

NAME: Bacterial regulatory proteins, marR family signature.

CONSENSUS: [STNA]-[LIA]-x-[RNGS]-x(4)-[LM]-[EIV]-x(2)-[GES]-[LFYW]-[LIVC]-x(7)-

CONSENSUS: [DN]-[RKQG]-[RK]-x(6)-T-x(2)-[GA].

NAME: Bacterial regulatory proteins, merR family signature.

CONSENSUS: [GSA]-x-[LIVMFA]-[ASM]-x(2)-[STACLIV]-[GSDENQR]-[LIVC]-[STANHK]-x(3)-

CONSENSUS: [LIVM]-[RHF]-x-[YW]-[DEQ]-x(2,3)-[GHDNQ]-[LIVMF](2).

NAME: Bacterial regulatory proteins, tetR family signature.

CONSENSUS: G-[LIVMFYS]-x(2,3)-[TS]-[LIVMT]-x(2)-[LIVM]-x(5)-[LIVQS]-[STAGENQH]-x-

CONSENSUS: [GPAR]-x-[LIVMF]-[FYST]-x-[HFY]-[FV]-x-[DNST]-K-x(2)-[LIVM].

NAME: Transcriptional antiterminators bglG family signature.

CONSENSUS: [ST]-x-H-x(2)-[FA](2)-[LIVM]-[EQK]-R-x(2)-[QNK].

NAME: Sigma-54 factors family signature-1.

CONSENSUS: P-[LIVM]-x-[LIVM]-x(2)-[LIVM]-A-x(2)-[LIVMF]-x(2)-[HS]-x-S-T-[LIVM]-S-R.

NAME: Sigma-54 factors family signature 2.

CONSENSUS: R-R-T-[IV]-[AT]-K-Y-R.

NAME: Sigma-54 factors family profile.

NAME: Sigma-70 factors family signature 1.

CONSENSUS: [DE]-[LIVMF](2)-[HEQS]-x-G-x-[LIVMFA]-G-L-[LIVMFYE]-x-[GSAM]-[LIVMAP].

NAME: Sigma-70 factors family signature 2.

CONSENSUS: [STN]-x(2)-[DEQ]-[LIVM]-[GAS]-x(4)-[LIVMF]-[PSTG]-x(3)-[LIVMA]-x-[NQR]-

CONSENSUS: [LIVMA]-[EQH]-x(3)-[LIVMF]-x(2)-[LIVM].
NAME: Sigma-70 factors ECF subfamily signature.
CONSENSUS: [STAIV]-[PQDEL]-[DE]-[LIV]-[LIVTA]-Q-x-[STAV]-[LIVMFYC]-[LIVMAX]-x-
CONSENSUS: [GSTAIV]-[LIMFYWQ]-x(12,14)-[STAP]-[FYW]-[LIF]-x(2)-[IV].
NAME: Sigma-54 interaction domain ATP-binding region A signature.
CONSENSUS: [LIVMFY](3)-x-G-[DEQ]-[STE]-G-[STAV]-G-K-x(2)-[LIVMFY].
NAME: Sigma-54 interaction domain ATP-binding region B signature.
CONSENSUS: [GS]-x-[LIVMF]-x(2)-A-[DNEQASH]-[GNEK]-G-[STIM]-[LIVMFY](3)-[DE]-[EK]-
CONSENSUS: [LIVM].
NAME: Sigma-54 interaction domain C-terminal part signature.
CONSENSUS: [FYW]-P-[GS]-N-[LIVM]-R-[EQ]-L-x-[NHAT].
NAME: Sigma-54 interaction domain profile.
NAME: Single-strand binding protein family signature 1.
CONSENSUS: [LIVMF]-[NST]-[KRT]-[LIVM]-x-[LIVMF](2)-G-[NHRK]-[LIVM]-[GST]-x-[DET].
NAME: Single-strand binding protein family signature 2.
CONSENSUS: T-x-W-[HY]-[RNS]-[LIVM]-x-[LIVMF]-[FY]-[NGKR].
NAME: Bacterial histone-like DNA-binding proteins signature.
CONSENSUS: [GSK]-F-x(2)-[LIVMF]-x(4)-[RKEQA]-x(2)-[RST]-x-[GA]-x-[KN]-P-x-T.
NAME: Dps protein family signature 1.
CONSENSUS: H-[FW]-x-[LIVM]-x-G-x(5)-[LV]-H-x(3)-[DE].
NAME: Dps protein family signature 2.
CONSENSUS: [LIVMFY]-[DH]-x-[LIVM]-[GA]-E-R-x(3)-[LIF]-[GDN]-x(2)-[PA].
NAME: DNA repair protein radC family signature.
CONSENSUS: H-N-H-P-S-G.
NAME: recA signature.
CONSENSUS: A-L-[KR]-[IF]-[FY]-[STA]-[STAD]-[LIVMQ]-R.
NAME: RecF protein signature 1.
CONSENSUS: P-[ED]-x(3)-[LIVM](2)-x-G-[GSAD]-P-x(2)-R-R-x-[FY]-[LIVM]-D.
NAME: RecF protein signature 2.
CONSENSUS: [LIVMFY](2)-x-D-x(2,3)-[SA]-[EH]-L-D-x(2)-[KRH]-x(3)-L.
NAME: RecR protein signature.
CONSENSUS: C-x(2)-C-x(3)-[ST]-x(4)-C-x-I-C-x(4)-R.
NAME: Histone H2A signature.
CONSENSUS: [AC]-G-L-x-F-P-V.
NAME: Histone H2B signature.
CONSENSUS: [KR]-E-[LIVM]-[EQ]-T-x(2)-[KR]-x-[LIVM](2)-x-[PAG]-[DE]-L-x-[KR]-H-A-
CONSENSUS: [LIVM]-[STA]-E-G.
NAME: Histone H3 signature 1.
CONSENSUS: K-A-P-R-K-Q-L.
NAME: Histone H3 signature 2.
CONSENSUS: P-F-x-[RA]-L-[VA]-[KRQ]-[DEG]-[IV].
NAME: Histone H4 signature.
CONSENSUS: G-A-K-R-H.
NAME: HMG1/2 signature.
CONSENSUS: [FI]-S-[KR]-K-C-S-[EK]-R-W-K-T-M.
NAME: HMG-I and HMG-Y DNA-binding domain (A+T-hook).
CONSENSUS: [AT]-x(1,2)-[RK](2)-[GP]-R-G-R-P-[RK]-x.
NAME: HMG14 and HMG17 signature.
CONSENSUS: R-R-S-A-R-L-S-A-[RK]-P.
NAME: Bromodomain signature.

CONSENSUS: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-[LIVMFY]-x(3)-
 CONSENSUS: [LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

NAME: Bromodomain profile.

NAME: Chromo domain signature.

CONSENSUS: [FYL]-x-[LIVMC]-[KR]-W-x-[GDNR]-[FYWLE]-x(5,6)-[ST]-W-[ES]-[PSTDN]-x(3)-
 CONSENSUS: [LIVMC].

NAME: Chromo and chromo shadow domain profile.

NAME: Regulator of chromosome condensation (RCC1) signature 1.

CONSENSUS: G-x-N-D-x(2)-[AV]-L-G-R-x-T.

NAME: Regulator of chromosome condensation (RCC1) signature 2.

CONSENSUS: [LIVMFA]-[STAGC](2)-G-x(2)-H-[STAGLI]-[LIVMFA]-x-[LIVM].

NAME: Protamine P1 signature.

CONSENSUS: [AV]-R-[NFY]-R-x(2,3)-[ST]-x-S-x-S.

NAME: Nuclear transition protein 1 signature.

CONSENSUS: S-K-R-K-Y-R-K.

NAME: Nuclear transition protein 2 signature 1.

CONSENSUS: H-x(3)-H-S-[NS]-S-x-P-Q-S.

NAME: Nuclear transition protein 2 signature 2.

CONSENSUS: K-x-R-K-x(2)-E-G-K-x(2)-K-[KR]-K.

NAME: Ribosomal protein L1 signature.

CONSENSUS: [EM]-x(2)-[LIVA]-x(2,3)-[LIVM]-G-x(2)-[LMS]-[GSNH]-[PTKR]-[KRAV]-G-x-
 CONSENSUS: [LMF]-P-[DENSTK].

NAME: Ribosomal protein L2 signature.

CONSENSUS: P-x(2)-R-G-[STAIV](2)-x-N-[APK]-x-[DE].

NAME: Ribosomal protein L3 signature.

CONSENSUS: [FL]-x(6)-[DN]-x(2)-[AGS]-x-[ST]-x-G-[KRH]-G-x(2)-G-x(3)-R.

NAME: Ribosomal protein L5 signature.

CONSENSUS: [LIVM]-x(2)-[LIVM]-[STAC]-[GE]-[QV]-x(2)-[LIVMA]-x-[STC]-x-[STAG]-[KR]-
 CONSENSUS: x-[STA].

NAME: Ribosomal protein L6 signature 1.

CONSENSUS: [PS]-[DENS]-x-Y-K-[GA]-K-G-[LIVM].

NAME: Ribosomal protein L6 signature 2.

CONSENSUS: Q-x(3)-[LIVM]-x(2)-[KR]-x(2)-R-x-F-x-D-G-[LIVM]-Y-[LIVM]-x(2)-[KR].

NAME: Ribosomal protein L9 signature.

CONSENSUS: G-x(2)-[GN]-x(4)-V-x(2)-G-[FY]-x(2)-N-[FY]-L-x(5)-[GA]-x(3)-[STN].

NAME: Ribosomal protein L10 signature.

CONSENSUS: [DEH]-x(2)-[GS]-[LIVMF]-[STN]-[VA]-x-[DEQK]-[LIVMA]-x(2)-[LIM]-R.

NAME: Ribosomal protein L11 signature.

CONSENSUS: [RKN]-x-[LIVM]-x-G-[ST]-x(2)-[SNQ]-[LIVM]-G-x(2)-[LIVM]-x(0,1)-[DENG].

NAME: Ribosomal protein L13 signature.

CONSENSUS: [LIVM]-[KRV]-[GK]-M-[LIV]-[PS]-x(4,5)-[GS]-[NQEKRA]-x(5)-[LIVM]-x-[AIV]-
 CONSENSUS: [LFY]-x-[GDN].

NAME: Ribosomal protein L14 signature.

CONSENSUS: [GA]-[LIV](3)-x(9,10)-[DNS]-G-x(4)-[FY]-x(2)-[NT]-x(2)-V-[LIV].

NAME: Ribosomal protein L15 signature.

CONSENSUS: K-[LIVM](2)-[GAL]-x-[GT]-x-[LIVMA]-x(2,5)-[LIVM]-x-[LIVMF]-x(3,4)-
 CONSENSUS: [LIVMFC]-[ST]-x(2)-A-x(3)-[LIVM]-x(3)-G.

NAME: Ribosomal protein L16 signature 1.

CONSENSUS: [KR]-R-x-[GSAC]-[KQVA]-[LIVM]-W-[LIVM]-[KR]-[LIVM]-[LFY]-[AP].

NAME: Ribosomal protein L16 signature 2.

CONSENSUS: R-M-G-x-[GR]-K-G-x(4)-[FWKR].

NAME: Ribosomal protein L17 signature.
 CONSENSUS: I-x-[ST]-[GT]-x(2)-[KR]-x-K-x(6)-[DE]-x-[LIMV]-[LIVMT]-T-x-[STAG]-[KR].

NAME: Ribosomal protein L19 signature.
 CONSENSUS: [RT]-[KRSVY]-[GSA]-x-V-[RS]-[KR]-[SA]-K-L-Y-Y-L-R.

NAME: Ribosomal protein L20 signature.
 CONSENSUS: K-x(3)-[KRC]-x-[LIVM]-W-[IV]-[STNALV]-R-[LIVM]-N-x(3)-[RKH].

NAME: Ribosomal protein L21 signature.
 CONSENSUS: [IVT]-x(3)-[KR]-x(3)-[KRQ]-K-x(6)-G-[HF]-R-[RQ]-x(2)-T.

NAME: Ribosomal protein L22 signature.
 CONSENSUS: [RKQN]-x(4)-[RH]-[GAS]-x-G-[KRQS]-x(9)-[HDN]-[LIVM]-x-[LIVMS]-x-[LIVM].

NAME: Ribosomal protein L23 signature.
 CONSENSUS: [RK](2)-[AM]-[IVFYT]-[IV]-[RKT]-L-[STANQK]-x(7)-[LIVMFT].

NAME: Ribosomal protein L24 signature.
 CONSENSUS: [GDEN]-D-x-V-x-[IV]-[LIVMA]-x-G-x(2)-[KA]-[GN]-x(2,3)-[GA]-x-[IV].

NAME: Ribosomal protein L27 signature.
 CONSENSUS: G-x-[LIVM](2)-x-R-Q-R-G-x(5)-G.

NAME: Ribosomal protein L29 signature.
 CONSENSUS: [KNQS]-[PSTL]-x(2)-[LIMFA]-[KRGSAN]-x-[LIVYSTA]-[KR]-[KRH]-[DESTANRL]-
 CONSENSUS: [LIV]-A-[KRCQVT]-[LIVMA].

NAME: Ribosomal protein L30 signature.
 CONSENSUS: [IVT]-[LIVM]-x(2)-[LF]-x-[LI]-x-[KRHQEG]-x(2)-[STNQH]-x-[IVT]-
 CONSENSUS: x(10)-[LMS]-[LIV]-x(2)-[LIVA]-x(2)-[LMFY]-[IVT].

NAME: Ribosomal protein L31 signature.
 CONSENSUS: H-P-F-[FY]-[TI]-x(9)-G-R-[AV]-x-[KR].

NAME: Ribosomal protein L33 signature.
 CONSENSUS: Y-x-[ST]-x-[KR]-[NS]-x(4)-[PAT]-x(1,2)-[LIVM]-[EA]-x(2)-K-[FY]-[CSD].

NAME: Ribosomal protein L34 signature.
 CONSENSUS: K-[RG]-T-[FYWL]-[EQS]-x(5)-[KRHS]-x(4,5)-G-F-x(2)-R.

NAME: Ribosomal protein L35 signature.
 CONSENSUS: [LIVM]-K-[TV]-x(2)-[GSA]-[SAIL]-x-K-R-[LIVMFY]-[KRL].

NAME: Ribosomal protein L36 signature.
 CONSENSUS: C-x(2)-C-x(2)-[LIVM]-x-R-x(3)-[LIVMN]-x-[LIVM]-x-C-x(3,4)-[KR]-H-x-Q-x-Q.

NAME: Ribosomal protein L1e signature.
 CONSENSUS: N-x(3)-[KR]-x(2)-A-[LIVT]-x-S-A-[LIV]-x-A-[ST]-[SGA]-x(7)-[RK]-G-H.

NAME: Ribosomal protein L6e signature.
 CONSENSUS: N-x(2)-P-L-R-R-x(4)-[FY]-V-I-A-T-S-x-K.

NAME: Ribosomal protein L7Ae signature.
 CONSENSUS: [CA]-x(4)-[IV]-P-[FY]-x(2)-[LIVM]-x-[GSQ]-[KRQ]-x(2)-L-G.

NAME: Ribosomal protein L10e signature.
 CONSENSUS: R-x-A-[FYW]-G-K-[PA]-x-G-x(2)-A-R-V.

NAME: Ribosomal protein L13e signature.
 CONSENSUS: [KR]-Y-x(2)-K-[LIVM]-R-[STA]-G-[KR]-G-F-[ST]-L-x-E.

NAME: Ribosomal protein L15e signature.
 CONSENSUS: [DE]-[KR]-A-R-x-L-G-[FY]-x-[SAP]-x(2)-G-[LIVMFY](4)-R-x-R-V-x-R-G.

NAME: Ribosomal protein L18e signature.
 CONSENSUS: [KRE]-x-L-x(2)-[PS]-[KR]-x(2)-[RH]-[PSA]-x-[LIVM]-[NS]-[LIVM]-x-[RK]-
 CONSENSUS: [LIVM].

NAME: Ribosomal protein L19e signature.
 CONSENSUS: R-x-[KR]-x(5)-[KR]-x(3)-[KRH]-x(2)-G-x-G-x-R-x-G-x(3)-A-R-x(3)-[KQ]-
 CONSENSUS: x(2)-W-x(7)-R-x(2)-L-x(3)-R.

NAME: Ribosomal protein L21e signature.

CONSENSUS: G-[DE]-x-V-x(10)-[GV]-x(2)-[FYH]-x(2)-[FY]-x-G-x-T-G.

NAME: Ribosomal protein L24e signature.

CONSENSUS: [FY]-x-[GS]-x(2)-[IV]-x-P-G-x-G-x(2)-[FYV]-x-[KRHE]-x-D.

NAME: Ribosomal protein L27e signature.

CONSENSUS: G-K-N-x-W-F-F-x-K-L-R-F>.

NAME: Ribosomal protein L30e signature 1.

CONSENSUS: [STA]-x(5)-G-x-[QKR]-x(2)-[LIVM]-[KQT]-x(2)-[KR]-x-G-x(2)-K-x-[LIVM](3).

NAME: Ribosomal protein L30e signature 2.

CONSENSUS: [DE]-L-G-[STA]-x(2)-G-[KR]-x(6)-[LIVM]-x-[LIVM]-x-[DEN]-x-G.

NAME: Ribosomal protein L31e signature.

CONSENSUS: V-[KR]-[LIVM]-x(3)-[LIVM]-N-x-[AK]-x-W-x-[KR]-G.

NAME: Ribosomal protein L32e signature.

CONSENSUS: F-x-R-x(4)-[KR]-x(2)-[KR]-[LIVM]-x(3)-W-R-[KR]-x(2)-G.

NAME: Ribosomal protein L34e signature.

CONSENSUS: Y-x-[ST]-x-S-[NY]-x(5)-[KR]-T-P-G.

NAME: Ribosomal protein L35Ae signature.

CONSENSUS: G-K-[LIVM]-x-R-x-H-G-x(2)-G-x-V-x-A-x-F-x(3)-[LI]-P.

NAME: Ribosomal protein L36e signature.

CONSENSUS: P-Y-E-[KR]-R-x-[LIVM]-[DE]-[LIVM](2)-[KR].

NAME: Ribosomal protein L37e signature.

CONSENSUS: G-T-x-[SA]-x-G-x-[KR]-x(3)-[ST]-x(0,1)-H-x(2)-C-x-R-C-G.

NAME: Ribosomal protein L39e signature.

CONSENSUS: [KRA]-T-x(3)-[LIVM]-[KRQF]-x-[NHS]-x(3)-R-[NHY]-W-R-R.

NAME: Ribosomal protein L44e signature.

CONSENSUS: K-x-[TV]-K-K-x(2)-L-[KR]-x(2)-C.

NAME: Ribosomal protein S2 signature 1.

CONSENSUS: [LIVMFA]-x(2)-[LIVMFYC](2)-x-[STAC]-[GSTANQEK]-[STALV]-[HY]-[LIVMF]-G.

NAME: Ribosomal protein S2 signature 2.

CONSENSUS: P-x(2)-[LIVMF](2)-[LIVMS]-x-[GDN]-x(3)-[DENL]-x(3)-[LIVM]-x-E-x(4)-

CONSENSUS: [GNQKRH]-[LIVM]-[AP].

NAME: Ribosomal protein S3 signature.

CONSENSUS: [GSTA]-[KR]-x(6)-G-x-[LIVMT]-x(2)-[NQSCH]-x(1,3)-[LIVFCA]-x(3)-[LIV]-

CONSENSUS: [DENQ]-x(7)-[LMT]-x(2)-G-x(2)-G.

NAME: Ribosomal protein S4 signature.

CONSENSUS: [LIVM]-[DE]-x-R-L-x(3)-[LIVMC]-[VMFYHQ]-[KRT]-x(3)-[STAGCF]-x-[ST]-x(3)-

CONSENSUS: [SAI]-[KR]-x-[LIVMF](2).

NAME: Ribosomal protein S5 signature.

CONSENSUS: G-[KRQ]-x(3)-[FY]-x-[ACV]-x(2)-[LIVMA]-[LIVM]-[AG]-[DN]-x(2)-G-x-

CONSENSUS: [LIVM]-G-x-[SAG]-x(5,6)-[DEQ]-[LIVM]-x(2)-A-[LIVMF].

NAME: Ribosomal protein S6 signature.

CONSENSUS: G-x-[KRC]-[DENQRH]-L-[SA]-Y-x-I-[KRNSA].

NAME: Ribosomal protein S7 signature.

CONSENSUS: [DENSK]-x-[LIVMET]-x(3)-[LIVMFT](2)-x(6)-G-K-[KR]-x(5)-[LIVMF]-[LIVMFC]-

CONSENSUS: x(2)-[STA].

NAME: Ribosomal protein S8 signature.

CONSENSUS: [GE]-x(2)-[LIV](2)-[STY]-T-x(2)-G-[LIVM](2)-x(4)-[AG]-[KRHAYT].

NAME: Ribosomal protein S9 signature.

CONSENSUS: G-G-G-x(2)-[GSA]-Q-x(2)-[SA]-x(3)-[GSA]-x-[GSTAV]-[KR]-[GSAL]-[LIF].

NAME: Ribosomal protein S10 signature.

CONSENSUS: [AV]-x(3)-[GDNSR]-[LIVMSTA]-x(3)-G-P-[LIVM]-x-[LIVM]-P-T.

NAME: Ribosomal protein S11 signature.
 CONSENSUS: [LIVMF]-x-[GSTAC]-[LIVMF]-x(2)-[GSTAL]-x(0,1)-[GSN]-[LIVMF]-x-[LIVM]-
 CONSENSUS: x(4)-[DEN]-x-T-P-x-[PA]-[STCH]-[DN].

NAME: Ribosomal protein S12 signature.
 CONSENSUS: [RK]-x-P-N-S-[AR]-x-R.

NAME: Ribosomal protein S13 signature.
 CONSENSUS: [KRQS]-G-x-R-H-x(2)-[GSNH]-x(2)-[LIVMC]-R-G-Q.

NAME: Ribosomal protein S14 signature.
 CONSENSUS: [RP]-x(0,1)-C-x(11,12)-[LIVMF]-x-[LIVMF]-[SC]-[RG]-x(3)-[RN].

NAME: Ribosomal protein S15 signature.
 CONSENSUS: [LIVM]-x(2)-H-[LIVMFY]-x(5)-D-x(2)-[SAGN]-x(3)-[LF]-x(9)-[LIVM]-x(2)-
 CONSENSUS: [FY].

NAME: Ribosomal protein S16 signature.
 CONSENSUS: [LIVMT]-x-[LIVM]-[KR]-L-[STAK]-R-x-G-[AKR].

NAME: Ribosomal protein S17 signature.
 CONSENSUS: G-D-x-[LIV]-x-[LIVA]-x-[QEK]-x-[RK]-P-[LIV]-S.

NAME: Ribosomal protein S18 signature.
 CONSENSUS: [IV]-[DY]-Y-x(2)-[LIVMT]-x(2)-[LIVM]-x(2)-[FYT]-[LIVM]-[ST]-[DERP]-x-
 CONSENSUS: [GY]-K-[LIVM]-x(3)-R-[LIVMAS].

NAME: Ribosomal protein S19 signature.
 CONSENSUS: [STDNQ]-G-[KRQM]-x(6)-[LIVM]-x(4)-[LIVM]-[GSD]-x(2)-[LF]-[GAS]-[DE]-F-
 CONSENSUS: x(2)-[ST].

NAME: Ribosomal protein S21 signature.
 CONSENSUS: [DE]-x-A-[LY]-[KR]-R-F-K-[KR]-x(3)-[KR].

NAME: Ribosomal protein S3Ae signature.
 CONSENSUS: [LIV]-x-[GH]-R-[IV]-x-E-x-[SC]-L-x-D-L.

NAME: Ribosomal protein S4e signature.
 CONSENSUS: H-x-K-R-[LIVM]-[SAN]-x-P-x(2)-W-x-[LIVM]-x-[KR].

NAME: Ribosomal protein S6e signature.
 CONSENSUS: [LIVM]-[STAMR]-G-G-x-D-x(2)-G-x-P-M.

NAME: Ribosomal protein S7e signature.
 CONSENSUS: [KR]-L-x-R-E-L-E-K-K-F-[SAP]-x-[KR]-H.

NAME: Ribosomal protein S8e signature.
 CONSENSUS: R-x(2)-T-G-[GA]-x(5)-[HR]-K-[KR]-x-K-x-E-[LM]-G.

NAME: Ribosomal protein S12e signature.
 CONSENSUS: A-L-[KRQP]-x-V-L-x(2)-[SA]-x(3)-[DN]-G-L.

NAME: Ribosomal protein S17e signature.
 CONSENSUS: A-x-I-x-[ST]-K-x-L-R-N-[KR]-I-A-G-[FY]-x-T-H.

NAME: Ribosomal protein S19e signature.
 CONSENSUS: P-x(6)-[SAN]-x(2)-[LIVMA]-x-R-x-[ALIV]-[LV]-Q-x-L-[EQ].

NAME: Ribosomal protein S21e signature.
 CONSENSUS: L-Y-V-P-R-K-C-S-[SA].

NAME: Ribosomal protein S24e signature.
 CONSENSUS: [FA]-G-x(2)-[KR]-[STA]-x-G-[FY]-[GA]-x-[LIVM]-Y-[DN]-[SN].

NAME: Ribosomal protein S26e signature.
 CONSENSUS: [YH]-C-V-S-C-A-I-H.

NAME: Ribosomal protein S27e signature.
 CONSENSUS: [QK]-C-x(2)-C-x(6)-F-[GS]-x-[PSA]-x(5)-C-x(2)-C-[GS]-x(2)-L-x(2)-P-x-G.

NAME: Ribosomal protein S28e signature.
 CONSENSUS: E-[ST]-E-R-E-A-R-x-L.

NAME: DNA mismatch repair proteins mutL / hexB / PMS1 signature.

CONSENSUS: G-F-R-G-E-A-L.

NAME: DNA mismatch repair proteins mutS family signature.

CONSENSUS: [ST]-[LIVM]-x-[LIVM]-x-D-E-[LIVMY]-[GC]-[RKH]-G-[GST]-x(4)-G.

NAME: mutT domain signature.

CONSENSUS: G-x(5)-E-x(4)-[STAGC]-[LIVMAC]-x-R-E-[LIVMFT]-x-E-E.

NAME: DnaA protein signature.

CONSENSUS: I-[GA]-x(2)-[LIVMF]-[SGDNK]-x(0,1)-[KR]-x-H-[STP]-[STV]-[LIVM](2)-x-

CONSENSUS: [SA]-x(2)-[KRE]-[LIVM].

NAME: Small, acid-soluble spore proteins, alpha/beta type, signature 1.

CONSENSUS: K-x-E-[LIV]-A-x-[DE]-[LIVMF]-G-[LIVMF].

NAME: Small, acid-soluble spore proteins, alpha/beta type, signature 2.

CONSENSUS: [KR]-[SAQ]-x-G-x-V-G-x-[LIVM]-x-[KR](2)-[LIVM](2).

NAME: Zinc-containing alcohol dehydrogenases signature.

CONSENSUS: G-H-E-x(2)-G-x(5)-[GA]-x(2)-[IVSAC].

NAME: Quinone oxidoreductase / zeta-crystallin signature.

CONSENSUS: [GSD]-[DEQH]-x(2)-L-x(3)-[SA](2)-G-G-x-G-x(4)-Q-x(2)-[KR].

NAME: Iron-containing alcohol dehydrogenases signature 1.

CONSENSUS: [STALIV]-[LIVF]-x-[DE]-x(6,7)-P-x(4)-[ALIV]-x-[GST]-x(2)-D-[TAIVM]-

CONSENSUS: [LIVMF]-x(4)-E.

NAME: Iron-containing alcohol dehydrogenases signature 2.

CONSENSUS: [GSW]-x-[LIVTSACD]-[GH]-x(2)-[GSAE]-[GSHYQ]-x-[LIVTP]-[GAST]-[GAS]-x(3)-

CONSENSUS: [LIVMT]-x-[HNS]-[GA]-x-[GTAC].

NAME: Short-chain dehydrogenases/reductases family signature.

CONSENSUS: [LIVSPADNK]-x(12)-Y-[PSTAGNCV]-[STAGNQCIVM]-[STAGC]-K-[PC]-[SAGFR]-

CONSENSUS: [LIVMSTAGD]-x(2)-[LIVMFYW]-x(3)-[LIVMFYWGAPTHQ]-[GSACQRHM].

NAME: Aldo/keto reductase family signature 1.

CONSENSUS: G-[FY]-R-[HSAL]-[LIVMF]-D-[STAGC]-[AS]-x(5)-E-x(2)-[LIVM]-G.

NAME: Aldo/keto reductase family signature 2.

CONSENSUS: [LIVMFY]-x(9)-[KREQ]-x-[LIVM]-G-[LIVM]-[SC]-N-[FY].

NAME: Aldo/keto reductase family putative active site signature.

CONSENSUS: [LIVM]-[PAIV]-[KR]-[ST]-x(4)-R-x(2)-[GSTAEQK]-[NSL]-x(2)-[LIVMFA].

NAME: Homoserine dehydrogenase signature.

CONSENSUS: A-x(3)-G-[LIVMFY]-[STAG]-x(2,3)-[DNS]-P-x(2)-D-[LIVM]-x-G-x-D-x(3)-K.

NAME: NAD-dependent glycerol-3-phosphate dehydrogenase signature.

CONSENSUS: G-[AT]-[LIVM]-K-[DN]-[LIVM](2)-A-x-[GA]-x-G-[LIVMF]-x-[DE]-G-[LIVM]-x-

CONSENSUS: [LIVMFYW]-G-x-N.

NAME: FAD-dependent glycerol-3-phosphate dehydrogenase signature 1.

CONSENSUS: [IV]-G-G-G-x(2)-G-[STACV]-G-x-A-x-D-x(3)-R-G.

NAME: FAD-dependent glycerol-3-phosphate dehydrogenase signature 2.

CONSENSUS: G-G-K-x(2)-[GSTE]-Y-R-x(2)-A.

NAME: Mannitol dehydrogenases signature.

CONSENSUS: [LIVMY]-x-[FS]-x(2)-[STAGCV]-x-V-D-R-[IV]-x-[PS].

NAME: Histidinol dehydrogenase signature.

CONSENSUS: I-D-x(2)-A-G-P-[ST]-E-[LIVS]-[LIVMA](3)-[AC]-x(3)-A-x(4)-[LIVM]-[AV]-

CONSENSUS: [SACL]-[DE]-[LIVMFC]-[LIVM]-[SA]-x(2)-E-H.

NAME: L-lactate dehydrogenase active site.

CONSENSUS: [LIVMA]-G-[EQ]-H-G-[DN]-[ST].

NAME: D-isomer specific 2-hydroxyacid dehydrogenases NAD-binding signature.

CONSENSUS: [LIVMA]-[AG]-[IVT]-[LIVMFY]-[AG]-x-G-[NHKRQGSAC]-[LIV]-G-x(13,14)-

CONSENSUS: [LIVfMT]-x(2)-[FYwCTH]-[DNSTK].

NAME: D-isomer specific 2-hydroxyacid dehydrogenases signature 2.

CONSENSUS: [LIVMFYWA]-[LIVFYWC]-x(2)-[SAC]-[DNQHR]-[IVFA]-[LIVF]-x-[LIVF]-[HNI]-x-

CONSENSUS: P-x(4)-[STN]-x(2)-[LIVMF]-x-[GSDN].

NAME: D-isomer specific 2-hydroxyacid dehydrogenases signature 3.

CONSENSUS: [LMFATC]-[KPQ]-x-[GSTDN]-x-[LIVMFYWR]-[LIVMFYW](2)-N-x-[STAGC]-R-[GP]-x-

CONSENSUS: [LIVH]-[LIVMC]-[DNV].

NAME: 3-hydroxyisobutyrate dehydrogenase signature.

CONSENSUS: [LIVMFY](2)-G-L-G-x-[MQ]-G-x-[PGS]-[MA]-[SA].

NAME: Hydroxymethylglutaryl-coenzyme A reductases signature 1.

CONSENSUS: [RKH]-x(6)-D-x-M-G-x-N-x-[LIVMA].

NAME: Hydroxymethylglutaryl-coenzyme A reductases signature 2.

CONSENSUS: [LIVM]-G-x-[LIVM]-G-G-[AG]-T.

NAME: Hydroxymethylglutaryl-coenzyme A reductases signature 3.

CONSENSUS: A-[LIVM]-x-[STAN]-x(2)-[LI]-x-[KRNQ]-[GSA]-H-[LM]-x-[FYLH].

NAME: Hydroxymethylglutaryl-coenzyme A reductases profile.

NAME: 3-hydroxyacyl-CoA dehydrogenase signature.

CONSENSUS: [DNE]-x(2)-[GA]-F-[LIVMFY]-x-[NT]-R-x(3)-[PA]-[LIVMFY](2)-x(5)-

CONSENSUS: [LIVMFYCT]-[LIVMFY]-x(2)-[GV].

NAME: Malate dehydrogenase active site signature.

CONSENSUS: [LIVM]-T-[TRKMN]-L-D-x(2)-R-[STA]-x(3)-[LIVMFY].

NAME: Malic enzymes signature.

CONSENSUS: F-x-[DV]-D-x(2)-G-T-[GSA]-x-[IV]-x-[LIVMA]-[GAST](2)-[LIVMF](2).

NAME: Isocitrate and isopropylmalate dehydrogenases signature.

CONSENSUS: [NS]-[LIMYT]-[FYDN]-G-[DNT]-[IMVY]-x-[STGDN]-[DN]-x(2)-[SGAP]-x(3,4)-G-

CONSENSUS: [STG]-[LIVMPA]-G-[LIVMF].

NAME: 6-phosphogluconate dehydrogenase signature.

CONSENSUS: [LIVM]-x-D-x(2)-[GA]-[NQS]-K-G-T-G-x-W.

NAME: Glucose-6-phosphate dehydrogenase active site.

CONSENSUS: D-H-Y-L-G-K-[EQK].

NAME: IMP dehydrogenase / GMP reductase signature.

CONSENSUS: [LIVM]-[RK]-[LIVM]-G-[LIVM]-G-x-G-S-[LIVM]-C-x-T.

NAME: Bacterial quinoprotein dehydrogenases signature 1.

CONSENSUS: [DEN]-W-x(3)-G-[RK]-x(6)-[FYW]-S-x(4)-[LIVM]-N-x(2)-N-V-x(2)-L-[RK].

NAME: Bacterial quinoprotein dehydrogenases signature 2.

CONSENSUS: W-x(4)-Y-D-x(3)-[DN]-[LIVMFY](4)-x(2)-G-x(2)-[STA]-P.

NAME: FMN-dependent alpha-hydroxy acid dehydrogenases active site.

CONSENSUS: S-N-H-G-[AG]-R-Q.

NAME: GMC oxidoreductases signature 1.

CONSENSUS: [GA]-[RKN]-x-[LIV]-G(2)-[GST](2)-x-[LIVM]-N-x(3)-[FYWA]-x(2)-[PAG]-x(5)-

CONSENSUS: [DNESH].

NAME: GMC oxidoreductases signature 2.

CONSENSUS: [GS]-[PSTA]-x(2)-[ST]-P-x-[LIVM](2)-x(2)-S-G-[LIVM]-G.

NAME: Eukaryotic molybdopterin oxidoreductases signature.

CONSENSUS: [GA]-x(3)-[KRNQHT]-x(11,14)-[LIVMFYWS]-x(8)-[LIVMF]-x-C-x(2)-[DEN]-R-

CONSENSUS: x(2)-[DE].

NAME: Prokaryotic molybdopterin oxidoreductases signature 1.

CONSENSUS: [STAN]-x-[CH]-x(2,3)-C-[STAG]-[GSTVMF]-x-C-x-[LIVMFYW]-x-[LIVMA]-x(3,4)-

CONSENSUS: [DENQKHT].

NAME: Prokaryotic molybdopterin oxidoreductases signature 2.

CONSENSUS: [STA]-x-[STAC](2)-x(2)-[STA]-D-[LIVMY](2)-L-P-x-[STAC](2)-x(2)-E.

NAME: Prokaryotic molybdopterin oxidoreductases signature 3.

CONSENSUS: A-x(3)-[IGDT]-I-x-[DNQTK]-x-[DEA]-x-[LIVM]-x-[LIVMC]-x-[NS]-x(2)-[GS]-

CONSENSUS: x(5)-A-x-[LIVM]-[ST].

NAME: Aldehyde dehydrogenases glutamic acid active site.
 CONSENSUS: [LIVMFGA]-E-[LIMSTAC]-[GS]-G-[KNLM]-[SADN]-[TAPFV].

NAME: Aldehyde dehydrogenases cysteine active site.
 CONSENSUS: [FYLVA]-x(3)-G-[QE]-x-C-[LIVMGSTANC]-[AGCN]-x-[GSTADNEKR].

NAME: Aspartate-semialdehyde dehydrogenase signature.
 CONSENSUS: [LIVM]-[SADN]-x(2)-C-x-R-[LIVM]-x(4)-[GSC]-H-[STA].

NAME: Glyceraldehyde 3-phosphate dehydrogenase active site.
 CONSENSUS: [ASV]-S-C-[NT]-T-x(2)-[LIM].

NAME: N-acetyl-gamma-glutamyl-phosphate reductase active site.
 CONSENSUS: [LIVM]-[GSA]-x-P-G-C-[FY]-[AVP]-T-[GA]-x(3)-[GTAC]-[LIVM]-x-P.

NAME: Gamma-glutamyl phosphate reductase signature.
 CONSENSUS: V-x(5)-A-[LIV]-x-H-I-x(2)-[HY]-[GS]-[ST]-x-H-[ST]-[DE]-x-I.

NAME: Dihydrodipicolinate reductase signature.
 CONSENSUS: E-[IV]-x-E-x-H-x(3)-K-x-D-x-P-S-G-T-A.

NAME: Dihydroorotate dehydrogenase signature 1.
 CONSENSUS: [GS]-x(4)-[GK]-[STA]-[IVSTA]-[GT]-x(3)-[NQR]-x-G-[NH]-x(2)-P-[RT].

NAME: Dihydroorotate dehydrogenase signature 2.
 CONSENSUS: [LIV](2)-[GSA]-x-G-G-[IV]-x-[STGN]-x(3)-[ACV]-x(6)-G-A.

NAME: Coproporphyrinogen III oxidase signature.
 CONSENSUS: K-x-W-C-x(2)-[FYH](3)-[LIVM]-x-H-R-x-E-x-R-G-[LIVM]-G-G-[LIVM]-F-F-D.

NAME: Fumarate reductase / succinate dehydrogenase FAD-binding site.
 CONSENSUS: R-[ST]-H-[ST]-x(2)-A-x-G-G.

NAME: Acyl-CoA dehydrogenases signature 1.
 CONSENSUS: [GAC]-[LIVM]-[ST]-E-x(2)-[GSAN]-G-[ST]-D-x(2)-[GSA].

NAME: Acyl-CoA dehydrogenases signature 2.
 CONSENSUS: [QDE]-x(2)-G-[GS]-x-G-[LIVMFY]-x(2)-[DEN]-x(4)-[KR]-x(3)-[DEN].

NAME: Alanine dehydrogenase & pyridine nucleotide transhydrogenase signature 1.
 CONSENSUS: G-[LIVM]-P-x-E-x(3)-N-E-x(1,3)-R-V-A-x-[ST]-P-x-[GST]-V-x(2)-L-x-[KRH]-
 CONSENSUS: x-G.

NAME: Alanine dehydrogenase & pyridine nucleotide transhydrogenase signature 2.
 CONSENSUS: [LIVM](2)-G-[GA]-G-x-A-G-x(2)-[SA]-x(3)-[GA]-x-[SG]-[LIVM]-G-A-x-V-
 CONSENSUS: x(3)-D.

NAME: Glu / Leu / Phe / Val dehydrogenases active site.
 CONSENSUS: [LIV]-x(2)-G-G-[SAG]-K-x-[GV]-x(3)-[DNST]-[PL].

NAME: D-amino acid oxidases signature.
 CONSENSUS: [LIVM](2)-H-[NHA]-Y-G-x-[GSA](2)-x-G-x(5)-G-x-A.

NAME: Pyridoxamine 5'-phosphate oxidase signature.
 CONSENSUS: [LIVF]-E-F-W-[QHG]-x(4)-R-[LIVM]-H-[DNE]-R.

NAME: Copper amine oxidase topaquinone signature.
 CONSENSUS: [LIVM]-[LIVMA]-[LIVM]-x(4)-T-x(2)-N-Y-[DE]-[YN].

NAME: Copper amine oxidase copper-binding site signature.
 CONSENSUS: T-x-G-x(2)-H-[LIVMF]-x(3)-E-[DE]-x-P.

NAME: Lysyl oxidase putative copper-binding region signature.
 CONSENSUS: W-E-W-H-S-C-H-Q-H-Y-H.

NAME: Delta 1-pyrroline-5-carboxylate reductase signature.
 CONSENSUS: [PALF]-x(2,3)-[LIV]-x(3)-[LIVM]-[STAC]-[STV]-x-[GAN]-G-x-T-x(2)-[AG]-
 CONSENSUS: [LIV]-x(2)-[LMF]-[DENQK].

NAME: Dihydrofolate reductase signature.
 CONSENSUS: [LVAGC]-[LIF]-G-x(4)-[LIVMF]-P-W-x(4,5)-[DE]-x(3)-[FYIV]-x(3)-[STIQ].

NAME: Tetrahydrofolate dehydrogenase/cyclohydrolase signature 1.
 CONSENSUS: [EQ]-x-[EQK]-[LIVM](2)-x(2)-[LIVM]-x(2)-[LIVMY]-N-x-[DN]-x(5)-[LIVMF](3)-

CONSENSUS: Q-L-P-[LV].
NAME: Tetrahydrofolate dehydrogenase/cyclohydrolase signature 2.
CONSENSUS: P-G-G-V-G-P-[MF]-T-[IV].
NAME: Oxygen oxidoreductases covalent FAD-binding site.
CONSENSUS: P-x(10)-[DE]-[LIVM]-x(3)-[LIVM]-x(9)-[LIVM]-x(3)-[GSA]-[GST]-G-H.
NAME: Pyridine nucleotide-disulphide oxidoreductases class-I active site.
CONSENSUS: G-G-x-C-[LIVA]-x(2)-G-C-[LIVM]-P.
NAME: Pyridine nucleotide-disulphide oxidoreductases class-II active site.
CONSENSUS: C-x(2)-C-D-[GA]-x(2,4)-[FY]-x(4)-[LIVM]-x-[LIVM](2)-G(3)-[DN].
NAME: Respiratory-chain NADH dehydrogenase subunit 1 signature 1.
CONSENSUS: G-[LIVMFYKRS]-[LIVMAGP]-Q-x-[LIVMFY]-x-D-[AGIM]-[LIVMFTA]-K-[LVMYST]-
CONSENSUS: [LIVMFYG]-x-[KR]-[EQG].
NAME: Respiratory-chain NADH dehydrogenase subunit 1 signature 2.
CONSENSUS: P-F-D-[LIVMFYQ]-[STAGPVM]-E-[GAC]-E-x-[EQ]-[LIVMS]-x(2)-G.
NAME: Respiratory-chain NADH dehydrogenase 20 Kd subunit signature.
CONSENSUS: [GN]-x-D-[KRST]-[LIVMF](2)-P-[IV]-D-[LIVMFYW](2)-x-P-x-C-P-[PT].
NAME: Respiratory-chain NADH dehydrogenase 24 Kd subunit signature.
CONSENSUS: D-x(2)-F-[ST]-x(5)-C-L-G-x-C-x(2)-[GA]-P.
NAME: Respiratory chain NADH dehydrogenase 30 Kd subunit signature.
CONSENSUS: E-R-E-x(2)-[DE]-[LIVMF](2)-x(6)-[HK]-x(3)-[KRP]-x-[LIVM]-[LIVMS].
NAME: Respiratory chain NADH dehydrogenase 49 Kd subunit signature.
CONSENSUS: [LIVMH]-H-[RT]-[GA]-x-E-K-[LIVMT]-x-E-x-[KRQ].
NAME: Respiratory-chain NADH dehydrogenase 51 Kd subunit signature 1.
CONSENSUS: G-[AM]-G-[AR]-Y-[LIVM]-C-G-[DE](2)-[STA](2)-[LIM](2)-[EN]-S.
NAME: Respiratory-chain NADH dehydrogenase 51 Kd subunit signature 2.
CONSENSUS: E-S-C-G-x-C-x-P-C-R-x-G.
NAME: Respiratory-chain NADH dehydrogenase 75 Kd subunit signature 1.
CONSENSUS: P-x(2)-C-[YWS]-x(7)-G-x-C-R-x-C.
NAME: Respiratory-chain NADH dehydrogenase 75 Kd subunit signature 2.
CONSENSUS: C-P-x-C-[DE]-x-[GS](2)-x-C-x-L-Q.
NAME: Respiratory-chain NADH dehydrogenase 75 Kd subunit signature 3.
CONSENSUS: R-C-[LIVM]-x-C-x-R-C-[LIVM]-x-[FY].
NAME: Nitrite and sulfite reductases iron-sulfur/siroheme-binding site.
CONSENSUS: [STV]-G-C-x(3)-C-x(6)-[DE]-[LIVMF]-[GAT]-[LIVMF].
NAME: Uricase signature.
CONSENSUS: L-x-[LV]-L-K-[ST]-T-x-S-x-F-x(2)-[FY]-x(4)-[FY].
NAME: Heme-copper oxidase catalytic subunit, copper B binding region signature.
CONSENSUS: [YWG]-[LIVFYWTA](2)-[VGS]-H-[LNP]-x-V-x(44,47)-H-H.
NAME: CO II and nitrous oxide reductase dinuclear copper centers signature.
CONSENSUS: V-x-H-x(33,40)-C-x(3)-C-x(3)-H-x(2)-M.
NAME: Cytochrome c oxidase subunit Vb, zinc binding region signature.
CONSENSUS: [LIVM](2)-[FYW]-x(10)-C-x(2)-C-G-x(2)-[FY]-K-L.
NAME: Multicopper oxidases signature 1.
CONSENSUS: G-x-[FYW]-x-[LIVMFYW]-x-[CST]-x(8)-G-[LM]-x(3)-[LIVMFYW].
NAME: Multicopper oxidases signature 2.
CONSENSUS: H-C-H-x(3)-H-x(3)-[AG]-[LM].
NAME: Peroxidases proximal heme-ligand signature.
CONSENSUS: [DET]-[LIVMTA]-x(2)-[LIVM]-[LIVMSTAG]-[SAG]-[LIVMSTAG]-H-[STA]-[LIVMFY].
NAME: Peroxidases active site signature.
CONSENSUS: [SGATV]-x(3)-[LIVMA]-R-[LIVMA]-x-[FW]-H-x-[SAC].

NAME: Catalase proximal heme-ligand signature.
 CONSENSUS: R-[LIVMFSTAN]-F-[GASTNP]-Y-x-D-[AST]-[QEH].

NAME: Catalase proximal active site signature.
 CONSENSUS: [IF]-x-[RH]-x(4)-[EQ]-R-x(2)-H-x(2)-[GAS]-[GASTF]-[GAST].

NAME: Glutathione peroxidases selenocysteine active site.
 CONSENSUS: [GN]-[RKHNFC]-x-[LIVMFC]-[LIVMF](2)-x-N-[VT]-x-[STC]-x-C-[GA]-x-T.

NAME: Glutathione peroxidases signature 2.
 CONSENSUS: [LIV]-[AGD]-F-P-[CS]-[NG]-Q-F.

NAME: Lipoxigenases iron-binding region signature 1.
 CONSENSUS: H-[EQ]-x(3)-H-x-[LM]-[NQRC]-[GST]-H-[LIVMSTAC](3)-E.

NAME: Lipoxigenases iron-binding region signature 2.
 CONSENSUS: [LIVMA]-H-P-[LIVM]-x-[KRQ]-[LIVMF](2)-x-[AP]-H.

NAME: Extradiol ring-cleavage dioxygenases signature.
 CONSENSUS: [GNTIV]-x-H-x(5,7)-[LIVMF]-Y-x(2)-[DENTA]-P-x-[GP]-x(2,3)-E.

NAME: Intradiol ring-cleavage dioxygenases signature.
 CONSENSUS: [LIVM]-x-G-x-[LIVM]-x(4)-[GS]-x(2)-[LIVM]-x(4)-[LIVM]-[DE]-[LIVMFY]-
 CONSENSUS: x(6)-G-x-[FY].

NAME: Indoleamine 2,3-dioxygenase signature 1.
 CONSENSUS: G-G-S-[AN]-[GA]-Q-S-S-x(2)-Q.

NAME: Indoleamine 2,3-dioxygenase signature 2.
 CONSENSUS: [FY]-L-[DQ]-[DE]-[LIVM]-x(2)-Y-M-x(3)-H-[KR].

NAME: Bacterial ring hydroxylating dioxygenases alpha-subunit signature.
 CONSENSUS: C-x-H-R-[GA]-x(8)-G-N-x(5)-C-x-[FY]-H.

NAME: Bacterial luciferase subunits signature.
 CONSENSUS: [GA]-[LIVM]-P-[LIVM]-x-[LIVMFY]-x-W-x(6)-[RK]-x(6)-Y-x(3)-[AR].

NAME: ubiH/COQ6 monooxygenase family signature.
 CONSENSUS: H-P-[LIV]-[AG]-G-Q-G-x-N-x-G-x(2)-D.

NAME: Bipterin-dependent aromatic amino acid hydroxylases signature.
 CONSENSUS: P-D-x(2)-H-[DE]-[LI]-[LIVMF]-G-H-[LIVMC]-P.

NAME: Copper type II, ascorbate-dependent monooxygenases signature 1.
 CONSENSUS: H-H-M-x(2)-F-x-C.

NAME: Copper type II, ascorbate-dependent monooxygenases signature 2.
 CONSENSUS: H-x-F-x(4)-H-T-H-x(2)-G.

NAME: Tyrosinase CuA-binding region signature.
 CONSENSUS: H-x(4,5)-F-[LIVMFTP]-x-[FW]-H-R-x(2)-[LM]-x(3)-E.

NAME: Tyrosinase and hemocyanins CuB-binding region signature.
 CONSENSUS: D-P-x-F-[LIVMFYW]-x(2)-H-x(3)-D.

NAME: Fatty acid desaturases family 1 signature.
 CONSENSUS: G-E-x-[FY]-H-N-[FY]-H-H-x-F-P-x-D-Y.

NAME: Fatty acid desaturases family 2 signature.
 CONSENSUS: [ST]-[SA]-x(3)-[QR]-[LI]-x(5,6)-D-Y-x(2)-[LIVMFYW]-[LIVM]-[DE].

NAME: Cytochrome P450 cysteine heme-iron ligand signature.
 CONSENSUS: [FW]-[SGNH]-x-[GD]-x-[RHPT]-x-C-[LIVMFAP]-[GAD].

NAME: Heme oxygenase signature.
 CONSENSUS: L-L-V-A-H-A-Y-T-R.

NAME: Copper/Zinc superoxide dismutase signature 1.
 CONSENSUS: [GA]-[IFAT]-H-[LIVF]-H-x(2)-[GP]-[SDG]-x-[STAGD].

NAME: Copper/Zinc superoxide dismutase signature 2.
 CONSENSUS: G-[GN]-[SGA]-G-x-R-x-[SGA]-C-x(2)-[IV].

NAME: Manganese and iron superoxide dismutases signature.

CONSENSUS: D-x-W-E-H-[STA]-[FY](2).

NAME: Ribonucleotide reductase large subunit signature.

CONSENSUS: W-x(2)-[LF]-x(6,7)-G-[LIVM]-[FYRA]-[NH]-x(3)-[STAQLIVM]-[ASC]-x(2)-

CONSENSUS: [PA].

NAME: Ribonucleotide reductase small subunit signature.

CONSENSUS: [IVMSEQ]-E-x(1,2)-[LIVTA]-[HY]-[GSA]-x-[STAVM]-Y-x(2)-[LIVMQ]-x(3)-

CONSENSUS: [LIFY]-[IVFYCSA].

NAME: Nitrogenases component I alpha and beta subunits signature 1.

CONSENSUS: [LIVMFYH]-[LIVMFST]-H-[AG]-[AGSP]-[LIVMNQA]-[AG]-C.

NAME: Nitrogenases component I alpha and beta subunits signature 2.

CONSENSUS: [STANQ]-[ET]-C-x(5)-G-D-[DN]-[LIVMT]-x-[STAGR]-[LIVMFYST].

NAME: NifH/frxC family signature 1.

CONSENSUS: E-x-G-G-P-x(2)-[GA]-x-G-C-[AG]-G.

NAME: NifH/frxC family signature 2.

CONSENSUS: D-x-L-G-D-V-V-C-G-G-F-[AG]-x-P.

NAME: Nickel-dependent hydrogenases large subunit signature 1.

CONSENSUS: R-G-[LIVMF]-E-x(15)-[QESM]-R-x-C-G-[LIVM]-C.

NAME: Nickel-dependent hydrogenases large subunit signature 2.

CONSENSUS: [FY]-D-P-C-[LIM]-[ASG]-C-x(2,3)-H.

NAME: Glutamyl-tRNA reductase signature.

CONSENSUS: H-[LIVM]-x(2)-[LIVM]-[GSTAC](3)-[LIVM]-[DEQ]-S-[LIVMA]-[LIVM](2)-[GF]-E-

CONSENSUS: x-[QR]-[IV]-[LIT]-[STAG]-Q-[LIVM]-[KR].

NAME: Bacterial-type phytoene dehydrogenase signature.

CONSENSUS: [NG]-x-[FYWV]-[LIVMF]-x-G-[AGC]-[GS]-[TA]-[HQT]-P-G-[STAV]-G-[LIVM]-

CONSENSUS: x(5)-[GS].

NAME: Glycine radical signature.

CONSENSUS: [STIV]-x-R-[IVT]-[CSA]-G-Y-x-[GACV].

NAME: Ergosterol biosynthesis ERG4/ERG24 family signature 1.

CONSENSUS: G-x(2)-[LIVM]-Y-D-x-[FY]-x-G-x(2)-L-N-P-R.

NAME: Ergosterol biosynthesis ERG4/ERG24 family signature 2.

CONSENSUS: [LIVM](2)-H-R-x(2)-R-D-x(3)-C-x(2)-K-Y-G.

NAME: NNMT/PNMT/TEMT family of methyltransferases signature.

CONSENSUS: L-I-D-I-G-S-G-P-T-[IV]-Y-Q-L-L-S-A-C.

NAME: RNA methyltransferase trmA family signature 1.

CONSENSUS: [DN]-P-[PA]-R-x-G-x(14,16)-[LIVM](2)-Y-x-S-C-N-x(2)-T.

NAME: RNA methyltransferase trmA family signature 2.

CONSENSUS: [LIVMF]-D-x-F-P-[QHY]-[ST]-x-H-[LIVMFY]-E.

NAME: Thymidylate synthase active site.

CONSENSUS: R-x(2)-[LIVM]-x(3)-[FW]-[QN]-x(8,9)-[LV]-x-P-C-[HAVM]-x(3)-[QMT]-[FYW]-

CONSENSUS: x-[LV].

NAME: Ribosomal RNA adenine dimethylases signature.

CONSENSUS: [LIVM]-[LIVMFY]-[DE]-x-G-[STAPV]-G-x-[GA]-x-[LIVMF]-[ST]-x(2)-[LIVM]-

CONSENSUS: x(6)-[LIVMY]-x-[STAGV]-[LIVMFYHC]-E-x-D.

NAME: Methylated-DNA--protein-cysteine methyltransferase active site.

CONSENSUS: [LIVMF]-P-C-H-R-[LIVMF](2).

NAME: N-6 Adenine-specific DNA methylases signature.

CONSENSUS: [LIVMAC]-[LIVFYWA]-x-[DN]-P-P-[FYW].

NAME: N-4 cytosine-specific DNA methylases signature.

CONSENSUS: [LIVMF]-T-S-P-P-[FY].

NAME: C-5 cytosine-specific DNA methylases active site.

CONSENSUS: [DENKS]-x-[FLIV]-x(2)-[GSTC]-x-P-C-x(2)-[FYWLIM]-S.

NAME: C-5 cytosine-specific DNA methylases C-terminal signature.
 CONSENSUS: [RKQGTG]-x(2)-G-N-[STAG]-[LIVMF]-x(3)-[LIVMT]-x(3)-[LIVM]-x(3)-[LIVM].

NAME: Protein-L-isoaspartate(D-aspartate) O-methyltransferase signature.
 CONSENSUS: [GSA]-D-G-x(2)-G-[FYWV]-x(3)-[AS]-P-[FY]-[DN]-x-I.

NAME: Uroporphyrin-III C-methyltransferase signature 1.
 CONSENSUS: [LIVM]-[GS]-[STAL]-G-P-G-x(3)-[LIVMFY]-[LIVM]-T-[LIVM]-[KRHQG]-[AG].

NAME: Uroporphyrin-III C-methyltransferase signature 2.
 CONSENSUS: V-x(2)-[LI]-x(2)-G-D-x(3)-[FYW]-[GS]-x(8)-[LIVF]-x(5,6)-[LIVMFYWPAC]-
 CONSENSUS: x-[LIVMY]-x-P-G.

NAME: ubiE/COQ5 methyltransferase family signature 1.
 CONSENSUS: Y-D-x-M-N-x(2)-[LIVM]-S-x(3)-H-x(2)-W.

NAME: ubiE/COQ5 methyltransferase family signature 2.
 CONSENSUS: R-V-[LIVM]-K-[PV]-G-G-x-[LIVMF]-x(2)-[LIVM]-E-x-S.

NAME: Serine hydroxymethyltransferase pyridoxal-phosphate attachment site.
 CONSENSUS: [DEH]-[LIVMFY]-x-[STMV]-[GST]-[ST](2)-H-K-[ST]-[LF]-x-G-[PAC]-[RQ]-
 CONSENSUS: [GSA]-[GA].

NAME: Phosphoribosylglycinamide formyltransferase active site.
 CONSENSUS: G-x-[STM]-[IVT]-x-[FYWVQ]-[VMAT]-x-[DEV]-x-[LIVMY]-D-x-G-x(2)-[LIVT]-
 CONSENSUS: x(6)-[LIVM].

NAME: Aspartate and ornithine carbamoyltransferases signature.
 CONSENSUS: F-x-[EK]-x-S-[GT]-R-T.

NAME: Transketolase signature 1.
 CONSENSUS: R-x(3)-[LIVMTA]-[DENQSTHKF]-x(5,6)-[GSN]-G-H-[PLIVMF]-[GSTA]-x(2)-
 CONSENSUS: [LMC]-[GS].

NAME: Transketolase signature 2.
 CONSENSUS: G-[DEQGSA]-[DN]-G-[PAEQ]-[ST]-[HQ]-x-[PAGM]-[LIVMYAC]-[DEFYW]-x(2)-
 CONSENSUS: [STAP]-x(2)-[RGA].

NAME: Transaldolase signature 1.
 CONSENSUS: [DG]-[IVSA]-T-[ST]-N-P-[STA]-[LIVMF](2).

NAME: Transaldolase active site.
 CONSENSUS: [LIVM]-x-[LIVM]-K-[LIVM]-[PAS]-x-[ST]-x-[DENQPAS]-G-[LIVM]-x-[AGV]-x-
 CONSENSUS: [QEKIRST]-x-[LIVM].

NAME: Acyltransferases ChoActase / COT / CPT family signature 1.
 CONSENSUS: [LI]-P-x-[LVP]-P-[IVTA]-P-x-[LIVM]-x-[DENQAS]-[ST]-[LIVM]-x(2)-[LY].

NAME: Acyltransferases ChoActase / COT / CPT family signature 2.
 CONSENSUS: R-[FYW]-x-[DA]-[KA]-x(0,1)-[LIVMFY]-x-[LIVMFY](2)-x(3)-[DNS]-[GSA]-x(6)-
 CONSENSUS: [DE]-[HS]-x(3)-[DE]-[GA].

NAME: Thiolases acyl-enzyme intermediate signature.
 CONSENSUS: [LIVM]-[NST]-x(2)-C-[SAGLI]-[ST]-[SAG]-[LIVMFYNS]-x-[STAG]-[LIVM]-x(6)-
 CONSENSUS: [LIVM].

NAME: Thiolases signature 2.
 CONSENSUS: N-x(2)-G-G-x-[LIVM]-[SA]-x-G-H-P-x-G-x-[ST]-G.

NAME: Thiolases active site.
 CONSENSUS: [AG]-[LIVMA]-[STAGLIVM]-[STAG]-[LIVMA]-C-x-[AG]-x-[AG]-x-[AG]-x-[SAG].

NAME: Chloramphenicol acetyltransferase active site.
 CONSENSUS: Q-[LIV]-H-H-[SA]-x(2)-D-G-[FY]-H.

NAME: Hexapeptide-repeat containing-transferases signature.
 CONSENSUS: [LIV]-[GAED]-x(2)-[STAV]-x-[LIV]-x(3)-[LIVAC]-x-[LIV]-[GAED]-x(2)-
 CONSENSUS: [STAVR]-x-[LIV]-[GAED]-x(2)-[STAV]-x-[LIV]-x(3)-[LIV].

NAME: Beta-ketoacyl synthases active site.
 CONSENSUS: G-x(4)-[LIVMFAP]-x(2)-[AGC]-C-[STA](2)-[STAG]-x(3)-[LIVMF].

NAME: Chalcone and stilbene synthases active site.

CONSENSUS: R-[LIVMFYS]-x-[LIVM]-x-[QHG]-x-G-C-[FYNA]-[GA]-G-[GA]-[STAV]-x-[LIVMF]-
CONSENSUS: [RA].

NAME: Myristoyl-CoA:protein N-myristoyltransferase signature 1.
CONSENSUS: E-I-N-F-L-C-x-H-K.

NAME: Myristoyl-CoA:protein N-myristoyltransferase signature 2.
CONSENSUS: K-F-G-x-G-D-G.

NAME: Gamma-glutamyltranspeptidase signature.
CONSENSUS: T-[STA]-H-x-[ST]-[LIVMA]-x(4)-G-[SN]-x-V-[STA]-x-T-x-T-[LIVM]-[NE]-
CONSENSUS: x(1,2)-[FY]-G.

NAME: Transglutaminases active site.
CONSENSUS: [GT]-Q-[CA]-W-V-x-[SA]-[GA]-[IVT]-x(2)-T-x-[LMSC]-R-[CSA]-[LV]-G.

NAME: Phosphorylase pyridoxal-phosphate attachment site.
CONSENSUS: E-A-[SC]-G-x-[GS]-x-M-K-x(2)-[LM]-N.

NAME: UDP-glycosyltransferases signature.
CONSENSUS: [FW]-x(2)-Q-x(2)-[LIVMYA]-[LIMV]-x(4,6)-[LVGAC]-[LVFYA]-[LIVMF]-[STAGCM]-
CONSENSUS: [HNQ]-[STAGC]-G-x(2)-[STAG]-x(3)-[STAGL]-[LIVMFA]-x(4)-[PQR]-[LIVMT]-
CONSENSUS: x(3)-[PA]-x(3)-[DES]-[QEHN].

NAME: Purine/pyrimidine phosphoribosyl transferases signature.
CONSENSUS: [LIVMFYWCTA]-[LIVM]-[LIVMA]-[LIVMFC]-[DE]-D-[LIVMS]-[LIVM]-[STAVD]-
CONSENSUS: [STAR]-[GAC]-x-[STAR].

NAME: Glutamine amidotransferases class-I active site.
CONSENSUS: [PAS]-[LIVMFYT]-[LIVMFY]-G-[LIVMFY]-C-[LIVMFYN]-G-x-[QEH]-x-[LIVMFA].

NAME: Glutamine amidotransferases class-II active site.
CONSENSUS: < x(0,11)-C-[GS]-[IV]-[LIVMFYW]-[AG].

NAME: Purine and other phosphorylases family 1 signature.
CONSENSUS: [GST]-x-G-[LIVM]-G-x-[PA]-S-x-[GSTA]-I-x(3)-E-L.

NAME: Purine and other phosphorylases family 2 signature.
CONSENSUS: [LIV]-x(3)-G-x(2)-H-x-[LIVMFY]-x(4)-[LIVMF]-x(3)-[ATV]-x(1,2)-[LIVM]-x-
CONSENSUS: [ATV]-x(4)-[GN]-x(3,4)-[LIVMF](2)-x(2)-[STN]-[SA]-x-G-[GS]-[LIVM].

NAME: Thymidine and pyrimidine-nucleoside phosphorylases signature.
CONSENSUS: S-[GS]-R-[GA]-[LIV]-x(2)-[TA]-[GA]-G-T-x-D-x-[LIV]-E.

NAME: ATP phosphoribosyltransferase signature.
CONSENSUS: E-x(5)-G-x-[SAG]-x(2)-[IV]-x-D-[LIV]-x(2)-[ST]-G-x-T-[LM].

NAME: NAD:arginine ADP-ribosyltransferases signature.
CONSENSUS: [FY]-x-[FY]-K-x(2)-H-[FY]-x-L-[ST]-x-A.

NAME: Prolipoprotein diacylglycerol transferase signature.
CONSENSUS: G-R-x-[GA]-N-F-[LIVMF]-N-x-E-x(2)-G.

NAME: S-adenosylmethionine synthetase signature 1.
CONSENSUS: G-A-G-D-Q-G-x(3)-G-Y.

NAME: S-adenosylmethionine synthetase signature 2.
CONSENSUS: G-[GA]-G-[ASC]-F-S-x-K-[DE].

NAME: Polyprenyl synthetases signature 1.
CONSENSUS: [LIVM](2)-x-D-D-x(2,4)-D-x(4)-R-R-[GH].

NAME: Polyprenyl synthetases signature 2.
CONSENSUS: [LIVMFY]-G-x(2)-[FYL]-Q-[LIVM]-x-D-D-[LIVMFY]-x-[DNG].

NAME: Squalene and phytoene synthases signature 1.
CONSENSUS: Y-[CSAM]-x(2)-[VSG]-A-[GSA]-[LIVAT]-[IV]-G-x(2)-[LMSC]-x(2)-[LIV].

NAME: Squalene and phytoene synthases signature 2.
CONSENSUS: [LIVM]-G-x(3)-Q-x(2,3)-N-[IF]-x-R-D-[LIVMFY]-x(2)-[DE]-x(4,7)-R-x-[FY]-
CONSENSUS: x-P.

NAME: Protein prenyltransferases alpha subunit repeat signature.
CONSENSUS: [PSIAV]-x-[NDFV]-[NEQIY]-x-[LIVMAGP]-W-[NQSTHF]-[FYHQ]-[LIVMR].

NAME: Riboflavin synthase alpha chain family signature.
 CONSENSUS: [LIVMF]-x(5)-G-[STADNQ]-[KREQIW]-V-N-[LIVM]-E.

NAME: Dihydropteroate synthase signature 1.
 CONSENSUS: [LIVM]-x-[AG]-[LIVMF](2)-N-x-T-x-D-S-F-x-D-x-[SG].

NAME: Dihydropteroate synthase signature 2.
 CONSENSUS: [GE]-[SA]-x-[LIVM](2)-D-[LIVM]-G-[GP]-x(2)-[STA]-x-P.

NAME: EPSP synthase signature 1.
 CONSENSUS: [LIVM]-x(2)-[GN]-N-[SA]-G-T-[STA]-x-R-x-[LIVMY]-x-[GSTA].

NAME: EPSP synthase signature 2.
 CONSENSUS: [KR]-x-[KH]-E-[CST]-[DNE]-R-[LIVM]-x-[STA]-[LIVMC]-x(2)-[EN]-[LIVMF]-x-
 CONSENSUS: [KRA]-[LIVMF]-G.

NAME: FLAP/GST2/LTC4S family signature.
 CONSENSUS: G-x(3)-F-E-R-V-[FY]-x-A-[NQ]-x-N-C.

NAME: Aminotransferases class-I pyridoxal-phosphate attachment site.
 CONSENSUS: [GS]-[LIVMFYTAC]-[GSTA]-K-x(2)-[GSALVN]-[LIVMFA]-x-[GNAR]-x-R-[LIVMA]-
 CONSENSUS: [GA].

NAME: Aminotransferases class-II pyridoxal-phosphate attachment site.
 CONSENSUS: T-[LIVMFYW]-[STAG]-K-[SAG]-[LIVMFYWR]-[SAG]-x(2)-[SAG].

NAME: Aminotransferases class-III pyridoxal-phosphate attachment site.
 CONSENSUS: [LIVMFYWC](2)-x-D-E-[LIVMA]-x(2)-[GP]-x(0,1)-[LIVMFYWAG]-x(0,1)-[SACR]-x-
 CONSENSUS: [GSAD]-x(12,16)-D-[LIVMFYWC]-x(2,3)-[GSA]-K-x(3)-[GSTADN]-[GSA].

NAME: Aminotransferases class-IV signature.
 CONSENSUS: E-x-[STAGCI]-x(2)-N-[LIVMFAC]-[FY]-x(6,12)-[LIVMF]-x-T-x(6,8)-[LIVM]-x-
 CONSENSUS: [GS]-[LIVM]-x-[KR].

NAME: Aminotransferases class-V pyridoxal-phosphate attachment site.
 CONSENSUS: [LIVFYCHT]-[DGH]-[LIVMFYAC]-[LIVMFYA]-x(2)-[GSTAC]-[GSTA]-[HQR]-K-
 CONSENSUS: x(4,6)-G-x-[GSAT]-x-[LIVMFYSAC].

NAME: Hexokinases signature.
 CONSENSUS: [LIVM]-G-F-[TN]-F-S-[FY]-P-x(5)-[LIVM]-[DNST]-x(3)-[LIVM]-x(2)-W-T-K-x-
 CONSENSUS: [LF].

NAME: Galactokinase signature.
 CONSENSUS: G-R-x-N-[LIV]-I-G-E-H-x-D-Y.

NAME: GHMP kinases putative ATP-binding domain.
 CONSENSUS: [LIVM]-[PK]-x-[GSTA]-x(0,1)-G-L-[GS]-S-S-[GSA]-[GSTAC].

NAME: Phosphofructokinase signature.
 CONSENSUS: [RK]-x(4)-G-H-x-Q-[QR]-G-G-x(5)-D-R.

NAME: pfkB family of carbohydrate kinases signature 1.
 CONSENSUS: [AG]-G-x(0,1)-[GAP]-x-N-x-[STA]-x(6)-[GS]-x(9)-G.

NAME: pfkB family of carbohydrate kinases signature 2.
 CONSENSUS: [DNSK]-[PSTV]-x-[SAG](2)-[GD]-D-x(3)-[SAGV]-[AG]-[LIVMFY]-[LIVMSTAP].

NAME: ROK family signature.
 CONSENSUS: [LIVM]-x(2)-G-[LIVMFCT]-G-x-[GA]-[LIVMFA]-x(8)-G-x(3,5)-[GATP]-x(2)-
 CONSENSUS: G-[RKH].

NAME: Phosphoribulokinase signature.
 CONSENSUS: K-[LIVM]-x-R-D-x(3)-R-G-x-[ST]-x-E.

NAME: Thymidine kinase cellular-type signature.
 CONSENSUS: [GA]-x(1,2)-[DE]-x-Y-x-[STAP]-x-C-[NKR]-x-[CH]-[LIVMFYWH].

NAME: FGGY family of carbohydrate kinases signature 1.
 CONSENSUS: [MFYGS]-x-[PST]-x(2)-K-[LIVMFYW]-x-W-[LIVMF]-x-[DENQTKR]-[ENQH].

NAME: FGGY family of carbohydrate kinases signature 2.
 CONSENSUS: [GSA]-x-[LIVMFYW]-x-G-[LIVM]-x(7,8)-[HDENQ]-[LIVMF]-x(2)-[AS]-[STAIVM]-
 CONSENSUS: [LIVMFY]-[DEQ].

NAME: Protein kinases ATP-binding region signature.

CONSENSUS: [LIV]-G-{P}-G-{P}-{FYWMGSTNH}-[SGA]-{PW}-{LIVCAT}-{PD}-x-[GSTACLIVMFY]-
CONSENSUS: x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K.

NAME: Serine/Threonine protein kinases active-site signature.

CONSENSUS: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3).

NAME: Tyrosine protein kinases specific active-site signature.

CONSENSUS: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC](3).

NAME: Protein kinase domain profile.

NAME: Casein kinase II regulatory subunit signature.

CONSENSUS: C-P-x-[LIVMY]-x-C-x(5)-L-P-[LIVMC]-G-x(9)-V-[KR]-x(2)-C-P-x-C.

NAME: Pyruvate kinase active site signature.

CONSENSUS: [LIVAC]-x-[LIVM](2)-[SAPCV]-K-[LIV]-E-[NKRST]-x-[DEQH]-[GSTA]-[LIVM].

NAME: Shikimate kinase signature.

CONSENSUS: [KR]-x(2)-E-x(3)-[LIVMF]-x(8,12)-[LIVMF](2)-[SA]-x-G(3)-x-[LIVMF].

NAME: Prokaryotic diacylglycerol kinase signature.

CONSENSUS: E-x-[LIVM]-N-[ST]-[SA]-[LIV]-E-x(2)-V-D.

NAME: Phosphatidylinositol 3- and 4-kinases signature 1.

CONSENSUS: [LIVMFAC]-K-x(1,3)-[DEA]-[DE]-[LIVMC]-R-Q-[DE]-x(4)-Q.

NAME: Phosphatidylinositol 3- and 4-kinases signature 2.

CONSENSUS: [GS]-x-[AV]-x(3)-[LIVM]-x(2)-[FYH]-[LIVM](2)-x-[LIVMF]-x-D-R-H-x(2)-N.

NAME: Acetate and butyrate kinases family signature 1.

CONSENSUS: [LIVM](2)-x-[LIVM]-N-x-G-S-[ST]-S-x-[KE].

NAME: Acetate and butyrate kinases family signature 2.

CONSENSUS: [LIVMA](2)-x(2)-H-x-G-x-G-x-[ST]-[LIVM]-x-[AV]-x(3)-G.

NAME: Phosphoglycerate kinase signature.

CONSENSUS: [KRHGTCV]-[VT]-[LIVMF]-[LIVMC]-R-x-D-x-N-[SACV]-P.

NAME: Aspartokinase signature.

CONSENSUS: [LIVM]-x-K-[FY]-G-G-[ST]-[SC]-[LIVM].

NAME: Glutamate 5-kinase signature.

CONSENSUS: [GSTN]-x(2)-G-x-G-[GC]-[IM]-x-[STA]-K-[LIVM]-x-[SA]-[TCA]-x(2)-[GALV]-
CONSENSUS: x(3)-G.

NAME: ATP:guanido phosphotransferases active site.

CONSENSUS: C-P-x(0,1)-[ST]-N-[IL]-G-T.

NAME: PTS HPR component histidine phosphorylation site signature.

CONSENSUS: G-[LIVM]-H-[STA]-R-[PA]-[GSTA]-[STAM].

NAME: PTS HPR component serine phosphorylation site signature.

CONSENSUS: [GSADE]-[KREQTV]-x(4)-[KRN]-S-[LIVMF](2)-x-[LIVM]-x(2)-[LIVM]-[GAD].

NAME: PTS EIIA domains phosphorylation site signature 1.

CONSENSUS: G-x(2)-[LIVMF](3)-H-[LIVMF]-G-[LIVMF]-x-T-[ALV].

NAME: PTS EIIA domains phosphorylation site signature 2.

CONSENSUS: [DENQ]-x(6)-[LIVMF]-[GA]-x(2)-[LIVM]-A-[LIVM]-P-H-[GAC].

NAME: PTS EIIB domains cysteine phosphorylation site signature.

CONSENSUS: N-[LIVMFY]-x(5)-C-x-T-R-[LIVMF]-x-[LIVMF]-x-[LIVM]-x-[DQ].

NAME: Adenylate kinase signature.

CONSENSUS: [LIVMFYW](3)-D-G-[FY]-P-R-x(3)-[NQ].

NAME: Nucleoside diphosphate kinases active site.

CONSENSUS: N-x(2)-H-[GA]-S-D-[SA]-[LIVMPKNE].

NAME: Guanylate kinase signature.

CONSENSUS: T-[ST]-R-x(2)-[KR]-x(2)-[DE]-x(2)-G-x(2)-Y-x-[FY]-[LIVMK].

NAME: Guanylate kinase domain profile.

NAME: Phosphoribosyl pyrophosphate synthetase signature.

CONSENSUS: D-[LI]-H-[SA]-x-Q-[IMST]-[QM]-G-[FY]-F-x(2)-P-[LIVMFC]-D.

NAME: 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature.

CONSENSUS: G-[PE]-R-x(2)-D-L-D-[LIVM](2).

NAME: Bacteriophage-type RNA polymerase family active site signature 1.

CONSENSUS: P-[LIVM]-x(2)-D-[GA]-[ST]-[AC]-[SN]-[GA]-[LIVMFY]-Q.

NAME: Bacteriophage-type RNA polymerase family active site signature 2.

CONSENSUS: [LIVMF]-x-R-x(3)-K-x(2)-[LIVMF]-M-[PT]-x(2)-Y.

NAME: Eukaryotic RNA polymerase II heptapeptide repeat.

CONSENSUS: Y-[ST]-P-[ST]-S-P-[STANK].

NAME: RNA polymerases beta chain signature.

CONSENSUS: G-x-K-[LIVMFA]-[STAC]-[GSTN]-x-[HSTA]-[GS]-[QNH]-K-G-[IVT].

NAME: RNA polymerases M / 15 Kd subunits signature.

CONSENSUS: F-C-x-[DEKST]-C-[GNK]-[DNSA]-[LIVMH]-[LIVM]-x(8,14)-C-x(2)-C.

NAME: RNA polymerases D / 30 to 40 Kd subunits signature.

CONSENSUS: N-[SGA]-[LIVMF]-R-R-x(9)-[SA]-x(3)-V-x(4)-N-x-[STA]-x(3)-[DN]-E-x-[LI]-

CONSENSUS: [GA]-x-R-[LI]-[GA]-[LIVM](2)-P.

NAME: RNA polymerases H / 23 Kd subunits signature.

CONSENSUS: H-[NEI]-[LIVM]-V-P-x-H-x(2)-[LIVM]-x(2)-[DE].

NAME: RNA polymerases K / 14 to 18 Kd subunits signature.

CONSENSUS: [ST]-x-[FY]-E-x-[AT]-R-x-[LIVM]-[GSA]-x-R-[SA]-x-Q.

NAME: RNA polymerases L / 13 to 16 Kd subunits signature.

CONSENSUS: [DE](2)-H-[ST]-[LIVM]-[GAP]-N-x(11)-V-x-[FM]-x(2)-Y-x(3)-H-P.

NAME: RNA polymerases N / 8 Kd subunits signature.

CONSENSUS: [LIVMF](2)-P-[LIVM]-x-C-F-[ST]-C-G.

NAME: DNA polymerase family A signature.

CONSENSUS: R-x(2)-[GSAV]-K-x(3)-[LIVMFY]-[AGQ]-x(2)-Y-x(2)-[GS]-x(3)-[LIVMA].

NAME: DNA polymerase family B signature.

CONSENSUS: [YA]-[GLIVMSTAC]-D-T-D-[SG]-[LIVMFTC]-x-[LIVMSTAC].

NAME: DNA polymerase family X signature.

CONSENSUS: G-[SG]-[LFY]-x-R-[GE]-x(3)-[SGCL]-x-D-[LIVM]-D-[LIVMFY](3)-x(2)-[SAP].

NAME: Galactose-1-phosphate uridyl transferase family 1 active site signature.

CONSENSUS: F-E-N-[RK]-G-x(3)-G-x(4)-H-P-H-x-Q.

NAME: Galactose-1-phosphate uridyl transferase family 2 signature.

CONSENSUS: D-L-P-I-V-G-G-[ST]-[LIVM](2)-[SA]-H-[DEN]-H-[FY]-Q-G-G.

NAME: ADP-glucose pyrophosphorylase signature 1.

CONSENSUS: [AG]-G-G-x-G-[STK]-x-L-x(2)-L-[TA]-x(3)-A-x-P-A-[LV].

NAME: ADP-glucose pyrophosphorylase signature 2.

CONSENSUS: W-[FY]-x-G-[ST]-A-[DNSH]-[AS]-[LIVMFYW].

NAME: ADP-glucose pyrophosphorylase signature 3.

CONSENSUS: [APV]-[GS]-M-G-[LIVMN]-Y-[IVC]-[LIVMFY]-x(2)-[DENPHK].

NAME: Phosphatidate cytidylyltransferase signature.

CONSENSUS: S-x-[LIVMF]-K-R-x(4)-K-D-x-[GSA]-x(2)-[LI]-[PG]-x-H-G-G-[LIVM]-x-D-R-

CONSENSUS: [LIVMFT]-D.

NAME: Ribonuclease PH signature.

CONSENSUS: C-[DE]-[LIVM](2)-Q-[GTA]-D-G-[SG]-x(2)-[TA]-A.

NAME: 2'-5'-oligoadenylate synthetases signature 1.

CONSENSUS: G-G-S-x-[AG]-[KR]-x-T-x-L-[KR]-[GST]-x-S-D-[AG].

NAME: 2'-5'-oligoadenylate synthetases signature 2.

CONSENSUS: R-P-V-I-L-D-P-x-[DE]-P-T.
NAME: CDP-alcohol phosphatidyltransferases signature.
CONSENSUS: D-G-x(2)-A-R-x(8)-G-x(3)-D-x(3)-D.
NAME: PEP-utilizing enzymes phosphorylation site signature.
CONSENSUS: G-[GA]-x-[TN]-x-H-[STA]-[STAV]-[LIVM](2)-[STAV]-[RG].
NAME: PEP-utilizing enzymes signature 2.
CONSENSUS: [DEQS]-x-[LIVMF]-S-[LIVMF]-G-[ST]-N-D-[LIVM]-x-Q-[LIVMFYGT]-[STALIV]-
CONSENSUS: [LIVMF]-[GAS]-x(2)-R.
NAME: Rhodanese signature 1.
CONSENSUS: [FY]-x(3)-H-[LIV]-P-G-A-x(2)-[LIVF].
NAME: Rhodanese C-terminal signature.
CONSENSUS: [AV]-x(2)-[FY]-[DEAP]-G-[GSA]-[WF]-x-E-[FYW].
NAME: CoA transferases signature 1.
CONSENSUS: [DN]-[GN]-x(2)-[LIVMFA](3)-G-G-F-x(3)-G-x-P.
NAME: CoA transferases signature 2.
CONSENSUS: [LF]-[HQ]-S-E-N-G-[LIVF](2)-[GA].
NAME: Phospholipase A2 histidine active site.
CONSENSUS: C-C-x(2)-H-x(2)-C.
NAME: Phospholipase A2 aspartic acid active site.
CONSENSUS: [LIVMA]-C-{LIVMFYWPCST}-C-D-x(5)-C.
NAME: Lipases, serine active site.
CONSENSUS: [LIV]-x-[LIVFY]-[LIVMST]-G-[HYWV]-S-x-G-[GSTAC].
NAME: Colipase signature.
CONSENSUS: Y-x(2)-Y-Y-x-C-x-C.
NAME: Lipolytic enzymes "G-D-S-L" family, serine active site.
CONSENSUS: [LIVMFYAG](4)-G-D-S-[LIVM]-x(1,2)-[TAG]-G.
NAME: Lipolytic enzymes "G-D-X-G" family, putative histidine active site.
CONSENSUS: [LIVMF](2)-x-[LIVMF]-H-G-G-[SAG]-[FY]-x(3)-[STDN]-x(2)-[ST]-H.
NAME: Lipolytic enzymes "G-D-X-G" family, putative serine active site.
CONSENSUS: [LIVM]-x-[LIVMF]-[SA]-G-D-S-[CA]-G-[GA]-x-L-[CA].
NAME: Carboxylesterases type-B serine active site.
CONSENSUS: F-[GR]-G-x(4)-[LIVM]-x-[LIV]-x-G-x-S-[STAG]-G.
NAME: Carboxylesterases type-B signature 2.
CONSENSUS: [ED]-D-C-L-[YT]-[LIV]-[DNS]-[LIV]-[LIVFYW]-x-[PQR].
NAME: Pectinesterase signature 1.
CONSENSUS: [GSTN]-x(5)-[LIVM]-x-[LIVM]-x(2)-G-x-Y-[DNK]-E-x-[LIVM]-x-[LIVM].
NAME: Pectinesterase signature 2.
CONSENSUS: G-[STAD]-[LIVMT]-D-F-I-F-G.
NAME: Peptidyl-tRNA hydrolase signature 1.
CONSENSUS: [FY]-x(2)-T-R-H-N-x-G-x(2)-[LIVMFA](2)-[DE].
NAME: Peptidyl-tRNA hydrolase signature 2.
CONSENSUS: [GS]-x(3)-H-N-G-[LIVM]-[KR]-[DNS]-[LIVMT].
NAME: Alkaline phosphatase active site.
CONSENSUS: [IV]-x-D-S-[GAS]-[GASC]-[GAST]-[GA]-T.
NAME: Histidine acid phosphatases phosphohistidine signature.
CONSENSUS: [LIVM]-x(2)-[LIVMA]-x(2)-[LIVM]-x-R-H-[GN]-x-R-x-[PAS].
NAME: Histidine acid phosphatases active site signature.
CONSENSUS: [LIVMF]-x-[LIVMFAG]-x(2)-[STAGI]-H-D-[STANQ]-x-[LIVM]-x(2)-[LIVMFY]-x(2)-
CONSENSUS: [STA].
NAME: Class A bacterial acid phosphatases signature.

CONSENSUS: G-S-Y-P-S-G-H-T.

NAME: 5'-nucleotidase signature 1.

CONSENSUS: [LIVM]-x-[LIVM](2)-[HEA]-[TI]-x-D-x-H-[GSA]-x-[LIVMF].

NAME: 5'-nucleotidase signature 2.

CONSENSUS: [FYP]-x(4)-[LIVM]-G-N-H-E-F-[DN].

NAME: Fructose-1-6-bisphosphatase active site.

CONSENSUS: [AG]-[RK]-L-x(1,2)-[LIV]-[FY]-E-x(2)-P-[LIVM]-[GSA].

NAME: Serine/threonine specific protein phosphatases signature.

CONSENSUS: [LIVM]-R-G-N-H-E.

NAME: Protein phosphatase 2A regulatory subunit PR55 signature 1.

CONSENSUS: E-F-D-Y-L-K-S-L-E-I-E-E-K-I-N.

NAME: Protein phosphatase 2A regulatory subunit PR55 signature 2.

CONSENSUS: N-[AG]-H-[TA]-Y-H-I-N-S-I-S-[LIVM]-N-S-D.

NAME: Protein phosphatase 2C signature.

CONSENSUS: [LIVMFY]-[LIVMFYA]-[GSAC]-[LIVM]-[FYC]-D-G-H-[GAV].

NAME: Tyrosine specific protein phosphatases active site.

CONSENSUS: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY].

NAME: Tyrosine specific protein phosphatases profile.

NAME: Dual specificity protein phosphatase profile.

NAME: PTP type protein phosphatase profile.

NAME: Inositol monophosphatase family signature 1.

CONSENSUS: [FWV]-x(0,1)-[LIVM]-D-P-[LIVM]-D-[SG]-[ST]-x(2)-[FY]-x-[HKRNSTY].

NAME: Inositol monophosphatase family signature 2.

CONSENSUS: [WV]-D-x-[AC]-[GSA]-[GSAPV]-x-[LIVACP]-[LIV]-[LIVAC]-x(3)-[GH]-[GA].

NAME: Prokaryotic zinc-dependent phospholipase C signature.

CONSENSUS: H-Y-x-[GT]-D-[LIVM]-[DNS]-x-P-x-H-[PA]-x-N.

NAME: Phosphatidylinositol-specific phospholipase X-box domain profile.

NAME: Phosphatidylinositol-specific phospholipase Y-box domain profile.

NAME: 3'5'-cyclic nucleotide phosphodiesterases signature.

CONSENSUS: H-D-[LIVMFY]-x-H-x-[AG]-x(2)-[NQ]-x-[LIVMFY].

NAME: cAMP phosphodiesterases class-II signature.

CONSENSUS: H-x-H-L-D-H-[LIVM]-x-[GS]-[LIVMA]-[LIVM](2)-x-S-[AP].

NAME: Sulfatases signature 1.

CONSENSUS: [SAP]-[LIVMST]-[CS]-[STAC]-P-[STA]-R-x(2)-[LIVMFW](2)-[TR]-G.

NAME: Sulfatases signature 2.

CONSENSUS: G-[YV]-x-[ST]-x(2)-[IVA]-G-K-x(0,1)-[FYWK]-[HL].

NAME: AP endonucleases family 1 signature 1.

CONSENSUS: [APF]-D-[LIVMF](2)-x-[LIVM]-Q-E-x-K.

NAME: AP endonucleases family 1 signature 2.

CONSENSUS: D-[ST]-[FY]-R-[KH]-x(7,8)-[FYW]-[ST]-[FYW](2).

NAME: AP endonucleases family 1 signature 3.

CONSENSUS: N-x-G-x-R-[LIVM]-D-[LIVMFYH]-x-[LV]-x-S.

NAME: AP endonucleases family 2 signature 1.

CONSENSUS: H-x(2)-Y-[LIVMF]-[IM]-N-[LIVMCA]-[AG].

NAME: AP endonucleases family 2 signature 2.

CONSENSUS: [GR]-[LIVMF]-C-[LIVM]-D-T-C-H.

NAME: AP endonucleases family 2 signature 3.

CONSENSUS: [LIVMW]-H-x-N-[DE]-[SA]-K-x(3)-G-[SA]-x(2)-D.

NAME: Deoxyribonuclease I signature 1.
 CONSENSUS: [LIVM](2)-[AP]-L-H-[STA](2)-P-x(5)-E-[LIVM]-[DN]-x-L-x-[DE]-V.

NAME: Deoxyribonuclease I signature 2.
 CONSENSUS: G-D-F-N-A-x-C-[SA].

NAME: Endonuclease III iron-sulfur binding region signature.
 CONSENSUS: C-x(3)-[KRS]-P-[KRAGL]-C-x(2)-C-x(5)-C.

NAME: Endonuclease III family signature.
 CONSENSUS: [GST]-x-[LIVMF]-P-x(5)-[LIVMW]-x(2,3)-[LI]-[PAS]-G-V-[GA]-x(3)-[GAC]-
 CONSENSUS: x(3)-[LIVM]-x(2)-[SALV]-[LIVMFYW]-[GANK].

NAME: Ribonuclease II family signature.
 CONSENSUS: [HI]-[FYE]-[GSTAM]-[LIVM]-x(4,5)-Y-[STAL]-x-[FWVAC]-[TV]-[SA]-P-[LIVMA]-
 CONSENSUS: [RQ]-[KR]-[FY]-x-D-x(3)-[HQ].

NAME: Ribonuclease III family signature.
 CONSENSUS: [DEQ]-[RQ]-[LM]-E-[FYW]-[LV]-G-D-[SAR].

NAME: Bacterial Ribonuclease P protein component signature.
 CONSENSUS: [LIVMFYS]-x(2)-A-x(2)-R-[NH]-[KRQL]-[LIVM]-[KRA]-R-x-[LIVMTA]-[KR].

NAME: Ribonuclease T2 family histidine active site 1.
 CONSENSUS: [FYWL]-x-[LIVM]-H-G-L-W-P.

NAME: Ribonuclease T2 family histidine active site 2.
 CONSENSUS: [LIVMF]-x(2)-[HDGTY]-[EQ]-[FYW]-x-[KR]-H-G-x-C.

NAME: Pancreatic ribonuclease family signature.
 CONSENSUS: C-K-x(2)-N-T-F.

NAME: DNA/RNA non-specific endonucleases active site.
 CONSENSUS: D-R-G-H-[QIL]-x(3)-A.

NAME: Thermonuclease family signature 1.
 CONSENSUS: D-G-D-T-[LIVM]-x-[LIVMC]-x(9,10)-R-[LIVM]-x(2)-[LIVM]-D-x-P-E.

NAME: Thermonuclease family signature 2.
 CONSENSUS: D-[KR]-Y-[GQ]-R-x-[LV]-[GA]-x-[IV]-[FYW].

NAME: Beta-amylase active site 1.
 CONSENSUS: H-x-C-G-G-N-V-G-D.

NAME: Beta-amylase active site 2.
 CONSENSUS: G-x-[SA]-G-E-[LIVM]-R-Y-P-S-Y.

NAME: Glucoamylase active site region signature.
 CONSENSUS: [STN]-[GP]-x(1,2)-[DE]-x-W-E-E-x(2)-[GS].

NAME: Polygalacturonase active site.
 CONSENSUS: [GSDENKRH]-x(2)-[VMFC]-x(2)-[GS]-H-G-[LIVMAG]-x(1,2)-[LIVM]-G-S.

NAME: Clostridium cellulosome enzymes repeated domain signature.
 CONSENSUS: D-[LIVMFY]-[DNV]-x-[DNS]-x(2)-[LIVM]-[DN]-[SALM]-x-D-x(3)-[LIVMF]-x-
 CONSENSUS: [RKS]-x-[LIVMF].

NAME: Chitinases family 18 active site.
 CONSENSUS: [LIVMFY]-[DN]-G-[LIVMF]-[DN]-[LIVMF]-[DN]-x-E.

NAME: Chitinases family 19 signature 1.
 CONSENSUS: C-x(4,5)-F-Y-[ST]-x(3)-[FY]-[LIVMF]-x-A-x(3)-[YF]-x(2)-F-[GSA].

NAME: Chitinases family 19 signature 2.
 CONSENSUS: [LIVM]-[GSA]-F-x-[STAG](2)-[LIVMFY]-W-[FY]-W-[LIVM].

NAME: Alpha-lactalbumin / lysozyme C signature.
 CONSENSUS: C-x(3)-C-x(2)-[LMF]-x(3)-[DEN]-[LI]-x(5)-C.

NAME: Alpha-galactosidase signature.
 CONSENSUS: G-[LIVMFY]-x(2)-[LIVMFY]-x-[LIVM]-D-D-x-W-x(3,4)-R-[DNSF].

NAME: Trehalase signature 1.

CONSENSUS: P-G-G-R-F-x-E-x-Y-x-W-D-x-Y.

NAME: Trehalase signature 2.

CONSENSUS: Q-W-D-x-P-x-[GA]-W-[PA]-P.

NAME: Alpha-L-fucosidase putative active site.

CONSENSUS: P-x(2)-L-x(3)-K-W-E-x-C.

NAME: Glycosyl hydrolases family 1 active site.

CONSENSUS: [LIVMFSTC]-[LIVFYS]-[LIV]-[LIVMST]-E-N-G-[LIVMFAR]-[CSAGN].

NAME: Glycosyl hydrolases family 1 N-terminal signature.

CONSENSUS: F-x-[FYWM]-[GSTA]-x-[GSTA]-x-[GSTA](2)-[FYNH]-[NQ]-x-E-x-[GSTA].

NAME: Glycosyl hydrolases family 2 signature 1.

CONSENSUS: N-x-[LIVMFYWD]-R-[STACN](2)-H-Y-P-x(4)-[LIVMFYW](2)-x(3)-[DN]-x(2)-

CONSENSUS: G-[LIVMFYW](4).

NAME: Glycosyl hydrolases family 2 acid/base catalyst.

CONSENSUS: [DENQF]-[KRVW]-N-H-[AP]-[SAC]-[LIVMF](3)-W-[GS]-x(2,3)-N-E.

NAME: Glycosyl hydrolases family 3 active site.

CONSENSUS: [LIVM](2)-[KR]-x-[EQK]-x(4)-G-[LIVMFT]-[LIVT]-[LIVMF]-[ST]-D-x(2)-

CONSENSUS: [SGADNI].

NAME: Glycosyl hydrolases family 5 signature.

CONSENSUS: [LIV]-[LIVMFYWGA](2)-[DNEQG]-[LIVMGST]-x-N-E-[PV]-[RHDNSTLIVFY].

NAME: Glycosyl hydrolases family 6 signature 1.

CONSENSUS: V-x-Y-x(2)-P-x-R-D-C-[GSAF]-x(2)-[GSA](2)-x-G.

NAME: Glycosyl hydrolases family 6 signature 2.

CONSENSUS: [LIVMYA]-[LIVA]-[LIVT]-[LIV]-E-P-D-[SAL]-[LI]-[PSAG].

NAME: Glycosyl hydrolases family 8 signature.

CONSENSUS: A-[ST]-D-[AG]-D-x(2)-[IM]-A-x-[SA]-[LIVM]-[LIVMG]-x-A-x(3)-[FW].

NAME: Glycosyl hydrolases family 9 active sites signature 1.

CONSENSUS: [STV]-x-[LIVMFY]-[STV]-x(2)-G-x-[NKR]-x(4)-[PLIVM]-H-x-R.

NAME: Glycosyl hydrolases family 9 active sites signature 2.

CONSENSUS: [FYW]-x-D-x(4)-[FYW]-x(3)-E-x-[STA]-x(3)-N-[STA].

NAME: Glycosyl hydrolases family 10 active site.

CONSENSUS: [GTA]-x(2)-[LIVN]-x-[IVMF]-[ST]-E-[LIY]-[DN]-[LIVMF].

NAME: Glycosyl hydrolases family 11 active site signature 1.

CONSENSUS: [PSA]-[LQ]-x-E-Y-Y-[LIVM](2)-[DE]-x-[FYWHN].

NAME: Glycosyl hydrolases family 11 active site signature 2.

CONSENSUS: [LIVMF]-x(2)-E-[AG]-[YWG]-[QRFGS]-[SG]-[STAN]-G-x-[SAF].

NAME: Glycosyl hydrolases family 16 active sites.

CONSENSUS: E-[LIV]-D-[LIV]-x(0,1)-E-x(2)-[GQ]-[KRNF]-x-[PSTA].

NAME: Glycosyl hydrolases family 17 signature.

CONSENSUS: [LIVM]-x-[LIVMFYWA](3)-[STAG]-E-[STA]-G-W-P-[STN]-x-[SAGQ].

NAME: Glycosyl hydrolases family 25 active sites signature.

CONSENSUS: D-[LIVM]-x(3)-[NQ]-[PG]-x(9,10)-G-x(4)-[LIVMFY](2)-K-x-[ST]-E-[GS]-x(2)-

CONSENSUS: Y-x-[DN].

NAME: Glycosyl hydrolases family 31 active site.

CONSENSUS: [GF]-[LIVMF]-W-x-D-M-[NSA]-E.

NAME: Glycosyl hydrolases family 31 signature 2.

CONSENSUS: G-[AV]-D-[LIVMT]-C-G-[FY]-x(3)-[ST]-x(3)-L-C-x-R-W-x(2)-[LV]-[GS]-[SA]-

CONSENSUS: F-x-P-F-x-R-[DN].

NAME: Glycosyl hydrolases family 32 active site.

CONSENSUS: H-x(2)-P-x(4)-[LIVM]-N-D-P-N-G.

NAME: Glycosyl hydrolases family 35 putative active site.

CONSENSUS: G-G-P-[LIVM](2)-x(2)-Q-x-E-N-E-[FY].

NAME: Glycosyl hydrolases family 39 active site.

CONSENSUS: W-x-F-E-x-W-N-E-P-[DN].

NAME: Glycosyl hydrolases family 45 active site.

CONSENSUS: [STA]-T-R-Y-[FYW]-D-x(5)-[CA].

NAME: Prokaryotic transglycosylases signature.

CONSENSUS: [LIVM]-x(3)-E-S-x(3)-[AP]-x(3)-S-x(5)-G-[LIVM]-[LIVMFYW]-x-[LIVMFYW]-

CONSENSUS: x(4)-[SAG].

NAME: Inosine-uridine preferring nucleoside hydrolase family signature.

CONSENSUS: D-x-D-[PT]-[GA]-x-D-D-[TAV]-[VI]-A.

NAME: Alkylbase DNA glycosidases alkA family signature.

CONSENSUS: G-I-G-x-W-[ST]-[AV]-x-[LIVMFY](2)-x-[LIVM]-x(8)-[MF]-x(2)-[ED]-D.

NAME: Formamidopyrimidine-DNA glycosylase signature.

CONSENSUS: C-x(2,4)-C-x-[GTAQ]-x-[IV]-x(7)-R-[GSTAN]-[STA]-x-[FYI]-C-x(2)-C-Q.

NAME: Uracil-DNA glycosylase signature.

CONSENSUS: [KR]-[LIV]-[LIVC]-[LIVM]-x-G-[QI]-D-P-Y.

NAME: S-adenosyl-L-homocysteine hydrolase signature 1.

CONSENSUS: [CS]-N-x-[FYL]-S-[ST]-[QA]-[DEN]-x-[AV](2)-A-A-[LIV]-[SAV].

NAME: S-adenosyl-L-homocysteine hydrolase signature 2.

CONSENSUS: G-K-x(3)-[LIV]-x-G-Y-G-x-V-G-[KR]-G-x-A.

NAME: Cytosol aminopeptidase signature.

CONSENSUS: N-T-D-A-E-G-R-L.

NAME: Aminopeptidase P and proline dipeptidase signature.

CONSENSUS: [HA]-[GSYR]-[LIVMT]-[SG]-H-x-[LIV]-G-[LIVM]-x-[IV]-H-[DE].

NAME: Methionine aminopeptidase subfamily 1 signature.

CONSENSUS: [MFY]-x-G-H-G-[LIVMC]-[GSH]-x(3)-H-x(4)-[LIVM]-x-[HN]-[YWV].

NAME: Methionine aminopeptidase subfamily 2 signature.

CONSENSUS: [DA]-[LIVMY]-x-K-[LIVM]-D-x-G-x-[HQ]-[LIVM]-[DNS]-G-x(3)-[DN].

NAME: Renal dipeptidase active site.

CONSENSUS: [LIVM]-E-G-[GA]-x(2)-[LIVMF]-x(6)-L-x(3)-Y-x(2)-G-[LIVM]-R.

NAME: Serine carboxypeptidases, serine active site.

CONSENSUS: [LIVM]-x-[GTA]-E-S-Y-[AG]-[GS].

NAME: Serine carboxypeptidases, histidine active site.

CONSENSUS: [LIVF]-x(2)-[LIVSTA]-x-[IVPST]-x-[GSDNQL]-[SAGV]-[SG]-H-x-[IVAQ]-P-x(3)-

CONSENSUS: [PSA].

NAME: Zinc carboxypeptidases, zinc-binding region 1 signature.

CONSENSUS: [PK]-x-[LIVMFY]-x-[LIVMFY]-x(4)-H-[STAG]-x-E-x-[LIVM]-[STAG]-x(6)-

CONSENSUS: [LIVMFYTA].

NAME: Zinc carboxypeptidases, zinc-binding region 2 signature.

CONSENSUS: H-[STAG]-x(3)-[LIVME]-x(2)-[LIVMFYW]-P-[FYW].

NAME: Serine proteases, trypsin family, histidine active site.

CONSENSUS: [LIVM]-[ST]-A-[STAG]-H-C.

NAME: Serine proteases, trypsin family, serine active site.

CONSENSUS: [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]-[LIVMFYWH]-

CONSENSUS: [LIVMFYSTANQH].

NAME: Serine proteases, subtilase family, aspartic acid active site.

CONSENSUS: [STAIV]-x-[LIVMF]-[LIVM]-D-[DSTA]-G-[LIVMFC]-x(2,3)-[DNH].

NAME: Serine proteases, subtilase family, histidine active site.

CONSENSUS: H-G-[STM]-x-[VIC]-[STAGC]-[GS]-x-[LIVMA]-[STAGCLV]-[SAGM].

NAME: Serine proteases, subtilase family, serine active site.

CONSENSUS: G-T-S-x-[SA]-x-P-x(2)-[STAVC]-[AG].

NAME: Serine proteases, V8 family, histidine active site.

CONSENSUS: [ST]-G-[LIVMFYW](3)-[GN]-x(2)-T-[LIVM]-x-T-x(2)-H.

NAME: Serine proteases, V8 family, serine active site.

CONSENSUS: T-x(2)-[GC]-[NQ]-S-G-S-x-[LIVM]-[FY].

NAME: Serine proteases, omptin family signature 1.

CONSENSUS: W-T-D-x-S-x-H-P-x-T.

NAME: Serine proteases, omptin family signature 2.

CONSENSUS: A-G-Y-Q-E-[ST]-R-[FYW]-S-[FYW]-[TN]-A-x-G-G-[ST]-Y.

NAME: Prolyl endopeptidase family serine active site.

CONSENSUS: D-x(3)-A-x(3)-[LIVMFYW]-x(14)-G-x-S-x-G-G-[LIVMFYW](2).

NAME: Endopeptidase Clp serine active site.

CONSENSUS: T-x(2)-[LIVMF]-G-x-A-[SAC]-S-[MSA]-[PAG]-[STA].

NAME: Endopeptidase Clp histidine active site.

CONSENSUS: R-x(3)-[EAP]-x(3)-[LIVMFYT]-M-[LIVM]-H-Q-P.

NAME: ATP-dependent serine proteases, lon family, serine active site.

CONSENSUS: D-G-[PD]-S-A-[GS]-[LIVMCA]-[TA]-[LIVM].

NAME: Eukaryotic thiol (cysteine) proteases cysteine active site.

CONSENSUS: Q-x(3)-[GE]-x-C-[YW]-x(2)-[STAGC]-[STAGCV].

NAME: Eukaryotic thiol (cysteine) proteases histidine active site.

CONSENSUS: [LIVMGSTAN]-x-H-[GSACE]-[LIVM]-x-[LIVMAT](2)-G-x-[GSADNH].

NAME: Eukaryotic thiol (cysteine) proteases asparagine active site.

CONSENSUS: [FYCH]-[WI]-[LIVT]-x-[KRQAG]-N-[ST]-W-x(3)-[FYW]-G-x(2)-G-[LFYW]-

CONSENSUS: [LIVMFYG]-x-[LIVMF].

NAME: Ubiquitin carboxyl-terminal hydrolase family 1 cysteine active-site.

CONSENSUS: Q-x(3)-N-[SA]-C-G-x(3)-[LIVM](2)-H-[SA]-[LIVM]-[SA].

NAME: Ubiquitin carboxyl-terminal hydrolases family 2 signature 1.

CONSENSUS: G-[LIVMFY]-x(1,3)-[AGC]-[NASM]-x-C-[FYW]-[LIVMC]-[NST]-[SACV]-x-[LIVMS]-

CONSENSUS: Q.

NAME: Ubiquitin carboxyl-terminal hydrolases family 2 signature 2.

CONSENSUS: Y-x-L-x-[SAG]-[LIVMFT]-x(2)-H-x-G-x(4,5)-G-H-Y.

NAME: Caspase family histidine active site.

CONSENSUS: H-x(2,4)-[SC]-x(4)-[LIVMF](2)-[ST]-H-G.

NAME: Caspase family cysteine active site.

CONSENSUS: K-P-K-[LIVMF](4)-Q-A-C-[RQG]-G.

NAME: Eukaryotic and viral aspartyl proteases active site.

CONSENSUS: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]-x-[LIVMFSTNC]-

CONSENSUS: x-[LIVMFGTA].

NAME: Neutral zinc metalloproteases, zinc-binding region signature.

CONSENSUS: [GSTALIVN]-x(2)-H-E-[LIVMFYW]-[DEHRKP]-H-x-[LIVMFYWGSPQ].

NAME: Matrixins cysteine switch.

CONSENSUS: P-R-C-[GN]-x-P-[DR]-[LIVSAPKQ].

NAME: Insulinase family, zinc-binding region signature.

CONSENSUS: G-x(8,9)-G-x-[STA]-H-[LIVMFY]-[LIVMC]-[DERN]-[HRKL]-[LMFAT]-x-[LFSTH]-x-

CONSENSUS: [GSTAN]-[GST].

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DE Glycoprotease family signature.

CONSENSUS: [KR]-[GSAT]-x(4)-[FYWHL]-[DQNGK]-x-P-x-[LIVMFY]-x(3)-H-x(2)-[AG]-H-

CONSENSUS: [LIVM].

NAME: Proteasome A-type subunits signature.

CONSENSUS: [FY]-x(4)-[STNV]-x-[FYW]-S-P-x-G-[RKH]-x(2)-Q-[LIVM]-[DE]-Y-[SAD]-x(2)-

CONSENSUS: [SAG].

NAME: Proteasome B-type subunits signature.

CONSENSUS: [LIVMA]-[GSA]-[LIVMF]-x-[FYLVGAC]-x(2)-[GSACFY]-[LIVMSTAC](3)-[GAC]-
CONSENSUS: [GSTACV]-[DES]-x(15)-[RK]-x(12,13)-G-x(2)-[GSTA]-D.

NAME: Signal peptidases I serine active site.

CONSENSUS: [GS]-x-S-M-x-[PS]-[AT]-[LF].

NAME: Signal peptidases I lysine active site.

CONSENSUS: K-R-[LIVMSTA](2)-G-x-[PG]-G-[DE]-x-[LIVM]-x-[LIVMFY].

NAME: Signal peptidases I signature 3.

CONSENSUS: [LIVMFYW](2)-x(2)-G-D-[NH]-x(3)-[SND]-x(2)-[SG].

NAME: Signal peptidases II signature.

CONSENSUS: [GAF]-[GA]-[GAS]-[LIVM]-[GAS]-N-[LVMFG]-[LIVMFY]-D-R-[LIMFA].

NAME: Peptidase family U32 signature.

CONSENSUS: E-x-F-x(2)-G-[SA]-[LIVM]-C-x(4)-G-x-C-x-[LIVM]-S.

NAME: Amidases signature.

CONSENSUS: G-[GA]-S-S-[GS]-G-x-[GSA]-[GSAVY]-x-[LIVM]-[GSA]-x(6)-[GSA]-x-[GA]-x-D-
CONSENSUS: x-[GA]-x-S-[LIVM]-R-x-P-[GSAC].

NAME: Asparaginase / glutaminase active site signature 1.

CONSENSUS: [LIVM]-x(2)-T-G-G-T-[IV]-[AGS].

NAME: Asparaginase / glutaminase active site signature 2.

CONSENSUS: G-x-[LIVM]-x(2)-H-G-T-D-T-[LIVM].

NAME: Urease nickel ligands signature.

CONSENSUS: T-[AY]-[GA]-[GAT]-[LIVM]-D-x-H-[LIVM]-H-x(3)-P.

NAME: Urease active site.

CONSENSUS: [LIVM](2)-[CT]-H-[HN]-L-x(3)-[LIVM]-x(2)-D-[LIVM]-x-F-A.

NAME: ArgE / dapE / ACY1 / CPG2 / yscS family signature 1.

CONSENSUS: [LIV]-[GALMY]-[LIVMF]-x-[GSA]-H-x-D-[TV]-[STAV].

NAME: ArgE / dapE / ACY1 / CPG2 / yscS family signature 2.

CONSENSUS: [GSTAI]-[SANQ]-D-x-K-[GSACN]-x(2)-[LIVMA]-x(2)-[LIVMFY]-x(14,17)-[LIVM]-
CONSENSUS: x-[LIVMF]-[LIVMSTAG]-[LIVMFA]-x(2)-[DNG]-E-E-x-[GSTN].

NAME: Dihydroorotase signature 1.

CONSENSUS: D-[LIVMFYWSAP]-H-[LIVA]-H-[LIVF]-[RN]-x-[PGN].

NAME: Dihydroorotase signature 2.

CONSENSUS: [GA]-[ST]-D-x-A-P-H-x(4)-K.

NAME: Beta-lactamase class-A active site.

CONSENSUS: [FY]-x-[LIVMFY]-x-S-[TV]-x-K-x(4)-[AGLM]-x(2)-[LC].

NAME: Beta-lactamase class-C active site.

CONSENSUS: F-E-[LIVM]-G-S-[LIVMG]-[SA]-K.

NAME: Beta-lactamase class-D active site.

CONSENSUS: [PA]-x-S-[ST]-F-K-[LIV]-[PAL]-x-[STA]-[LI].

NAME: Beta-lactamases class B signature 1.

CONSENSUS: [LI]-x-[STN]-[HN]-x-H-[GSTA]-D-x(2)-G-[GP]-x(7,8)-[GS].

NAME: Beta-lactamases class B signature 2.

CONSENSUS: P-x(3)-[LIVM](2)-x-G-x-C-[LIVMF](2)-K.

NAME: Arginase family signature 1.

CONSENSUS: [LIVMF]-G-G-x-H-x-[LIVMT]-[STAV]-x-[PAG]-x(3)-[GSTA].

NAME: Arginase family signature 2.

CONSENSUS: [LIVM](2)-x-[LIVMFY]-D-[AS]-H-x-D.

NAME: Arginase family signature 3.

CONSENSUS: [ST]-[LIVMFY]-D-[LIVM]-D-x(3)-[PAQ]-x(3)-P-[GSA]-x(7)-G.

NAME: Adenosine and AMP deaminase signature.

CONSENSUS: [SA]-[LIVM]-[NGS]-[STA]-D-D-P.

NAME: Cytidine and deoxycytidylate deaminases zinc-binding region signature.

CONSENSUS: [CH]-[AGV]-E-x(2)-[LIVMFGAT]-[LIVM]-x(17,33)-P-C-x(2,8)-C-x(3)-[LIVM].

NAME: GTP cyclohydrolase I signature 1.

CONSENSUS: [EN]-[LIVM](2)-x(2)-[KRQN]-[DN]-[LIVM]-x(3)-[ST]-x-C-E-H-H.

NAME: GTP cyclohydrolase I signature 2.

CONSENSUS: [SA]-x-[RK]-x-Q-[LIVM]-Q-E-[RN]-[LI]-[TSN].

NAME: Nitrilases / cyanide hydratase signature 1.

CONSENSUS: G-x(2)-[LIVMFY](2)-x-[IF]-x-E-x(2)-[LIVM]-x-G-Y-P.

NAME: Nitrilases / cyanide hydratase active site signature.

CONSENSUS: G-[GAQ]-x(2)-C-[WA]-E-[NH]-x(2)-[PST]-[LIVMFYS]-x-[KR].

NAME: Inorganic pyrophosphatase signature.

CONSENSUS: D-[SGDN]-D-[PE]-[LIVMF]-D-[LIVMGAC].

NAME: Acylphosphatase signature 1.

CONSENSUS: [LIV]-x-G-x-V-Q-G-V-x-[FM]-R.

NAME: Acylphosphatase signature 2.

CONSENSUS: G-[FYW]-[AVC]-[KRQAM]-N-x(3)-G-x-V-x(5)-G.

NAME: ATP synthase alpha and beta subunits signature.

CONSENSUS: P-[SAP]-[LIV]-[DNH]-x(3)-S-x-S.

NAME: ATP synthase gamma subunit signature.

CONSENSUS: [IV]-T-x-E-x(2)-[DE]-x(3)-G-A-x-[SAKR].

NAME: ATP synthase delta (OSCP) subunit signature.

CONSENSUS: [LIVM]-x-[LIVMFYT]-x(3)-[LIVMT]-[DENQK]-x(2)-[LIVM]-x-[GSA]-G-[LIVMFYGA]-

CONSENSUS: x-[LIVM]-[KRHENQ]-x-[GSEN].

NAME: ATP synthase a subunit signature.

CONSENSUS: [STAGN]-x-[STAG]-[LIVMF]-R-L-x-[SAGV]-N-[LIVMT].

NAME: ATP synthase c subunit signature.

CONSENSUS: [GSTA]-R-[NQ]-P-x(10)-[LIVMFYW](2)-x(3)-[LIVMFYW]-x-[DE].

NAME: E1-E2 ATPases phosphorylation site.

CONSENSUS: D-K-T-G-T-[LI]-[TI].

NAME: Sodium and potassium ATPases beta subunits signature 1.

CONSENSUS: [FYW]-x(2)-[FYW]-x-[FYW]-[DN]-x(6)-[LIVM]-G-R-T-x(3)-W.

NAME: Sodium and potassium ATPases beta subunits signature 2.

CONSENSUS: [RK]-x(2)-C-[RKQWI]-x(5)-L-x(2)-C-[SA]-G.

NAME: GDA1/CD39 family of nucleoside phosphatases signature.

CONSENSUS: [LIVM]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LIVA]-[TAG]-x-N-[HY].

NAME: Iodothyronine deiodinases active site.

CONSENSUS: R-P-L-V-x-N-F-G-S-[CA]-T-C-P-x-F.

NAME: Cutinase, serine active site.

CONSENSUS: P-x-[STA]-x-[LIV]-[IVT]-x-[GS]-G-Y-S-[QL]-G.

NAME: Cutinase, aspartate and histidine active sites.

CONSENSUS: C-x(3)-D-x-[IV]-C-x-G-[GST]-x(2)-[LIVM]-x(2,3)-H.

NAME: DDC / GAD / HDC / TyrDC pyridoxal-phosphate attachment site.

CONSENSUS: S-[LIVMFYW]-x(5)-K-[LIVMFYWG](2)-x(3)-[LIVMFYW]-x-[CA]-x(2)-[LIVMFYWQ]-

CONSENSUS: x(2)-[RK].

NAME: Orn/Lys/Arg decarboxylases family 1 pyridoxal-P attachment site.

CONSENSUS: [STAV]-x-S-x-H-K-x(2)-[GSTAN](2)-x-[STA]-Q-[STA](2).

NAME: Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment site.

CONSENSUS: [FY]-[PA]-x-K-[SACV]-[NHCLFW]-x(4)-[LIVMF]-[LIVMTA]-x(2)-[LIVMA]-x(3)-

CONSENSUS: [GTE].

NAME: Orn/DAP/Arg decarboxylases family 2 signature 2.
 CONSENSUS: [GS]-x(2,6)-[LIVMSCP]-x(2)-[LIVMF]-[DNS]-[LIVMCA]-G-G-G-[LIVMFY]-
 CONSENSUS: [GSTPCEQ].

NAME: Orotidine 5'-phosphate decarboxylase active site.
 CONSENSUS: [LIVMFTA]-[LIVMF]-x-D-x-K-x(2)-D-I-[GP]-x-T-[LIVMTA].

NAME: Phosphoenolpyruvate carboxylase active site 1.
 CONSENSUS: [VT]-x-T-A-H-P-T-[EQ]-x(2)-R-[KRH].

NAME: Phosphoenolpyruvate carboxylase active site 2.
 CONSENSUS: [IV]-M-[LIVM]-G-Y-S-D-S-x-K-D-[STAG]-G.

NAME: Phosphoenolpyruvate carboxykinase (GTP) signature.
 CONSENSUS: F-P-S-A-C-G-K-T-N.

NAME: Phosphoenolpyruvate carboxykinase (ATP) signature.
 CONSENSUS: L-I-G-D-D-E-H-x-W-x-[DE]-x-G-[IV]-x-N.

NAME: Uroporphyrinogen decarboxylase signature 1.
 CONSENSUS: P-x-W-x-M-R-Q-A-G-R.

NAME: Uroporphyrinogen decarboxylase signature 2.
 CONSENSUS: G-F-[STAGCV]-[STAGC]-x-P-[FYW]-T-[LV]-x(2)-Y-x(2)-[AE]-[GK].

NAME: Indole-3-glycerol phosphate synthase signature.
 CONSENSUS: [LIVMFY]-[LIVMC]-x-E-[LIVMFYC]-K-[KRSP]-[STAK]-S-P-[ST]-x(3)-[LIVMFYST].

NAME: Ribulose biphosphate carboxylase large chain active site.
 CONSENSUS: G-x-[DN]-F-x-K-x-D-E.

NAME: Fructose-bisphosphate aldolase class-I active site.
 CONSENSUS: [LIVM]-x-[LIVMFYW]-E-G-x-[LS]-L-K-P-[SN].

NAME: Fructose-bisphosphate aldolase class-II signature 1.
 CONSENSUS: [FYVM]-x(1,3)-[LIVMH]-[APN]-[LIVM]-x(1,2)-[LIVM]-H-x-D-H-[GACH].

NAME: Fructose-bisphosphate aldolase class-II signature 2.
 CONSENSUS: [LIVM]-E-x-E-[LIVM]-G-x(2)-[GM]-[GSTA]-x-E.

NAME: Malate synthase signature.
 CONSENSUS: [KR]-[DENQ]-H-x(2)-G-L-N-x-G-x-W-D-Y-[LIVM]-F.

NAME: Hydroxymethylglutaryl-coenzyme A lyase active site.
 CONSENSUS: S-V-A-G-L-G-G-C-P-Y.

NAME: Hydroxymethylglutaryl-coenzyme A synthase active site.
 CONSENSUS: N-x-[DN]-[IV]-E-G-[IV]-D-x(2)-N-A-C-[FY]-x-G.

NAME: Citrate synthase signature.
 CONSENSUS: G-[FYA]-[GA]-H-x-[IV]-x(1,2)-[RKT]-x(2)-D-[PS]-R.

NAME: Alpha-isopropylmalate and homocitrate synthases signature 1.
 CONSENSUS: L-R-[DE]-G-x-Q-x(10)-K.

NAME: Alpha-isopropylmalate and homocitrate synthases signature 2.
 CONSENSUS: [LIVMFW]-x(2)-H-x-H-[DN]-D-x-G-x-[GAS]-x-[GASLI].

NAME: KDPG and KHG aldolases active site.
 CONSENSUS: G-[LIVM]-x(3)-E-[LIV]-T-[LF]-R.

NAME: KDPG and KHG aldolases Schiff-base forming residue.
 CONSENSUS: G-x(3)-[LIVMF]-K-[LF]-F-P-[SA]-x(3)-G.

NAME: Isocitrate lyase signature.
 CONSENSUS: K-[KR]-C-G-H-[LMQ].

NAME: Beta-eliminating lyases pyridoxal-phosphate attachment site.
 CONSENSUS: Y-x-D-x(3)-M-S-[GA]-K-K-D-x-[LIVM](2)-x-[LIVM]-G-G.

NAME: DNA photolyases class 1 signature 1.
 CONSENSUS: T-G-x-P-[LIVM](2)-D-A-x-M-[RA]-x-[LIVM].

NAME: DNA photolyases class 1 signature 2.

CONSENSUS: [DN]-R-x-R-[LIVM](2)-x-[STA](2)-F-[LIVMFA]-x-K-x-L-x(2,3)-W-[KRQ].

NAME: DNA photolyases class 2 signature 1.

CONSENSUS: F-x-E-E-x-[LIVM](2)-R-R-E-L-x(2)-N-F.

NAME: DNA photolyases class 2 signature 2.

CONSENSUS: G-x-H-D-x(2)-W-x-E-R-x-[LIVM]-F-G-K-[LIVM]-R-[FY]-M-N.

NAME: Eukaryotic-type carbonic anhydrases signature.

CONSENSUS: S-E-H-x-[LIVM]-x(4)-[FYH]-x(2)-E-[LIVM]-H-[LIVMFA](2).

NAME: Prokaryotic-type carbonic anhydrases signature 1.

CONSENSUS: C-[SA]-D-S-R-[LIVM]-x-[AP].

NAME: Prokaryotic-type carbonic anhydrases signature 2.

CONSENSUS: [EQ]-Y-A-[LIVM]-x(2)-[LIVM]-x(4)-[LIVMF](3)-x-G-H-x(2)-C-G.

NAME: Fumarate lyases signature.

CONSENSUS: G-S-x(2)-M-x(2)-K-x-N.

NAME: Aconitase family signature 1.

CONSENSUS: [LIVM]-x(2)-[GSACIVM]-x-[LIV]-[GTIV]-[STP]-C-x(0,1)-T-N-[GSTANI]-x(4)-

CONSENSUS: [LIVMA].

NAME: Aconitase family signature 2.

CONSENSUS: G-x(2)-[LIVWPQ]-x(3)-[GAC]-C-[GSTAM]-[LIMPTA]-C-[LIMV]-[GA].

NAME: Dihydroxy-acid and 6-phosphogluconate dehydratases signature 1.

CONSENSUS: C-D-K-x(2)-P-[GA]-x(3)-[GA].

NAME: Dihydroxy-acid and 6-phosphogluconate dehydratases signature 2.

CONSENSUS: [SA]-L-[LIVM]-T-D-[GA]-R-[LIVMF]-S-[GA]-[GAV]-[ST].

NAME: Dehydroquinase class I active site.

CONSENSUS: D-[LIVM]-[DE]-[LIVN]-x(18,20)-[LIVM](2)-x-[SC]-[INH]-H-[DN].

NAME: Dehydroquinase class II signature.

CONSENSUS: [LIVM]-[NQ]-G-P-N-[LV]-x(2)-L-G-x-R-[QED]-P-x(2)-[FY]-G.

NAME: Enolase signature.

CONSENSUS: [LIV](3)-K-x-N-Q-I-G-[ST]-[LIV]-[ST]-[DE]-[STA].

NAME: Serine/threonine dehydratases pyridoxal-phosphate attachment site.

CONSENSUS: [DESH]-x(4,5)-[STVG]-x-[AS]-[FYI]-K-[DLIFSA]-[RVMF]-[GA]-[LIVMGA].

NAME: Enoyl-CoA hydratase/isomerase signature.

CONSENSUS: [LIVM]-[STA]-x-[LIVM]-[DENQRHSTA]-G-x(3)-[AG](3)-x(4)-[LIVMST]-x-[CSTA]-

CONSENSUS: [DQHP]-[LIVMFY].

NAME: Imidazoleglycerol-phosphate dehydratase signature 1.

CONSENSUS: [LIVMY]-[DE]-x-H-H-x(2)-E-x(2)-[GCA]-[LIVM]-[STAC]-[LIVM].

NAME: Imidazoleglycerol-phosphate dehydratase signature 2.

CONSENSUS: G-x-[DN]-x-H-H-x(2)-E-[STAGC]-x-[FY]-K.

NAME: Tryptophan synthase alpha chain signature.

CONSENSUS: [LIVM]-E-[LIVM]-G-x(2)-[FYC]-[ST]-[DE]-[PA]-[LIVMY]-[AGLI]-[DE]-G.

NAME: Tryptophan synthase beta chain pyridoxal-phosphate attachment site.

CONSENSUS: [LIVM]-x-H-x-G-[STA]-H-K-x-N.

NAME: Delta-aminolevulinic acid dehydratase active site.

CONSENSUS: G-x-D-x-[LIVM](2)-[IV]-K-P-[GSA]-x(2)-Y.

NAME: Urocanase active site.

CONSENSUS: F-Q-G-L-P-x-R-I-C-W.

NAME: Prephenate dehydratase signature 1.

CONSENSUS: [FY]-x-[LIVM]-x(2)-[LIVM]-x(5)-[DN]-x(5)-T-R-F-[LIVMW]-x-[LIVM].

NAME: Prephenate dehydratase signature 2.

CONSENSUS: [LIVM]-[ST]-[KR]-[LIVM]-E-[ST]-R-P.

NAME: Dihydrodipicolinate synthetase signature 1.

CONSENSUS: [GSA]-[LIVM]-[LIVMFY]-x(2)-G-[ST]-[TG]-G-E-[GASNF]-x(6)-[EQ].
NAME: Dihydrodipicolinate synthetase signature 2.
CONSENSUS: Y-[DNS]-[LIVMF]-P-x(2)-[ST]-x(3)-[LIVM]-x(13,14)-[LIVM]-x-[SGA]-[LIVMF]-
CONSENSUS: K-[DEQAF]-[STAC].
NAME: RsuA family of pseudouridine synthase signature.
CONSENSUS: G-R-L-D-x(2)-[ST]-x-G-[LIVMF](4)-[ST]-[DNT].
NAME: Cysteine synthase/cystathionine beta-synthase P-phosphate attachment site.
CONSENSUS: K-x-E-x(3)-[PA]-[STAGC]-x-S-[IVAP]-K-x-R-x-[STAG]-x(2)-[LIVM].
NAME: Phenylalanine and histidine ammonia-lyases signature.
CONSENSUS: G-[STG]-[LIVM]-[STG]-[AC]-S-G-[DH]-L-x-P-L-[SA]-x(2)-[SA].
NAME: Porphobilinogen deaminase cofactor-binding site.
CONSENSUS: E-R-x-[LIVMFA]-x(3)-[LIVMF]-x-G-[GSA]-C-x-[IVT]-P-[LIVMF]-[GSA].
NAME: Cys/Met metabolism enzymes pyridoxal-phosphate attachment site.
CONSENSUS: [DQ]-[LIVMF]-x(3)-[STAGC]-[STAGCI]-T-K-[FYWQ]-[LIVMF]-x-G-[HQ]-[SGNH].
NAME: Glyoxalase I signature 1.
CONSENSUS: [HQ]-[IVT]-x-[LIVFY]-x-[IV]-x(5)-[STA]-x(2)-F-[YM]-x(2,3)-[LMF]-G-[LMF].
NAME: Glyoxalase I signature 2.
CONSENSUS: G-[NTKQ]-x(0,5)-[GA]-[LVFY]-[GH]-H-[IVF]-[CGA]-x-[STAGL]-x(2)-[DNC].
NAME: Cytochrome c and c1 heme lyases signature 1.
CONSENSUS: H-N-x(2)-N-E-x(2)-W-[NQKR]-x(4)-W-E.
NAME: Cytochrome c and c1 heme lyases signature 2.
CONSENSUS: P-F-D-R-H-D-W.
NAME: Adenylate cyclases class-I signature 1.
CONSENSUS: E-Y-F-G-[SA](2)-L-W-x-L-Y-K.
NAME: Adenylate cyclases class-I signature 2.
CONSENSUS: Y-R-N-x-W-[NS]-E-[LIVM]-R-T-L-H-F-x-G.
NAME: Guanylate cyclases signature.
CONSENSUS: G-V-[LIVM]-x(0,1)-G-x(5)-[FY]-x-[LIVM]-[FYW]-[GS]-[DNTHKW]-[DNT]-[IV]-
CONSENSUS: [DNTA]-x(5)-[DE].
NAME: Chorismate synthase signature 1.
CONSENSUS: G-E-S-H-[GC]-x(2)-[LIVM]-[GTV]-x-[LIVM](2)-[DE]-G-x-[PV].
NAME: Chorismate synthase signature 2.
CONSENSUS: [GE]-R-[SA](2)-[SAG]-R-[EV]-[ST]-x(2)-[RH]-V-x(2)-G.
NAME: Chorismate synthase signature 3.
CONSENSUS: R-[SH]-D-[PSV]-[CSAV]-x(4)-[GAI]-x-[IVGSP]-[LIVM]-x-E-[STAH]-[LIVM].
NAME: 6-pyruvoyl tetrahydropterin synthase signature 1.
CONSENSUS: C-N-N-x(2)-G-H-G-H-N-Y.
NAME: 6-pyruvoyl tetrahydropterin synthase signature 2.
CONSENSUS: D-H-K-N-L-D-x-D.
NAME: Ferrochelatase signature.
CONSENSUS: [LIVMF](2)-x-S-x-H-[GS]-[LIVM]-P-x(4,5)-[DENQKR]-x-G-D-x-Y.
NAME: Alanine racemase pyridoxal-phosphate attachment site.
CONSENSUS: V-x-K-A-[DN]-[GA]-Y-G-H-G.
NAME: Aspartate and glutamate racemases signature 1.
CONSENSUS: [IVA]-[LIVM]-x-C-x(0,1)-N-[ST]-[MSA]-[STH]-[LIVFYSTANK].
NAME: Aspartate and glutamate racemases signature 2.
CONSENSUS: [LIVM](2)-x-[AG]-C-T-[DEH]-[LIVMFY]-[PNGRS]-x-[LIVM].
NAME: Mandelate racemase / muconate lactonizing enzyme family signature 1.
CONSENSUS: A-x-[SAG](2)-[LIVM]-[DE]-x-A-x(2)-D-x(2)-[GA]-[KR].
NAME: Mandelate racemase / muconate lactonizing enzyme family signature 2.

CONSENSUS: G-x(7)-D-x(9)-A-x(14)-[LIVM]-E-[DENQ]-P-x(4)-[DENQ].
NAME: Ribulose-phosphate 3-epimerase family signature 1.
CONSENSUS: [LIVMF]-H-[LIVMFY]-D-[LIVM]-x-D-x(1,2)-[FY]-[LIVM]-x-N-x-[STAV].
NAME: Ribulose-phosphate 3-epimerase family signature 2.
CONSENSUS: [LIVMA]-x-[LIVM]-M-[ST]-[VS]-x-P-x(3)-G-Q-x-F-x(6)-[NK]-[LIVMC].
NAME: Aldose 1-epimerase putative active site.
CONSENSUS: [NS]-x-T-N-H-x-Y-[FW]-N-[LI].
NAME: Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.
CONSENSUS: [FY]-x(2)-[STCNLV]-x-F-H-[RH]-[LIVMN]-[LIVM]-x(2)-F-[LIVM]-x-Q-[AG]-G.
NAME: Cyclophilin-type peptidyl-prolyl cis-trans isomerase profile.
NAME: FKBP-type peptidyl-prolyl cis-trans isomerase signature 1.
CONSENSUS: [LIVMC]-x-[YF]-x-[GVL]-x(1,2)-[LFT]-x(2)-G-x(3)-[DE]-[STAEQK]-[STAN].
NAME: FKBP-type peptidyl-prolyl cis-trans isomerase signature 2.
CONSENSUS: [LIVMFY]-x(2)-[GA]-x(3,4)-[LIVMF]-x(2)-[LIVMFHK]-x(2)-G-x(4)-[LIVMF]-
CONSENSUS: x(3)-[PSGAQ]-x(2)-[AG]-[FY]-G.
NAME: FKBP-type peptidyl-prolyl cis-trans isomerase domain profile.
NAME: PpiC-type peptidyl-prolyl cis-trans isomerase signature.
CONSENSUS: F-[GSADEI]-x-[LVAQ]-A-x(3)-[ST]-x(3,4)-[STQ]-x(3,5)-[GER]-G-x-[LIVM]-
CONSENSUS: [GS].
NAME: Triosephosphate isomerase active site.
CONSENSUS: [AV]-Y-E-P-[LIVM]-W-[SA]-I-G-T-[GK].
NAME: Xylose isomerase signature 1.
CONSENSUS: [LI]-E-P-K-P-x(2)-P.
NAME: Xylose isomerase signature 2.
CONSENSUS: [FL]-H-D-x-D-[LIV]-x-[PD]-x-[GDE].
NAME: Phosphomannose isomerase type I signature 1.
CONSENSUS: Y-x-D-x-N-H-K-P-E.
NAME: Phosphomannose isomerase type I signature 2.
CONSENSUS: H-A-Y-[LIVM]-x-G-x(2)-[LIVM]-E-x-M-A-x-S-D-N-x-[LIVM]-R-A-G-x-T-P-K.
NAME: Phosphoglucose isomerase signature 1.
CONSENSUS: [DENS]-x-[LIVM]-G-G-R-[FY]-S-[LIVMT]-x-[STA]-[PSAC]-[LIVMA]-G.
NAME: Phosphoglucose isomerase signature 2.
CONSENSUS: [GS]-x-[LIVM]-[LIVMFYW]-x(4)-[FY]-[DN]-Q-x-G-V-E-x(2)-K.
NAME: Glucosamine/galactosamine-6-phosphate isomerases signature.
CONSENSUS: [LIVM]-x(3)-G-x-[LIT]-x-[LIV]-x-[LIVM]-x-G-[LIVM]-G-x-[DEN]-G-H.
NAME: Phosphoglycerate mutase family phosphohistidine signature.
CONSENSUS: [LIVM]-x-R-H-G-[EQ]-x(3)-N.
NAME: Phosphoglucomutase and phosphomannomutase phosphoserine signature.
CONSENSUS: [GSA]-[LIVM]-x-[LIVM]-[ST]-[PGA]-S-H-x-P-x(4)-[GNHE].
NAME: Methylmalonyl-CoA mutase signature.
CONSENSUS: R-I-A-R-N-[TQ]-x(2)-[LIVMFY](2)-x-[EQ]-E-x(4)-[KRN]-x(2)-D-P-x-[GSA]-
CONSENSUS: G-S.
NAME: Terpene synthases signature.
CONSENSUS: [DE]-G-S-W-x-G-x-W-[GA]-[LIVM]-x-[FY]-x-Y-[GA].
NAME: Eukaryotic DNA topoisomerase I active site.
CONSENSUS: [DEN]-x(6)-[GS]-[IT]-S-K-x(2)-Y-[LIVM]-x(3)-[LIVM].
NAME: Prokaryotic DNA topoisomerase I active site.
CONSENSUS: [EQ]-x-L-Y-[DEQT]-x(3,12)-[LI]-[ST]-Y-x-R-[ST]-[DEQS].
NAME: DNA topoisomerase II signature.
CONSENSUS: [LIVMA]-x-E-G-[DN]-S-A-x-[STAG].

NAME: Aminoacyl-transfer RNA synthetases class-I signature.

CONSENSUS: P-x(0,2)-[GSTAN]-[DENQGAPK]-x-[LIVMFP]-[HT]-[LIVMYAC]-G-[HNTG]-
[LIVMFYSTAGPC].

NAME: Aminoacyl-transfer RNA synthetases class-II signature 1.

CONSENSUS: [FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE].

NAME: Aminoacyl-transfer RNA synthetases class-II signature 2.

CONSENSUS: [GSTALVF]-{DENQHRKP}-[GSTA]-[LIVMF]-[DE]-R-[LIVMF]-x-[LIVMSTAG]-[LIVMFY].

NAME: WHEP-TRS domain signature.

CONSENSUS: [QY]-G-[DNEA]-x-[LIV]-[KR]-x(2)-K-x(2)-[KRNG]-[AS]-x(4)-[LIV]-[DENK]-
x(2)-[IV]-x(2)-L-x(3)-K.

NAME: ATP-citrate lyase / succinyl-CoA ligases family signature 1.

CONSENSUS: S-[KR]-S-G-[GT]-[LIVM]-[GST]-x-[EQ]-x(8,10)-G-x(4)-[LIVM]-[GA]-[LIVM]-G-
G-D.

NAME: ATP-citrate lyase / succinyl-CoA ligases family active site.

CONSENSUS: G-x(2)-A-x(4,7)-[RQT]-[LIVMF]-G-H-[AS]-[GH].

NAME: ATP-citrate lyase / succinyl-CoA ligases family signature 3.

CONSENSUS: G-x-[IV]-x(2)-[LIVMF]-x-[NA]-G-[GA]-G-[LA]-[STAV]-x(4)-D-x-[LIVM]-x(3)-
G-[GRE].

NAME: Glutamine synthetase signature 1.

CONSENSUS: [FYWL]-D-G-S-S-x(6,8)-[DENQSTAK]-[SA]-[DE]-x(2)-[LIVMFY].

NAME: Glutamine synthetase putative ATP-binding region signature.

CONSENSUS: K-P-[LIVMFYA]-x(3,5)-[NPAT]-G-[GSTAN]-G-x-H-x(3)-S.

NAME: Glutamine synthetase class-I adenylation site.

CONSENSUS: K-[LIVM]-x(5)-[LIVMA]-D-[RK]-[DN]-[LI]-Y.

NAME: D-alanine--D-alanine ligase signature 1.

CONSENSUS: H-G-x(2)-G-E-D-G-x-[LIVMA]-[QSA]-[GSA].

NAME: D-alanine--D-alanine ligase signature 2.

CONSENSUS: [LIV]-x(3)-[GA]-x-[GSAIV]-R-[LIVCA]-D-[LIVMF](2)-x(7,9)-[LI]-x-E-
[LIVA]-N-[STP]-x-P-[GA].

NAME: SAICAR synthetase signature 1.

CONSENSUS: [LIVMF](2)-P-[LIVM]-E-x-[LIVM]-[LIVMCA]-R-x(3)-[TA]-G-S.

NAME: SAICAR synthetase signature 2.

CONSENSUS: [LIVM]-[LIVMA]-D-x-K-[LIVMFY]-E-F-G.

NAME: Folylpolylglutamate synthase signature 1.

CONSENSUS: [LIVMFY]-x-[LIVM]-[STAG]-G-T-[NK]-G-K-x-[ST]-x(7)-[LIVM](2)-x(3)-[GSK].

NAME: Folylpolylglutamate synthase signature 2.

CONSENSUS: [LIVMFY](2)-E-x-G-[LIVM]-[GA]-G-x(2)-D-x-[GST]-x-[LIVM](2).

NAME: Ubiquitin-activating enzyme signature 1.

CONSENSUS: K-A-C-S-G-K-F-x-P.

NAME: Ubiquitin-activating enzyme active site.

CONSENSUS: P-[LIVM]-C-T-[LIVM]-[KRH]-x-[FT]-P.

NAME: Ubiquitin-conjugating enzymes active site.

CONSENSUS: [FYWLSP]-H-[PC]-[NH]-[LIV]-x(3,4)-G-x-[LIV]-C-[LIV]-x-[LIV].

NAME: Formate--tetrahydrofolate ligase signature 1.

CONSENSUS: G-[LIVM]-K-G-G-A-A-G-G-G-Y.

NAME: Formate--tetrahydrofolate ligase signature 2.

CONSENSUS: V-A-T-[IV]-R-A-L-K-x-[HN]-G-G.

NAME: Adenylosuccinate synthetase GTP-binding site.

CONSENSUS: Q-W-G-D-E-G-K-G.

NAME: Adenylosuccinate synthetase active site.

CONSENSUS: G-I-[GR]-P-x-Y-x(2)-K-x(2)-R.

NAME: Argininosuccinate synthase signature 1.
 CONSENSUS: A-[FY]-S-G-G-L-D-T-S.

NAME: Argininosuccinate synthase signature 2.
 CONSENSUS: G-x-T-x-K-G-N-D-x(2)-R-F.

NAME: Phosphoribosylglycinamide synthetase signature.
 CONSENSUS: R-F-G-D-P-E-x-[QM].

NAME: Carbamoyl-phosphate synthase subdomain signature 1.
 CONSENSUS: [FYV]-[PS]-[LIVMC]-[LIVMA]-[LIVM]-[KR]-[PSA]-[STA]-x(3)-[SG]-G-x-[AG].

NAME: Carbamoyl-phosphate synthase subdomain signature 2.
 CONSENSUS: [LIVMF]-[LIMN]-E-[LIVMCA]-N-[PATLIVM]-[KR]-[LIVMSTAC].

NAME: ATP-dependent DNA ligase AMP-binding site.
 CONSENSUS: [EDQH]-x-K-x-[DN]-G-x-R-[GACIVM].

NAME: ATP-dependent DNA ligase signature 2.
 CONSENSUS: E-G-[LIVMA]-[LIVM](2)-[KR]-x(5,8)-[YW]-[QNEK]-x(2,6)-[KRH]-x(3,5)-K-
 CONSENSUS: [LIVMFY]-K.

NAME: NAD-dependent DNA ligase signature 1.
 CONSENSUS: K-[LIVM]-D-G-[LIVM]-[SA]-x(4)-Y-x(2)-G-x-L-x(4)-[ST]-R-G-[DN]-G-x(2)-G-
 CONSENSUS: [DE]-[DENL].

NAME: NAD-dependent DNA ligase signature 2.
 CONSENSUS: [IV]-G-[KR]-[ST]-G-x-[LIVM]-[STNK]-x-[VT]-x(2)-L-x-[PS]-V.

NAME: RNA 3'-terminal phosphate cyclase signature.
 CONSENSUS: [RH]-G-x(2)-P-x-G(3)-x-[LIV].

NAME: Lipote-protein ligase B signature.
 CONSENSUS: R-G-G-x(2)-T-[FYW]-H-x(2)-[GH]-Q-x-[LIV]-x-Y.

NAME: Isopenicillin N synthetase signature 1.
 CONSENSUS: [RK]-x-[STA]-x(2)-S-x-C-Y-[SL].

NAME: Isopenicillin N synthetase signature 2.
 CONSENSUS: [LIVM](2)-x-C-G-[STA]-x(2)-[STAG]-x(2)-T-x-[DNG].

NAME: Site-specific recombinases active site.
 CONSENSUS: Y-[LIVAC]-R-[VA]-S-[ST]-x(2)-Q.

NAME: Site-specific recombinases signature 2.
 CONSENSUS: G-[DE]-x(2)-[LIVM]-x(3)-[LIVM]-[DT]-R-[LIVM]-[GSA].

NAME: Transposases, Mutator family, signature.
 CONSENSUS: D-x(3)-G-[LIVMF]-x(6)-[STAV]-[LIVMFYW]-[PT]-x-[STAV]-x(2)-[QR]-x-C-x(2)-
 CONSENSUS: H.

NAME: Transposases, IS30 family, signature.
 CONSENSUS: R-G-x(2)-E-N-x-N-G-[LIVM](2)-R-[QE]-[LIVMFY](2)-P-K.

NAME: Autoinducers synthetases family signature.
 CONSENSUS: [LMFY]-R-x(3)-F-x(2)-[KR]-x(2)-W-x-[LIVM]-x(6,9)-E-x-D-x-[FY]-D.

NAME: Thiamine pyrophosphate enzymes signature.
 CONSENSUS: [LIVMF]-[GSA]-x(5)-P-x(4)-[LIVMFYW]-x-[LIVMF]-x-G-D-[GSA]-[GSAC].

NAME: Biotin-requiring enzymes attachment site.
 CONSENSUS: [GN]-[DEQTR]-x-[LIVMFY]-x(2)-[LIVM]-x-[AIV]-M-K-[LMAT]-x(3)-[LIVM]-x-
 CONSENSUS: [SAV].

NAME: 2-oxo acid dehydrogenases acyltransferase component lipoyl binding site.
 CONSENSUS: [GN]-x(2)-[LIVF]-x(5)-[LIVFC]-x(2)-[LIVFA]-x(3)-K-[STAIV]-[STAVQDN]-
 CONSENSUS: x(2)-[LIVMFS]-x(5)-[GCN]-x-[LIVMFY].

NAME: Putative AMP-binding domain signature.
 CONSENSUS: [LIVMFY]-x(2)-[STG]-[STAG]-G-[ST]-[STEI]-[SG]-x-[PASLIVM]-[KR].

NAME: Molybdenum cofactor biosynthesis proteins signature 1.
 CONSENSUS: [LIVM](3)-[LIT](2)-G-G-T-G-x(4)-D.

NAME: Molybdenum cofactor biosynthesis proteins signature 2.
 CONSENSUS: S-x-[GS]-x(2)-D-x(5)-[LIVW]-x(10,12)-[LIV]-x(2)-[KR]-P-G-[KRL]-P-x(2)-[LIVMF]-[GA].
 NAME: moaA / nifB / pqqE family signature.
 CONSENSUS: [LIV]-x(3)-C-[NP]-[LIVMF]-[QRS]-C-x-[FYM]-C.
 NAME: Radical activating enzymes signature.
 CONSENSUS: [GV]-x-G-x-[KR]-x(3)-F-x(2)-G-x(0,1)-C-x(3)-C-x(2)-C-x-[NL].
 NAME: Tpx family signature.
 CONSENSUS: S-x-D-L-P-F-A-x(2)-[KR]-[FW]-C.
 NAME: Cytochrome c family heme-binding site signature.
 CONSENSUS: C-{CPWHF}-{CPWR}-C-H-{CFYW}.
 NAME: Cytochrome b5 family, heme-binding domain signature.
 CONSENSUS: {FY}-[LIVMK]-x(2)-H-P-[GA]-G.
 NAME: Cytochrome b/b6 heme-ligand signature.
 CONSENSUS: [DENQ]-x(3)-G-[FYWMQ]-x-[LIVMF]-R-x(2)-H.
 NAME: Cytochrome b/b6 Qo site signature.
 CONSENSUS: P-[DE]-W-[FY]-[LFY](2).
 NAME: Cytochrome b559 subunits heme-binding site signature.
 CONSENSUS: [LIV]-x-[ST]-[LIVF]-R-[FYW]-x(2)-[IV]-H-[STGA]-[LIV]-[STGA]-[IV]-P.
 NAME: Nickel-dependent hydrogenases b-type cytochrome subunit signature 1.
 CONSENSUS: R-[LIVMFYW]-x-H-W-[LIVM]-x(2)-[LIVMF]-[STAC]-[LIVM]-x(2)-L-x-[LIVM]-T-G.
 NAME: Nickel-dependent hydrogenases b-type cytochrome subunit signature 2.
 CONSENSUS: [RH]-[STA]-[LIVMFYW]-H-[RH]-[LIVM]-x(2)-W-x-[LIVMF]-x(2)-F-x(3)-H.
 NAME: Succinate dehydrogenase cytochrome b subunit signature 1.
 CONSENSUS: R-P-[LIVMT]-x(3)-[LIVM]-x(6)-[LIVMWPK]-x(4)-S-x(2)-H-R-x-[ST].
 NAME: Succinate dehydrogenase cytochrome b subunit signature 2.
 CONSENSUS: H-x(3)-[GA]-[LIVMT]-R-[HF]-[LIVMF]-x-[FYWM]-D-x-[GVA].
 NAME: Thioredoxin family active site.
 CONSENSUS: [LIVMF]-[LIVMSTA]-x-[LIVMFYC]-[FYWSTHE]-x(2)-[FYWGNTN]-C-[GATPLVE]-[PHYWSTA]-C-x(6)-[LIVMFYWT].
 NAME: Glutaredoxin active site.
 CONSENSUS: [LIVD]-[FYSA]-x(4)-C-[PV]-[FYW]-C-x(2)-[TAV]-x(2,3)-[LIV].
 NAME: Type-1 copper (blue) proteins signature.
 CONSENSUS: [GA]-x(0,2)-[YSA]-x(0,1)-[VFY]-x-C-x(1,2)-[PG]-x(0,1)-H-x(2,4)-[MQ].
 NAME: 2Fe-2S ferredoxins, iron-sulfur binding region signature.
 CONSENSUS: C-{C}-{C}-[GA]-{C}-C-[GAST]-[CPDEKRHFYW]-C.
 NAME: Adrenodoxin family, iron-sulfur binding region signature.
 CONSENSUS: C-x(2)-[STAQ]-x-[STAMV]-C-[STA]-T-C-[HR].
 NAME: 4Fe-4S ferredoxins, iron-sulfur binding region signature.
 CONSENSUS: C-x(2)-C-x(2)-C-x(3)-C-[PEG].
 NAME: High potential iron-sulfur proteins signature.
 CONSENSUS: C-x(6,9)-[LIVM]-x(3)-G-[YW]-C-x(2)-[FYW].
 NAME: Rieske iron-sulfur protein signature 1.
 CONSENSUS: C-[TK]-H-L-G-C-[LIVT].
 NAME: Rieske iron-sulfur protein signature 2.
 CONSENSUS: C-P-C-H-x-[GSA].
 NAME: Flavodoxin signature.
 CONSENSUS: [LIV]-[LIVFY]-[FY]-x-[ST]-x(2)-[AGC]-x-T-x(3)-A-x(2)-[LIV].
 NAME: Rubredoxin signature.
 CONSENSUS: [LIVM]-x(3)-W-x-C-P-x-C-[AGD].

NAME: Electron transfer flavoprotein alpha-subunit signature.

CONSENSUS: [LI]-Y-[LIVM]-[AT]-x-G-[IV]-[SD]-G-x-[IV]-Q-H-x(2)-G-x(6)-[IV]-x-A-
CONSENSUS: [IV]-N.

NAME: Electron transfer flavoprotein beta-subunit signature.

CONSENSUS: [IVA]-x-[KR]-x(2)-[DE]-[GD]-[GDE]-x(1,2)-[EQ]-x-[LIV]-x(4)-P-x-[LIVM](2)-
CONSENSUS: [TAC].

NAME: Vertebrate metallothioneins signature.

CONSENSUS: C-x-C-[GSTAP]-x(2)-C-x-C-x(2)-C-x-C-x(2)-C-x-K.

NAME: Ferritin iron-binding regions signature 1.

CONSENSUS: E-x-[KR]-E-x(2)-E-[KR]-[LF]-[LIVMA]-x(2)-Q-N-x-R-x-G-R.

NAME: Ferritin iron-binding regions signature 2.

CONSENSUS: D-x(2)-[LIVMF]-[STAC]-[DH]-F-[LI]-[EN]-x(2)-[FY]-L-x(6)-[LIVM]-[KN].

NAME: Bacterioferritin signature.

CONSENSUS: <M-x-G-x(3)-V-[LIV]-x(2)-[LM]-x(3)-L-x(3)-L.

NAME: Transferrins signature 1.

CONSENSUS: Y-x(0,1)-[VAS]-V-[IVAC]-[IVA]-[IVA]-[RKH]-[RKS]-[GDENSA].

NAME: Transferrins signature 2.

CONSENSUS: Y-x-G-A-[FL]-[KRHNQ]-C-L-x(3,4)-G-[DENQ]-V-[GA]-[FYW].

NAME: Transferrins signature 3.

CONSENSUS: [DENQ]-[YF]-x-[LY]-L-C-x-[DN]-x(5,8)-[LIV]-x(4,5)-C-x(2)-A-x(4)-[HQR]-x-
CONSENSUS: [LIVMFYW]-[LIVM].

NAME: Globins profile.

NAME: Protozoan/cyanobacterial globins signature.

CONSENSUS: F-[LF]-x(5)-G-[PA]-x(4)-G-[KRA]-x-[LIVM]-x(3)-H.

NAME: Plant hemoglobins signature.

CONSENSUS: [SN]-P-x-L-x(2)-H-A-x(3)-F.

NAME: Hemerythrins signature.

CONSENSUS: W-L-x-[NQ]-H-I-x(3)-D-F.

NAME: Arthropod hemocyanins / insect LSPs signature 1.

CONSENSUS: Y-[FYW]-x-E-D-[LIVM]-x(2)-N-x(6)-H-x(3)-P.

NAME: Arthropod hemocyanins / insect LSPs signature 2.

CONSENSUS: T-x(2)-R-D-P-x-[FY]-[FYW].

NAME: Heavy-metal-associated domain.

CONSENSUS: [LIVN]-x(2)-[LIVMFA]-x-C-x-[STAGCDNH]-C-x(3)-[LIVFG]-x(3)-[LIV]-x(9,11)-
CONSENSUS: [IVA]-x-[LVFYS].

NAME: ABC transporters family signature.

CONSENSUS: [LIVMFYC]-[SA]-[SAPGLVFKQH]-G-[DENQMW]-[KRQASPLIMFW]-[KRNQSTAVM]-
CONSENSUS: [KRACLVM]-[LIVMFYPAN]-[PHY]-[LIVMFW]-[SAGCLIVP]-[FYWHP]-[KRHP]-
CONSENSUS: [LIVMFYWSTA].

NAME: Binding-protein-dependent transport systems inner membrane comp. sign.

CONSENSUS: [LIVMFY]-x(8)-[EQR]-[STAGV]-[STAG]-x(3)-G-[LIVMFYSTAC]-x(5)-[LIVMFYSTA]-
CONSENSUS: x(4)-[LIVMFY]-[PKR].

NAME: ABC-2 type transport system integral membrane proteins signature.

CONSENSUS: [LIMST]-x(2)-[LIMW]-x(2)-[LIMCA]-[GSTC]-x-[GSAIV]-x(6)-[LIMGA]-[PGSNQ]-
CONSENSUS: x(9,12)-P-[LIMFT]-x-[HRSY]-x(5)-[RQ].

NAME: Bacterial extracellular solute-binding proteins, family 1 signature.

CONSENSUS: [GAP]-[LIVMFA]-[STAVDN]-x(4)-[GSAV]-[LIVMFY](2)-Y-[ND]-x(3)-[LIVMF]-x-
CONSENSUS: [KNDE].

NAME: Bacterial extracellular solute-binding proteins, family 3 signature.

CONSENSUS: G-[FYIL]-[DE]-[LIVMT]-[DE]-[LIVMF]-x(3)-[LIVMA]-[VAGC]-x(2)-[LIVMAGN].

NAME: Bacterial extracellular solute-binding proteins, family 5 signature.

CONSENSUS: [AG]-x(6,7)-[DNEG]-x(2)-[STAVE]-[LIVMFYWA]-x-[LIVMFY]-x-[LIVM]-[KR]-

CONSENSUS: [KRHDE]-[GDN]-[LIVMA]-[KNGSP]-[FW].
NAME: Serum albumin family signature.
CONSENSUS: [FY]-x(6)-C-C-x(7)-C-[LFY]-x(6)-[LIVMFYW].
NAME: Transthyretin signature 1.
CONSENSUS: S-K-C-P-L-M-V-K-V-L-D-[AS]-V-R-G.
NAME: Transthyretin signature 2.
CONSENSUS: S-P-[FY]-S-[FY]-S-T-T-A-[LIVM]-V-[ST]-x-P.
NAME: Avidin / Streptavidin family signature.
CONSENSUS: [DEN]-x(2)-[KR]-[STA]-x(2)-V-G-x-[DN]-x-[FW]-T-[KR].
NAME: Eukaryotic cobalamin-binding proteins signature.
CONSENSUS: [SN]-V-D-T-[GA]-A-[LIVM]-A-x-L-A-[LIVMF]-T-C.
NAME: Lipocalin signature.
CONSENSUS: [DENG]-x-[DENQGSTARK]-x(0,2)-[DENQARK]-[LIVFY]-{CP}-G-{C}-W-[FYWLRH]-x-
CONSENSUS: [LIVMTA].
NAME: Cytosolic fatty-acid binding proteins signature.
CONSENSUS: [GSAIVK]-x-[FYW]-x-[LIVMF]-x(4)-[NHG]-[FY]-[DE]-x-[LIVMFY]-[LIVM]-x(2)-
CONSENSUS: [LIVMAKR].
NAME: Acyl-CoA-binding protein signature.
CONSENSUS: P-[STA]-x-[DEN]-x-[LIVMF]-x(2)-[LIVMFY]-Y-[GSTA]-x-[FY]-K-Q-[STA](2)-x-G.
NAME: LBP / BPI / CETP family signature.
CONSENSUS: [PA]-[GA]-[LIVMC]-x(2)-R-[IV]-[ST]-x(3)-L-x(5)-[EQ]-x(4)-[LIVM]-[EQK]-
CONSENSUS: x(8)-P.
NAME: Phosphatidylethanolamine-binding protein family signature.
CONSENSUS: [FY]-x-[LIVMF](3)-x-[DC]-P-D-x-P-[SN]-x(10)-H.
NAME: Plant lipid transfer proteins signature.
CONSENSUS: [LIVM]-[PA]-x(2)-C-x-[LIVM]-x-[LIVM]-x-[LIVMFY]-x-[LIVM]-[ST]-x(3)-
CONSENSUS: [DN]-C-x(2)-[LIVM].
NAME: Uteroglobin family signature 1.
CONSENSUS: [GA]-x(3)-I-C-P-x-[LIVMF]-x(3)-[LIVM]-[DE]-x-[LIVMF](2).
NAME: Uteroglobin family signature 2.
CONSENSUS: [DEQ]-x(4)-[SN]-x(5)-[DEQ]-x-I-x(2)-S-[PSE]-[LS]-C.
NAME: Mitochondrial energy transfer proteins signature.
CONSENSUS: P-x-[DE]-x-[LIVAT]-[RK]-x-[LRH]-[LIVMFY]-[QMAIGV].
NAME: Sugar transport proteins signature 1.
CONSENSUS: [LIVMSTAG]-[LIVMFSAG]-x(2)-[LIVMSA]-[DE]-x-[LIVMFYWA]-G-R-[RK]-x(4,6)-
CONSENSUS: [GSTA].
NAME: Sugar transport proteins signature 2.
CONSENSUS: [LIVMF]-x-G-[LIVMFA]-x(2)-G-x(8)-[LIFY]-x(2)-[EQ]-x(6)-[RK].
NAME: LacY family proton/sugar symporters signature 1.
CONSENSUS: G-[LIVM](2)-x-D-[RK]-L-G-L-[RK](2)-x-[LIVM](2)-W.
NAME: LacY family proton/sugar symporters signature 2.
CONSENSUS: P-x-[LIVMF](2)-N-R-[LIVM]-G-x-K-N-[STA]-[LIVM](3).
NAME: PTR2 family proton/oligopeptide symporters signature 1.
CONSENSUS: [GA]-[GAS]-[LIVMFYWA]-[LIVM]-[GAS]-D-x-[LIVMFYWT]-[LIVMFYW]-G-x(3)-[TAV]-
CONSENSUS: [IV]-x(3)-[GSTAV]-x-[LIVMF]-x(3)-[GA].
NAME: PTR2 family proton/oligopeptide symporters signature 2.
CONSENSUS: [FYT]-x(2)-[LMFY]-[FYV]-[LIVMFYWA]-x-[IVG]-N-[LIVMAG]-G-[GSA]-[LIMF].
NAME: Amiloride-sensitive sodium channels signature.
CONSENSUS: Y-x(2)-[EQTF]-x-C-x(2)-[GSTDNL]-C-x-[QT]-x(2)-[LIVMT]-[LIVMS]-x(2)-C-x-C.
NAME: Sodium:alanine symporter family signature.
CONSENSUS: G-G-x-[GA](2)-[LIVM]-F-W-M-W-[LIVM]-x-[STAV]-[LIVMFA](2)-G.

NAME: Sodium:dicarboxylate symporter family signature 1.
 CONSENSUS: P-x(0,1)-G-[DE]-x-[LIVMF](2)-x-[LIVM](2)-[KREQ]-[LIVM](3)-x-P.

NAME: Sodium:dicarboxylate symporter family signature 2.
 CONSENSUS: P-x-G-x-[STA]-x-[NT]-[LIVMC]-D-G-[STAN]-x-[LIVM]-[FY]-x(2)-[LIVM]-x(2)-[LIVM]-[FY]-[LI]-[SA]-Q.

NAME: Sodium:galactoside symporter family signature.
 CONSENSUS: D-x(3)-G-x(3)-[DN]-x(6,8)-G-[KH]-F-[KR]-P-[FYW]-[LIVM](2)-x-[GSTA](2).

NAME: Sodium:neurotransmitter symporter family signature 1.
 CONSENSUS: W-R-F-[GP]-Y-x(4)-N-G-G-G-x-[FY].

NAME: Sodium:neurotransmitter symporter family signature 2.
 CONSENSUS: Y-[LIVMFY]-x(2)-[SC]-[LIVMFY]-[STQ]-x(2)-L-P-W-x(2)-C-x(4)-N-[GST].

NAME: Sodium:solute symporter family signature 1.
 CONSENSUS: [GS]-x(2)-[LIY]-x(3)-[LIVMFYWSTAG](10)-[LIY]-[TAV]-x(2)-G-G-[LMF]-x-
 CONSENSUS: [SAP].

NAME: Sodium:solute symporter family signature 2.
 CONSENSUS: [GAST]-[LIVM]-x(3)-[KR]-x(4)-G-A-x(2)-[GAS]-[LIVMGS]-[LIVMW]-[LIVMGAT]-G-
 CONSENSUS: x-[LIVMG].

NAME: Sodium:sulfate symporter family signature.
 CONSENSUS: [STACP]-S-x(2)-F-x(2)-P-[LIVM]-[GSA]-x(3)-N-x-[LIVM]-V.

NAME: glpT family of transporters signature.
 CONSENSUS: R-G-x(5)-W-N-x(2)-H-N-x-G-G.

NAME: Ammonium transporters signature.
 CONSENSUS: D-[FYWS]-A-G-[GSC]-x(2)-[IV]-x(3)-[SAG](2)-x(2)-[SAG]-[LIVMF]-x(3)-
 CONSENSUS: [LIVMFYWA](2)-x-[GK]-x-R.

NAME: BCCT family of transporters signature.
 CONSENSUS: [GSDN]-W-T-[LIVM]-x-[FY]-W-x-W-W.

NAME: Flagellar motor protein motA family signature.
 CONSENSUS: A-[LMF]-x-[GAT]-T-[LIVF]-x-G-x-[LIVMF]-x(7)-P.

NAME: Formate and nitrite transporters signature 1.
 CONSENSUS: [LIVMA]-[LIVMY]-x-G-[GSTA]-[DES]-L-[FI]-[TN]-[GS].

NAME: Formate and nitrite transporters signature 2.
 CONSENSUS: [GA]-x(2)-[CA]-N-[LIVMFYW](2)-V-C-[LV]-A.

NAME: Prokaryotic sulfate-binding proteins signature 1.
 CONSENSUS: K-x-[NQEK]-[GT]-G-[DQ]-x-[LIVM]-x(3)-Q-S.

NAME: Prokaryotic sulfate-binding proteins signature 2.
 CONSENSUS: N-P-K-[ST]-S-G-x-A-R.

NAME: Sulfate transporters signature.
 CONSENSUS: P-x-Y-[GS]-L-Y-[STAG](2)-x(4)-[LIVMFY](3)-x(3)-[GSTA](2)-S-[KR].

NAME: Amino acid permeases signature.
 CONSENSUS: [STAGC]-G-[PAG]-x(2,3)-[LIVMFYWA](2)-x-[LIVMFYW]-x-[LIVMFWSTAGC](2)-
 CONSENSUS: [STAGC]-x(3)-[LIVMFYW]-x-[LIVMST]-x(3)-[LIMCTA]-[GA]-E-x(5)-[PSAL].

NAME: Aromatic amino acids permeases signature.
 CONSENSUS: I-G-[GA]-G-M-[LF]-[SA]-x-P-x(3)-[SA]-G-x(2)-F.

NAME: Xanthine/uracil permeases family signature.
 CONSENSUS: [LIVM]-P-x-[PASIF]-V-[LIVM]-G-G-x(4)-[LIVM]-[FY]-[GSA]-x-[LIVM]-x(3)-G.

NAME: Anion exchangers family signature 1.
 CONSENSUS: F-G-G-[LIVM](2)-[KR]-D-[LIVM]-[RK]-R-R-Y.

NAME: Anion exchangers family signature 2.
 CONSENSUS: [FI]-L-I-S-L-I-F-I-Y-E-T-F-x-K-L.

NAME: MIP family signature.
 CONSENSUS: [HNQA]-x-N-P-[STA]-[LIVMF]-[ST]-[LIVMF]-[GSTAFY].

NAME: General diffusion Gram-negative porins signature.

CONSENSUS: [LIVMFY]-x(2)-G-x(2)-Y-x-F-x-K-x(2)-[SN]-[STAV]-[LIVMFYW]-V.

NAME: OmpA-like domain.

CONSENSUS: [LIVMA]-x-[GT]-x-[TA]-[DA]-x(2)-[DG]-[GSTP]-x(2)-[LFYDE]-[NQS]-x(2)-

CONSENSUS: [LI]-[SG]-[QE]-[KRQE]-R-A-x(2)-[LV]-x(3)-[LIVMF]-x(4,5)-[LIVM]-x(4)-

CONSENSUS: [LIVM]-x(3)-[SG]-x-G.

NAME: Eukaryotic mitochondrial porin signature.

CONSENSUS: [YH]-x(2)-D-[SPA]-x-[STA]-x(3)-[TAG]-[KR]-[LIVMF]-[DNSTA]-[DNS]-x(4)-

CONSENSUS: [GSTAN]-[LIVMA]-x-[LIVMY].

NAME: Insulin-like growth factor binding proteins signature.

CONSENSUS: G-C-[GS]-C-C-x(2)-C-A-x(6)-C.

NAME: GPR1/FUN34/yaaH family signature.

CONSENSUS: N-P-[AV]-P-[LF]-G-L-x-[GSA]-F.

NAME: GNS1/SUR4 family signature.

CONSENSUS: L-x-F-L-H-x-Y-H-H.

NAME: 43 Kd postsynaptic protein signature.

CONSENSUS: G-Q-D-Q-T-K-Q-Q-I.

NAME: Actins signature 1.

CONSENSUS: [FY]-[LIV]-G-[DE]-E-A-Q-x-[RKQ](2)-G.

NAME: Actins signature 2.

CONSENSUS: W-[IV]-[STA]-[RK]-x-[DE]-Y-[DNE]-[DE].

NAME: Actins and actin-related proteins signature.

CONSENSUS: [LM]-[LIVM]-T-E-[GAPQ]-x-[LIVMFYWHQ]-N-[PSTAQ]-x(2)-N-[KR].

NAME: Annexins repeated domain signature.

CONSENSUS: [TG]-[STV]-x(8)-[LIVMF]-x(2)-R-x(3)-[DEQNH]-x(7)-[IFY]-x(7)-[LIVMF]-

CONSENSUS: x(3)-[LIVMF]-x(11)-[LIVMFA]-x(2)-[LIVMF].

NAME: Caveolins signature.

CONSENSUS: F-E-D-V-I-A-E-P.

NAME: Clathrin light chain signature 1.

CONSENSUS: F-L-A-Q-Q-E-S.

NAME: Clathrin light chain signature 2.

CONSENSUS: [KR]-D-x-S-[KR]-[LIVM]-[KR]-x-[LIVM](3)-x-L-K.

NAME: Clusterin signature 1.

CONSENSUS: C-K-P-C-L-K-x-T-C.

NAME: Clusterin signature 2.

CONSENSUS: C-L-[RK]-M-[RK]-x-[EQ]-C-[ED]-K-C.

NAME: Connexins signature 1.

CONSENSUS: C-[DN]-T-x-Q-P-G-C-x(2)-V-C-Y-D.

NAME: Connexins signature 2.

CONSENSUS: C-x(3,4)-P-C-x(3)-[LIVM]-[DEN]-C-[FY]-[LIVM]-[SA]-[KR]-P.

NAME: Crystallins beta and gamma 'Greek key' motif signature.

CONSENSUS: [LIVMFYWA]-x-[DEHRKSTP]-[FY]-[DEQHKY]-x(3)-[FY]-x-G-x(4)-[LIVMFCST].

NAME: Dynamins family signature.

CONSENSUS: L-P-[RK]-G-[STN]-[GN]-[LIVM]-V-T-R.

NAME: Dynein light chain type 1 signature.

CONSENSUS: H-x-I-x-G-[KR]-x-F-[GA]-S-x-V-[ST]-[HY]-E.

NAME: FtsZ protein signature 1.

CONSENSUS: N-[ST]-D-x-Q-x-L-x(16,18)-G-x-G-[ATV]-G-[GSAN]-x-P-x(2)-G.

NAME: FtsZ protein signature 2.

CONSENSUS: [DNHKR]-[LIVMF]-x-[LIVMF](2)-[VSTAC]-[STAC]-G-x-G-[GK]-G-T-G-[ST]-G-

CONSENSUS: [GSAR]-[STA]-P-[LIVMFT]-[LIVMF]-[SCAV].

NAME: Fungal hydrophobins signature.
 CONSENSUS: [GN]-[DNQPSA]-x-C-[GSTANK]-[GSTADNQ]-[STNQI]-[PTIV]-x-C-C-[DENQKPST].

NAME: Intermediate filaments signature.
 CONSENSUS: [IV]-x-[TACI]-Y-[RKH]-x-[LM]-L-[DE].

NAME: Involucrin signature.
 CONSENSUS: <M-S-[QH]-Q-x-T-[LV]-P-V-T-[LV].

NAME: Kinesin motor domain signature.
 CONSENSUS: [GSA]-[KRHPSTQVM]-[LIVMF]-x-[LIVMF]-[IVC]-D-L-[AH]-G-[SAN]-E.

NAME: Kinesin motor domain profile.

NAME: Kinesin light chain repeat.
 CONSENSUS: [DEQR]-A-L-x(3)-[GEQ]-x(3)-G-x-[DNS]-x-P-x-V-A-x(3)-N-x-L-[AS]-
 CONSENSUS: x(5)-[QR]-x-[KR]-[FY]-x(2)-[AV]-x(4)-[HKNQ].

NAME: Myelin basic protein signature.
 CONSENSUS: V-V-H-F-F-K-N.

NAME: Myelin P0 protein signature.
 CONSENSUS: S-[KR]-S-x-K-[AG]-x-[SA]-E-K-K-[STA]-K.

NAME: Myelin proteolipid protein signature 1.
 CONSENSUS: G-[MV]-A-L-F-C-G-C-G-H.

NAME: Myelin proteolipid protein signature 2.
 CONSENSUS: C-x-[ST]-x-[DE]-x(3)-[ST]-[FY]-x-L-[FY]-I-x(4)-G-A.

NAME: Neuromodulin (GAP-43) signature 1.
 CONSENSUS: <M-L-C-C-[LIVM]-R-R.

NAME: Neuromodulin (GAP-43) signature 2.
 CONSENSUS: S-F-R-G-H-I-x-R-K-K-[LIVM].

NAME: Osteopontin signature.
 CONSENSUS: [KQ]-x-[TA]-x(2)-[GA]-S-S-E-E-K.

NAME: Peripherin / rom-1 signature.
 CONSENSUS: D-[GS]-V-P-F-[ST]-C-C-N-P-x-S-P-R-P-C.

NAME: Profilin signature.
 CONSENSUS: <x(0,1)-[STA]-x(0,1)-W-[DENQH]-x-[YI]-x-[DEQ].

NAME: Surfactant associated polypeptide SP-C palmitoylation sites.
 CONSENSUS: I-P-C-C-P-V.

NAME: Synapsins signature 1.
 CONSENSUS: L-R-R-R-L-S-D-S.

NAME: Synapsins signature 2.
 CONSENSUS: G-H-A-H-S-G-M-G-K-V-K.

NAME: Synaptobrevin signature.
 CONSENSUS: N-[LIVM]-[DENS]-[KL]-V-x-[DEQ]-R-x(2)-[KR]-[LIVM]-[STDE]-x-[LIVM]-x-[DE]-
 CONSENSUS: [KR]-[TA]-[DE].

NAME: Synaptophysin / synaptoporin signature.
 CONSENSUS: L-S-V-[DE]-C-x-N-K-T.

NAME: Tropomyosins signature.
 CONSENSUS: L-K-E-A-E-x-R-A-E.

NAME: Tubulin subunits alpha, beta, and gamma signature.
 CONSENSUS: [SAG]-G-G-T-G-[SA]-G.

NAME: Tubulin-beta mRNA autoregulation signal.
 CONSENSUS: <M-R-[DE]-[IL].

NAME: Tau and MAP proteins tubulin-binding domain signature.
 CONSENSUS: G-S-x(2)-N-x(2)-H-x-[PA]-[AG]-G(2).

NAME: Neuraxin and MAP1B proteins repeated region signature.

CONSENSUS: [STAGDN]-Y-x-Y-E-x(2)-[DE]-[KR]-[STAGCI].
NAME: F-actin capping protein alpha subunit signature 1.
CONSENSUS: V-H-[FY](2)-E-D-G-N-V.
NAME: F-actin capping protein alpha subunit signature 2.
CONSENSUS: F-K-[AE]-L-R-R-x-L-P.
NAME: F-actin capping protein beta subunit signature.
CONSENSUS: C-D-Y-N-R-D.
NAME: Vinculin family talin-binding region signature.
CONSENSUS: [KR]-x-[LIVMF]-x(3)-[LIVMA]-x(2)-[LIVM]-x(6)-R-Q-Q-E-L.
NAME: Vinculin repeated domain signature.
CONSENSUS: [LIVM]-x-[QA]-A-x(2)-W-[IL]-x-[DN]-P.
NAME: Amyloidogenic glycoprotein extracellular domain signature.
CONSENSUS: G-[VT]-E-[FY]-V-C-C-P.
NAME: Amyloidogenic glycoprotein intracellular domain signature.
CONSENSUS: G-Y-E-N-P-T-Y-[KR].
NAME: Cadherins extracellular repeated domain signature.
CONSENSUS: [LIV]-x-[LIV]-x-D-x-N-D-[NH]-x-P.
NAME: Insect cuticle proteins signature.
CONSENSUS: G-x(7)-[DEN]-G-x(6)-Y-x-A-[DNG]-x(2,3)-G-[FY]-x-[AP].
NAME: Gas vesicles protein GVPa signature 1.
CONSENSUS: [LIVM]-x-[DE]-[LIVMFYT]-[LIVM]-[DE]-x-[LIVM](2)-[DKR](2)-G-x-[LIVM](2).
NAME: Gas vesicles protein GVPa signature 2.
CONSENSUS: R-[LIVA](3)-A-[GS]-[LIVMFY]-x-T-x(3)-Y-[AG].
NAME: Gas vesicles protein GVPc repeated domain signature.
CONSENSUS: F-L-x(2)-T-x(3)-R-x(3)-A-x(2)-Q-x(3)-L-x(2)-F.
NAME: Bacterial microcompartments proteins signature.
CONSENSUS: D-x(0,1)-M-x-K-[SAG](2)-x-[IV]-x-[LIVM]-[LIVMA]-[GCS]-x(4)-[GD]-[SGPD]-
CONSENSUS: [GA].
NAME: Flagella basal body rod proteins signature.
CONSENSUS: [GTARYQ]-x(9)-[LIVMYSTA](2)-[GSTA]-[STADEN]-N-[LIVM]-[SAN]-N-x-[SADNFR]-
CONSENSUS: [STV].
NAME: Flagella transport protein flp family signature 1.
CONSENSUS: [PA]-A-[FY]-x-[LIVT]-[STH]-[EQ]-[LI]-x(2)-[GA]-F-[KREQ]-[IM]-G-[LIF].
NAME: Flagella transport protein flp family signature 2.
CONSENSUS: P-[LIVMF]-K-[LIVMF](5)-x-[LIVMA]-[DNLS]-G-W.
NAME: Plant viruses icosahedral capsid proteins 'S' region signature.
CONSENSUS: [FYW]-x-[PSTA]-x(7)-G-x-[LIVM]-x-[LIVM]-x-[FYWI]-x(2)-D-x(5)-P.
NAME: Potexviruses and carlaviruses coat protein signature.
CONSENSUS: [RK]-[FYW]-A-[GAP]-F-D-x-F-x(2)-[LV]-x(3)-[GAST](2).
NAME: Neurotransmitter-gated ion-channels signature.
CONSENSUS: C-x-[LIVMFQ]-x-[LIVMF]-x(2)-[FY]-P-x-D-x(3)-C.
NAME: ATP P2X receptors signature.
CONSENSUS: G-G-x-[LIVM]-G-[LIVM]-x-[IV]-x-W-x-C-[DN]-L-D-x(5)-C-x-P-x-Y-x-F.
NAME: G-protein coupled receptors signature.
CONSENSUS: [GSTALIVMFYWC]-[GSTANCPDE]-[EDPKRH]-x(2)-[LIVMNQGA]-x(2)-[LIVMFT]-
CONSENSUS: [GSTANC]-[LIVMFYWSTAC]-[DENH]-R-[FYWCSTH]-x(2)-[LIVM].
NAME: G-protein coupled receptors family 2 signature 1.
CONSENSUS: C-x(3)-[FYWLIV]-D-x(3,4)-C-[FW]-x(2)-[STAGV]-x(8,9)-C-[PF].
NAME: G-protein coupled receptors family 2 signature 2.
CONSENSUS: Q-G-[LMFCA]-[LIVMFT]-[LIV]-x-[LIVFST]-[LIF]-[VFYH]-C-[LFY]-x-N-x(2)-V.

NAME: G-protein coupled receptors family 3 signature 1.

CONSENSUS: [LV]-x-N-[LIVM](2)-x-L-F-x-I-[PA]-Q-[LIVM]-[STA]-x-[STA](3)-[STAN].

NAME: G-protein coupled receptors family 3 signature 2.

CONSENSUS: C-C-[FYW]-x-C-x(2)-C-x(4)-[FYW]-x(2,4)-[DN]-x(2)-[STAH]-C-x(2)-C.

NAME: G-protein coupled receptors family 3 signature 3.

CONSENSUS: F-N-E-[STA]-K-x-I-[STAG]-F-[ST]-M.

NAME: Visual pigments (opsins) retinal binding site.

CONSENSUS: [LIVMWAC]-[PGAC]-x(3)-[SAC]-K-[STALIMR]-[GSACPNV]-[STACP]-x(2)-[DENF]-

CONSENSUS: [AP]-x(2)-[IY].

NAME: Bacterial rhodopsins signature 1.

CONSENSUS: R-Y-x-[DT]-W-x-[LIVMF]-[ST]-T-P-[LIVM](3).

NAME: Bacterial rhodopsins retinal binding site.

CONSENSUS: [FYIV]-x-[FYVG]-[LIVM]-D-[LIVMF]-x-[STA]-K-x(2)-[FY].

NAME: Receptor tyrosine kinase class II signature.

CONSENSUS: [DN]-[LIV]-Y-x(3)-Y-Y-R.

NAME: Receptor tyrosine kinase class III signature.

CONSENSUS: G-x-H-x-N-[LIVM]-V-N-L-L-G-A-C-T.

NAME: Receptor tyrosine kinase class V signature 1.

CONSENSUS: F-x-[DN]-x-[GAW]-[GA]-C-[LIVM]-[SA]-[LIVM](2)-[SA]-[LV]-[KRHQ]-[LIVA]-

CONSENSUS: x(3)-[KR]-C-[PSAW].

NAME: Receptor tyrosine kinase class V signature 2.

CONSENSUS: C-x(2)-[DE]-G-[DEQ]-W-x(2,3)-[PAQ]-[LIVMT]-[GT]-x-C-x-C-x(2)-G-[HFY]-

CONSENSUS: [EQ].

NAME: Growth factor and cytokines receptors family signature 1.

CONSENSUS: C-[LVFYR]-x(7,8)-[STIVDN]-C-x-W.

NAME: Growth factor and cytokines receptors family signature 2.

CONSENSUS: [STGL]-x-W-[SG]-x-W-S.

NAME: TNFR/NGFR family cysteine-rich region signature.

CONSENSUS: C-x(4,6)-[FYH]-x(5,10)-C-x(0,2)-C-x(2,3)-C-x(7,11)-C-x(4,6)-[DNEQSKP]-

CONSENSUS: x(2)-C.

NAME: TNFR/NGFR family cysteine-rich region domain.

NAME: Integrins alpha chain signature.

CONSENSUS: [FYWS]-[RK]-x-G-F-F-x-R.

NAME: Integrins beta chain cysteine-rich domain signature.

CONSENSUS: C-x-[GNQ]-x(1,3)-G-x-C-x-C-x(2)-C-x-C.

NAME: Natriuretic peptides receptors signature.

CONSENSUS: G-P-x-C-x-Y-x-A-A-x-V-x-R-x(3)-H-W.

NAME: Photosynthetic reaction center proteins signature.

CONSENSUS: [NH]-x(4)-P-x-H-x(2)-[SAG]-x(11)-[SAGC]-x-H-[SAG](2).

NAME: Antenna complexes alpha subunits signature.

CONSENSUS: [LIVFAG]-x-[GASV]-[LIVFA]-x-[IV]-H-x(3)-[LIVM]-[GSTAE]-[STANH]-x(1,3)-

CONSENSUS: [STN]-W-[LIVMFYW].

NAME: Antenna complexes beta subunits signature.

CONSENSUS: [EQ]-x(4)-H-x(5)-[GSTA]-x(3)-[FY]-x(3)-[AG]-x(2)-[AV]-H-x(7)-P.

NAME: Photosystem I psaA and psaB proteins signature.

CONSENSUS: C-D-G-P-G-R-G-G-T-C.

NAME: Photosystem I psaG and psaK proteins signature.

CONSENSUS: G-F-x-[LIVM]-x-[DEA]-x(2)-[GA]-x-[GTA]-[SA]-x-G-H-x-[LIVM]-[GA].

NAME: Phytochrome chromophore attachment site signature.

CONSENSUS: [RGS]-[GSA]-[PV]-H-x-C-H-x(2)-Y.

NAME: Phytochrome chromophore attachment site domain profile.

NAME: Speract receptor repeated domain signature.

CONSENSUS: G-x(5)-G-x(2)-E-x(6)-W-G-x(2)-C-x(3)-[FYW]-x(8)-C-x(3)-G.

NAME: TonB-dependent receptor proteins signature 1.

CONSENSUS: <x(10,115)-[DENF]-[ST]-[LIVMF]-[LIVSTEQ]-V-x-[AGP]-[STANEQPK].

NAME: TonB-dependent receptor proteins signature 2.

CONSENSUS: [LYGSTANE]-x(3)-[GSTAENQ]-x-[PGE]-R-x-[LIVFYWA]-x-[LIVMFTA]-[STAGNQ]-

CONSENSUS: [LIVMFYGT]-x-[LIVMFYWGTDQ]-x-F>.

NAME: Transmembrane 4 family signature.

CONSENSUS: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF](2)-G-C-x-[GA]-[STA]-x(2)-[EG]-x(2)-

CONSENSUS: [CWN]-[LIVM](2).

NAME: Bacterial chemotaxis sensory transducers signature.

CONSENSUS: R-T-E-[EQ]-Q-x(2)-[SA]-[LIVM]-x-[EQ]-T-A-A-S-M-E-Q-L-T-A-T-V.

NAME: ER lumen protein retaining receptor signature 1.

CONSENSUS: G-I-S-x-[KR]-x-Q-x-L-[FY]-x-[LIV](2)-F-x(2)-R-Y.

NAME: ER lumen protein retaining receptor signature 2.

CONSENSUS: L-E-[SA]-V-A-I-[LM]-P-Q-L.

NAME: Ephrins signature.

CONSENSUS: [KRQ]-[LF]-[CST]-x-K-[IF]-Q-x-[FY]-[ST]-[PA]-x(3)-G-x-E-F-x(5)-[FY](2)-

CONSENSUS: x(2)-[SA].

NAME: Granulins signature.

CONSENSUS: C-x-D-x(2)-H-C-C-P-x(4)-C.

NAME: HBGF/FGF family signature.

CONSENSUS: G-x-L-x-[STAGP]-x(6,7)-[DE]-C-x-[FM]-x-E-x(6)-Y.

NAME: PTN/MK heparin-binding protein family signature 1.

CONSENSUS: S-[DE]-C-x-[DE]-W-x-W-x(2)-C-x-P-x-[SN]-x-D-C-G-[LIVMA]-G-x-R-E-G.

NAME: PTN/MK heparin-binding protein family signature 2.

CONSENSUS: C-[KR]-[LIVM]-P-C-N-W-K-K-x-F-G-A-[DE]-C-K-Y-x-F-[EQ]-x-W-G-x-C.

NAME: Nerve growth factor family signature.

CONSENSUS: G-C-[KR]-G-[LIV]-[DE]-x(3)-[YW]-x-S-x-C.

NAME: Platelet-derived growth factor (PDGF) family signature.

CONSENSUS: P-[PS]-C-V-x(3)-R-C-[GSTA]-G-C-C.

NAME: Small cytokines (intercrine/chemokine) C-x-C subfamily signature.

CONSENSUS: C-x-C-[LIVM]-x(5,6)-[LIVMFY]-x(2)-[RKSEQ]-x-[LIVM]-x(2)-[LIVM]-x(5)-

CONSENSUS: [SAG]-x(2)-C-x(3)-[EQ]-[LIVM](2)-x(9,10)-C-L-[DN].

NAME: Small cytokines (intercrine/chemokine) C-C subfamily signature.

CONSENSUS: C-C-[LIFYT]-x(5,6)-[LI]-x(4)-[LIVMF]-x(2)-[FYW]-x(6,8)-C-x(3,4)-[SAG]-

CONSENSUS: [LIVM](2)-[FL]-x(8)-C-[STA].

NAME: TGF-beta family signature.

CONSENSUS: [LIVM]-x(2)-P-x(2)-[FY]-x(4)-C-x-G-x-C.

NAME: TNF family signature.

CONSENSUS: [LV]-x-[LIVM]-x(3)-G-[LIVMF]-Y-[LIVMFY](2)-x(2)-[QEKHL]-[LIVMGT]-x-

CONSENSUS: [LIVMFY].

NAME: TNF family profile.

NAME: Wnt-1 family signature.

CONSENSUS: C-K-C-H-G-[LIVMT]-S-G-x-C.

NAME: Interferon alpha, beta and delta family signature.

CONSENSUS: [FYH]-[FY]-x-[GNRC]-[LIVM]-x(2)-[FY]-L-x(7)-[CY]-A-W.

NAME: Granulocyte-macrophage colony-stimulating factor signature.

CONSENSUS: C-P-[LP]-T-x-E-[ST]-x-C.

NAME: Interleukin-1 signature.

CONSENSUS: [FC]-x-S-[ASLV]-x(2)-P-x(2)-[FYLV]-[LI]-[SCA]-T-x(7)-[LIVM].

NAME: Interleukin-2 signature.

CONSENSUS: T-E-[LF]-x(2)-L-x-C-L-x(2)-E-L.

NAME: Interleukins -4 and -13 signature.

CONSENSUS: L-x-E-[LIVM](2)-x(4,5)-[LIVM]-[TL]-x(5,7)-C-x(4)-[IVA]-x-[DNS]-[LIVMA].

NAME: Interleukin-6 / G-CSF / MGF signature.

CONSENSUS: C-x(9)-C-x(6)-G-L-x(2)-[FY]-x(3)-L.

NAME: Interleukin-7 and -9 signature.

CONSENSUS: N-x-[LAP]-[SCT]-F-L-K-x-L-L.

NAME: Interleukin-10 family signature.

CONSENSUS: [GS]-C-x(2)-[LV]-x(2)-[LIVM](2)-x-F-Y-L-x(2)-V.

NAME: LIF / OSM family signature.

CONSENSUS: [PST]-x(4)-F-[NQ]-x-K-x(3)-C-x-[LF]-L-x(2)-Y-[HK].

NAME: Macrophage migration inhibitory factor family signature.

CONSENSUS: [DE]-P-C-A-x(3)-[LIVM]-x-S-I-G-x-[LIVM]-G.

NAME: Adipokinetic hormone family signature.

CONSENSUS: Q-[LV]-[NT]-[FY]-[ST]-x(2)-W.

NAME: Bombesin-like peptides family signature.

CONSENSUS: W-A-x-G-[SH]-[LF]-M.

NAME: Calcitonin / CGRP / IAPP family signature.

CONSENSUS: C-[SAGDN]-[STN]-x(0,1)-[SA]-T-C-[VMA]-x(3)-[LYF]-x(3)-[LYF].

NAME: Corticotropin-releasing factor family signature.

CONSENSUS: [PQ]-x-[LIVM]-S-[LIVM]-x(2)-[PST]-[LIVMF]-x-[LIVM]-L-R-x(2)-[LIVM].

NAME: Crustacean CHH/MIH/GIH neurohormones family signature.

CONSENSUS: C-[DENK]-D-C-x-N-[LIV]-[FY]-R-x(7)-C-[KR]-x(2)-C.

NAME: Erythropoietin / thrombopoietin signature.

CONSENSUS: P-x(4)-C-D-x-R-[LIVM](2)-x-[KR]-x(14)-C.

NAME: Granins signature 1.

CONSENSUS: [DE]-[SN]-L-[SAN]-x(2)-[DE]-x-E-L.

NAME: Granins signature 2.

CONSENSUS: C-[LIVM](2)-E-[LIVM](2)-S-[DN]-[STA]-L-x-K-x-S-x(3)-[LIVM]-[STA]-x-E-C.

NAME: Galanin signature.

CONSENSUS: G-W-T-L-N-S-A-G-Y-L-L-G-P-H.

NAME: Gastrin / cholecystokinin family signature.

CONSENSUS: Y-x(0,1)-[GD]-[WH]-M-[DR]-F.

NAME: Glucagon / GIP / secretin / VIP family signature.

CONSENSUS: [YH]-[STAIVGD]-[DEQ]-[AGF]-[LIVMSTE]-[FYLR]-x-[DENSTAK]-[DENSTA]-

CONSENSUS: [LIVMFY]-x(9)-[KREQL]-[KRDENQL]-[LVFYWG]-[LIVQ].

NAME: Glycoprotein hormones alpha chain signature 1.

CONSENSUS: C-x-G-C-C-[FY]-S-R-A-[FY]-P-T-P.

NAME: Glycoprotein hormones alpha chain signature 2.

CONSENSUS: N-H-T-x-C-x-C-x-T-C-x(2)-H-K.

NAME: Glycoprotein hormones beta chain signature 1.

CONSENSUS: C-[STAGM]-G-[HFYL]-C-x-[ST].

NAME: Glycoprotein hormones beta chain signature 2.

CONSENSUS: [PA]-V-A-x(2)-C-x-C-x(2)-C-x(4)-[STD]-[DEY]-C-x(6,8)-[PGSTAVM]-x(2)-C.

NAME: Gonadotropin-releasing hormones signature.

CONSENSUS: Q-H-[FYW]-S-x(4)-P-G.

NAME: Insulin family signature.

CONSENSUS: C-C-[P]-x(2)-C-[STDNEKPI]-x(3)-[LIVMFS]-x(3)-C.

NAME: Natriuretic peptides signature.

CONSENSUS: C-F-G-x(3)-D-R-I-x(3)-S-x(2)-G-C.

NAME: Neurohypophysial hormones signature.

CONSENSUS: C-[LIFY](2)-x-N-[CS]-P-x-G.

NAME: Neuromedin U signature.

CONSENSUS: F-[LIVMF]-F-R-P-R-N.

NAME: Endogenous opioids neuropeptides precursors signature.

CONSENSUS: C-x(3)-C-x(2)-C-x(2)-[KRH]-x(6,7)-[LIF]-[DN]-x(3)-C-x-[LIVM]-[EQ]-C-

CONSENSUS: [EQ]-x(8)-W-x(2)-C.

NAME: Pancreatic hormone family signature.

CONSENSUS: [FY]-x(3)-[LIVM]-x(2)-Y-x(3)-[LIVMFY]-x-R-x-R-[YF].

NAME: Parathyroid hormone family signature.

CONSENSUS: V-S-E-x-Q-x(2)-H-x(2)-G.

NAME: Pyrokinins signature.

CONSENSUS: F-[GSTV]-P-R-L-[G >].

NAME: Somatotropin, prolactin and related hormones signature 1.

CONSENSUS: C-x-[ST]-x(2)-[LIVMFY]-x-[LIVMSTA]-P-x(5)-[TALIV]-x(7)-[LIVMFY]-x(6)-

CONSENSUS: [LIVMFY]-x(2)-[STA]-W.

NAME: Somatotropin, prolactin and related hormones signature 2.

CONSENSUS: C-[LIVMFY]-x(2)-D-[LIVMFYSTA]-x(5)-[LIVMFY]-x(2)-[LIVMFYT]-x(2)-C.

NAME: Tachykinin family signature.

CONSENSUS: F-[IVFY]-G-[LM]-M-[G >].

NAME: Thymosin beta-4 family signature.

CONSENSUS: K-L-K-K-T-E-T-Q-E-K-N.

NAME: Urotensin II signature.

CONSENSUS: C-F-W-K-Y-C.

NAME: Cecropin family signature.

CONSENSUS: W-x(0,2)-[KDN]-x(2)-K-[KRE]-[LI]-E-[RKN].

NAME: Mammalian defensins signature.

CONSENSUS: C-x-C-x(3,5)-C-x(7)-G-x-C-x(9)-C-C.

NAME: Arthropod defensins signature.

CONSENSUS: C-x(2,3)-[HN]-C-x(3,4)-[GR]-x(2)-G-G-x-C-x(4,7)-C-x-C.

NAME: Cathelicidins signature 1.

CONSENSUS: Y-x-[ED]-x-V-x-[RQ]-A-[LIVMA]-[DQG]-x-[LIVMFY]-N-[EQ].

NAME: Cathelicidins signature 2.

CONSENSUS: F-x-[LIVM]-K-E-T-x-C-x(10)-C-x-F-[KR]-[KE].

NAME: Endothelin family signature.

CONSENSUS: C-x-C-x(4)-D-x(2)-C-x(2)-[FY]-C.

NAME: Plant thionins signature.

CONSENSUS: C-C-x(5)-R-x(2)-[FY]-x(2)-C.

NAME: Gamma-thionins family signature.

CONSENSUS: [KR]-x-C-x(3)-[SV]-x(2)-[FYWH]-x-[GF]-x-C-x(5)-C-x(3)-C.

NAME: Snake toxins signature.

CONSENSUS: G-C-x(1,3)-C-P-x(8,10)-C-C-x(2)-[PDEN].

NAME: Myotoxins signature.

CONSENSUS: K-x-C-H-x-K-x(2)-H-C-x(2)-K-x(3)-C-x(8)-K-x(2)-C-x(2)-[RK]-x-K-C-C-K-K.

NAME: Scorpion short toxins signature.

CONSENSUS: C-x(3)-C-x(6,9)-[GAS]-K-C-[IMQT]-x(3)-C-x-C.

NAME: Heat-stable enterotoxins signature.

CONSENSUS: C-C-x(2)-C-C-x-P-A-C-x-G-C.

NAME: Aerolysin type toxins signature.

CONSENSUS: [KT]-x(2)-N-W-x(2)-T-[DN]-T.

NAME: Shiga/ricin ribosomal inactivating toxins active site signature.

CONSENSUS: [LIVMA]-x-[LIVMSTA](2)-x-E-[SAGV]-[STAL]-R-[FY]-[RKNQS]-x-[LIVM]-[EQS]-

CONSENSUS: x(2)-[LIVMF].

NAME: Channel forming colicins signature.

CONSENSUS: T-x(2)-W-x-P-[LIVMFY](3)-x(2)-E.

NAME: Hok/gef family cell toxic proteins signature.

CONSENSUS: [LIVMA](4)-C-[LIVMFA]-T-[LIVMA](2)-x(4)-[LIVM]-x-[RG]-x(2)-L-[CY].

NAME: Staphylococcal enterotoxin/Streptococcal pyrogenic exotoxin signature 1.

CONSENSUS: Y-G-G-[LIV]-T-x(4)-N.

NAME: Staphylococcal enterotoxin/Streptococcal pyrogenic exotoxin signature 2.

CONSENSUS: K-x(2)-[LIV]-x(4)-[LIV]-D-x(3)-R-x(2)-L-x(5)-[LIV]-Y.

NAME: Thiol-activated cytolysins signature.

CONSENSUS: [RK]-E-C-T-G-L-x-W-E-W-W-[RK].

NAME: Membrane attack complex components / perforin signature.

CONSENSUS: Y-x(6)-[FY]-G-T-H-[FY].

NAME: Pancreatic trypsin inhibitor (Kunitz) family signature.

CONSENSUS: F-x(3)-G-C-x(6)-[FY]-x(5)-C.

NAME: Bowman-Birk serine protease inhibitors family signature.

CONSENSUS: C-x(5,6)-[DENQKRHSTA]-C-[PASTDH]-[PASTDK]-[ASTDV]-C-[NDKS]-[DEKRHSTA]-C.

NAME: Kazal serine protease inhibitors family signature.

CONSENSUS: C-x(7)-C-x(6)-Y-x(3)-C-x(2,3)-C.

NAME: Soybean trypsin inhibitor (Kunitz) protease inhibitors family signature.

CONSENSUS: [LIVM]-x-D-x-[EDNTY]-[DG]-[RKHDENQ]-x-[LIVM]-x(5)-Y-x-[LIVM].

NAME: Serpins signature.

CONSENSUS: [LIVMFY]-x-[LIVMFYAC]-[DNQ]-[RKHQS]-[PST]-F-[LIVMFY]-[LIVMFYC]-x-

CONSENSUS: [LIVMFAH].

NAME: Potato inhibitor I family signature.

CONSENSUS: [FYW]-P-[EQH]-[LIV](2)-G-x(2)-[STAGV]-x(2)-A.

NAME: Squash family of serine protease inhibitors signature.

CONSENSUS: C-P-x(5)-C-x(2)-D-x-D-C-x(3)-C-x-C.

NAME: Streptomyces subtilisin-type inhibitors signature.

CONSENSUS: C-x-P-x(2,3)-G-x-H-P-x(4)-A-C-[ATD]-x-L.

NAME: Cysteine proteases inhibitors signature.

CONSENSUS: [GSTEQKRV]-Q-[LIVT]-[VAF]-[SAGQ]-G-x-[LIVMNK]-x(2)-[LIVMFY]-x-[LIVMFYA]-

CONSENSUS: [DENQKRHSIV].

NAME: Tissue inhibitors of metalloproteinases signature.

CONSENSUS: C-x-C-x-P-x-H-P-Q-x-A-F-C.

NAME: Cereal trypsin/alpha-amylase inhibitors family signature.

CONSENSUS: C-x(4)-[SAGD]-x(4)-[SPAL]-[LF]-x(2)-C-[RH]-x-[LIVMFY](2)-x(3,4)-C.

NAME: Alpha-2-macroglobulin family thiolester region signature.

CONSENSUS: [PG]-x-[GS]-C-[GA]-E-[EQ]-x-[LIVM].

NAME: Disintegrins signature.

CONSENSUS: C-x(2)-G-x-C-C-x-[NQRS]-C-x-[FM]-x(6)-C-[RK].

NAME: Lambdoid phages regulatory protein CIII signature.

CONSENSUS: E-S-x-L-x-R-x(2)-[KR]-x-L-x(4)-[KR](2)-x(2)-[DE]-x-L.

NAME: Chaperonins cpn60 signature.

CONSENSUS: A-[AS]-x-[DEQ]-E-x(4)-G-G-[GA].

NAME: Chaperonins cpn10 signature.

CONSENSUS: [LIVMFY]-x-P-[ILT]-x-[DEN]-[KR]-[LIVMFA](3)-[KREQ]-x(8,9)-[SG]-x-

CONSENSUS: [LIVMFY](3).

NAME: Chaperonins TCP-1 signature 1.

CONSENSUS: [RKEL]-[ST]-x-[LMFY]-G-P-x-[GSA]-x-x-K-[LIVMF](2).

NAME: Chaperonins TCP-1 signature 2.

CONSENSUS: [LIVM]-[TS]-[NK]-D-[GA]-[AVNHK]-[TAV]-[LIVM](2)-x(2)-[LIVM]-x-[LIVM]-x-

CONSENSUS: [SNH]-[PQH].

NAME: Chaperonins TCP-1 signature 3.

CONSENSUS: Q-[DEK]-x-x-[LIVMGTA]-[GA]-D-G-T.

NAME: Heat shock hsp20 proteins family profile.

NAME: Heat shock hsp70 proteins family signature 1.

CONSENSUS: [IV]-D-L-G-T-[ST]-x-[SC].

NAME: Heat shock hsp70 proteins family signature 2.

CONSENSUS: [LIVMF]-[LIVMFY]-[DN]-[LIVMFS]-G-[GSH]-[GS]-[AST]-x(3)-[ST]-[LIVM]-

CONSENSUS: [LIVMFC].

NAME: Heat shock hsp70 proteins family signature 3.

CONSENSUS: [LIVMY]-x-[LIVMF]-x-G-G-x-[ST]-x-[LIVM]-P-x-[LIVM]-x-[DEQKRSTA].

NAME: Heat shock hsp90 proteins family signature.

CONSENSUS: Y-x-[NQH]-K-[DE]-[IVA]-F-L-R-[ED].

NAME: Chaperonins clpA/B signature 1.

CONSENSUS: D-[AI]-[SGA]-N-[LIVMF](2)-K-[PT]-x-L-x(2)-G.

NAME: Chaperonins clpA/B signature 2.

CONSENSUS: R-[LIVMFY]-D-x-S-E-[LIVMFY]-x-E-[KRQ]-x-[STA]-x-[STA]-[KR]-[LIVM]-x-G-

CONSENSUS: [STA].

NAME: Nt-dnaJ domain signature.

CONSENSUS: [FY]-x(2)-[LIVMA]-x(3)-[FYWHNT]-[DENQSA]-x-L-x-[DN]-x(3)-[KR]-x(2)-[FYI].

NAME: dnaJ domain profile.

NAME: CXXCXGXXG dnaJ domain signature.

CONSENSUS: C-[DEGSTHKR]-x-C-x-G-x-[GK]-[AGSDM]-x(2)-[GSNKR]-x(4,6)-C-x(2,3)-C-x-G-x-G.

NAME: grpE protein signature.

CONSENSUS: [FL]-[DN]-[PHEA]-x(2)-[HM]-x-A-[LIVMTN]-x(16,20)-G-[FY]-x(3)-[DEG]-x(2)-

CONSENSUS: [LIVM]-[RI]-x-[SA]-x-V-x-[IV].

NAME: Bacterial type II secretion system protein C signature.

CONSENSUS: P-x(6)-F-x(4)-L-x(3)-D-[LIVM]-A-[LIVM]-x-[LIVM]-N-x-[LIVM]-x-L.

NAME: Bacterial type II secretion system protein D signature.

CONSENSUS: [GR]-[DEQKG]-[STVM]-[LIVMA](3)-[GA]-G-[LIVMFY]-x(11)-[LIVM]-P-

CONSENSUS: [LIVMFYWGS]-[LIVMF]-[GSAE]-x-[LIVM]-P-[LIVMFYW](2)-x(2)-[LV]-F.

NAME: Bacterial type II secretion system protein E signature.

CONSENSUS: [LIVM]-R-x(2)-P-D-x-[LIVM](3)-G-E-[LIVM]-R-D.

NAME: Bacterial type II secretion system protein F signature.

CONSENSUS: [KRQ]-[LIVMA]-x(2)-[SAIV]-[LIVM]-x-[TY]-P-x(2)-[LIVM]-x(3)-[STAGV]-x(6)-

CONSENSUS: [LMY]-x(3)-[LIVMF](2)-P.

NAME: Bacterial type II secretion system protein N signature.

CONSENSUS: G-T-L-W-x-G-x(11)-L-x(4)-W.

NAME: Bacterial export FHIPEP family signature.

CONSENSUS: R-[LIVM]-[GSA]-E-V-[GSA]-A-R-F-[STV]-L-D-[GSA]-M-P-G-K-Q-M-[GSA]-I-D-

CONSENSUS: [GSA]-D.

NAME: Protein secA signatures.

CONSENSUS: [IV]-x-[IV]-[SA]-T-[NQ]-M-A-G-R-G-x-D-I-x-L.

NAME: Protein secY signature 1.

CONSENSUS: [GST]-[LIVMF](2)-x-[LIVM]-G-[LIVM]-x-P-[LIVMFY](2)-x-[AS]-[GSTQ]-

CONSENSUS: [LIVMFAT](3)-Q-[LIVMFA](2).

NAME: Protein secY signature 2.

CONSENSUS: [LIVMFYW](2)-x-[DE]-x-[LIVMF]-[STN]-x(2)-G-[LIVMF]-[GST]-[NST]-G-x-[GST]-
CONSENSUS: [LIVMF](3).

NAME: Protein secE/sec61-gamma signature.

CONSENSUS: [LIVMFY]-x(2)-[DENQGA]-x(4)-[LIVMTA]-x-[KRV]-x(2)-[KW]-P-x(3)-[SEQ]-x(7)-
CONSENSUS: [LIVT]-[LIVGA]-[LIVFGAST].

NAME: Gram-negative pili assembly chaperone signature.

CONSENSUS: [LIVMFY]-[APN]-x-[DNS]-[KREQ]-E-[STR]-[LIVMAR]-x-[FYWT]-x-[NC]-[LIVM]-
CONSENSUS: x(2)-[LIVM]-P-[PAS].

NAME: Fimbrial biogenesis outer membrane usher protein signature.

CONSENSUS: [VL]-[PASQ]-[PAS]-G-[PAD]-[FY]-x-[LI]-[DNQSTAP]-[DNH]-[LIVMFY].

NAME: SRP54-type proteins GTP-binding domain signature.

CONSENSUS: P-[LIVM]-x-[FYL]-[LIVMAT]-[GS]-x-[GS]-[EQ]-x(4)-[LIVMF].

NAME: Cytochrome c oxidase assembly factor COX10/ctaB/cyoE signature.

CONSENSUS: [ED]-x-D-x(2)-M-x-R-T-x(2)-R-x(4)-G.

NAME: Cyclin-dependent kinases regulatory subunits signature 1.

CONSENSUS: Y-S-x-[KR]-Y-x-[DE](2)-x-[FY]-E-Y-R-H-V-x-[LV]-[PT]-[KRP].

NAME: Cyclin-dependent kinases regulatory subunits signature 2.

CONSENSUS: H-x-P-E-x-H-[IV]-L-L-F-[KR].

NAME: Pentaxin family signature.

CONSENSUS: H-x-C-x-[ST]-W-x-[ST].

NAME: Immunoglobulins and major histocompatibility complex proteins signature.

CONSENSUS: [FY]-x-C-x-[VA]-x-H.

NAME: Prion protein signature 1.

CONSENSUS: A-G-A-A-A-A-G-A-V-V-G-G-L-G-G-Y.

NAME: Prion protein signature 2.

CONSENSUS: E-x-[ED]-x-K-[LIVM](2)-x-[KR]-[LIVM](2)-x-[QE]-M-C-x(2)-Q-Y.

NAME: Cyclins signature.

CONSENSUS: R-x(2)-[LIVMSA]-x(2)-[FYWS]-[LIVM]-x(8)-[LIVMFC]-x(4)-[LIVMFYA]-x(2)-
CONSENSUS: [STAGC]-[LIVMFYQ]-x-[LIVMFYC]-[LIVMFY]-D-[RKH]-[LIVMFYW].

NAME: Proliferating cell nuclear antigen signature 1.

CONSENSUS: [GA]-[LIVMF]-x-[LIVMA]-x-[SAV]-[LIVM]-D-x-[NSAE]-[HKR]-[VI]-x-[LY]-
CONSENSUS: [VGA]-x-[LIVM]-x-[LIVM]-x(4)-F.

NAME: Proliferating cell nuclear antigen signature 2.

CONSENSUS: [RKA]-C-[DE]-[RH]-x(3)-[LIVMF]-x(3)-[LIVM]-x-[SGAN]-[LIVMF]-x-K-
CONSENSUS: [LIVMF](2).

NAME: Actin-depolymerizing proteins signature.

CONSENSUS: P-[DE]-x-[SA]-x-[LIVMT]-[KR]-x-[KR]-M-[LIVM]-[YA]-[STA](3)-x(3)-[LIVMF]-
CONSENSUS: [KR].

NAME: BCL2-like apoptosis inhibitors (spans part of BH3, BH1 and BH2).

NAME: Apoptosis regulator, Bcl-2 family BH1 domain signature.

CONSENSUS: [LVME]-[FT]-x-[GSD]-[GL]-x(1,2)-[NS]-[YW]-G-R-[LIV]-[LIVC]-[GAT]-
CONSENSUS: [LIVMF](2)-x-F-[GSAE]-[GSARY].

NAME: Apoptosis regulator, Bcl-2 family BH2 domain signature.

CONSENSUS: W-[LIM]-x(3)-[GR]-G-[WQ]-[DENSAV]-x-[FLGA]-[LIVFTC].

NAME: Apoptosis regulator, Bcl-2 family BH3 domain signature.

CONSENSUS: [LIVAT]-x(3)-L-[KARQ]-x-[IVAL]-G-D-[DESG]-[LIMFV]-[DENS HQ]-[LVSHRQ]-
CONSENSUS: [NSR].

NAME: Apoptosis regulator, Bcl-2 family BH4 domain signature.

CONSENSUS: [DS]-[NT]-R-[AE]-[LI]-V-x-[KD]-[FY]-[LIV]-[GHS]-Y-K-L-[SR]-Q-[RK]-G-
CONSENSUS: [HY]-x-[CW].

NAME: Apoptosis regulator, Bcl-2 family BH4 domain profile.

NAME: Arrestins signature.

CONSENSUS: [FY]-R-Y-G-x-[DE](2)-x-[DE]-[LIVM](2)-G-[LIVM]-x-F-x-[RK]-[DEQ]-[LIVM].

NAME: AAA-protein family signature.

CONSENSUS: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-

CONSENSUS: x-R.

NAME: Ubiquitin domain signature.

CONSENSUS: K-x(2)-[LIVM]-x-[DESAK]-x(3)-[LIVM]-[PA]-x(3)-Q-x-[LIVM]-[LIVMC]-

CONSENSUS: [LIVMFY]-x-G-x(4)-[DE].

NAME: Ubiquitin domain profile.

NAME: ADP-ribosylation factors family signature.

CONSENSUS: [HRQT]-x-[FYWI]-x-[LIVM]-x(4)-A-x(2)-G-x(2)-[LIVM]-x(2)-[GSA]-[LIVMF]-x-

CONSENSUS: [WK]-[LIVM].

NAME: GTP-binding nuclear protein ran signature.

CONSENSUS: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.

NAME: SAR1 family signature.

CONSENSUS: R-x-[LIVM]-E-V-F-M-C-S-[LIVM](2)-x-[KRQ]-x-G-Y-x-E-[AG]-[FI]-x-W-[LIVM]-

CONSENSUS: x-Q-Y.

NAME: Band 7 protein family signature.

CONSENSUS: R-x(2)-[LIV]-[SAN]-x(6)-[LIV]-D-x(2)-T-x(2)-W-G-[LIV]-[KRH]-[LIV]-x-

CONSENSUS: [KR]-[LIV]-E-[LIV]-[KR].

NAME: Trp-Asp (WD) repeats signature.

CONSENSUS: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-

CONSENSUS: [LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

NAME: G-protein gamma subunit profile.

NAME: Ras GTPase-activating proteins signature.

CONSENSUS: [GSN]-x-[LIVMF]-[FY]-[LIVMFY]-R-[LIVMFY](2)-[GACN]-P-[AV]-[LIV](2)-

CONSENSUS: [SGAN]-P.

NAME: Ras GTPase-activating proteins profile.

NAME: Guanine-nucleotide dissociation stimulators CDC24 family signature.

CONSENSUS: L-x(2)-[LIVMFYW]-L-x(2)-P-[LIVM]-x(2)-[LIVM]-x-[KRS]-x(2)-L-x-[LIVM]-x-

CONSENSUS: [DEQ]-[LIVM]-x(3)-[ST].

NAME: Guanine-nucleotide dissociation stimulators CDC25 family signature.

CONSENSUS: [GAP]-[CT]-V-P-[FY]-x(4)-[LIVMFY]-x-[DN]-[LIVM].

NAME: MARCKS family signature 1.

CONSENSUS: G-Q-E-N-G-H-V-[KR].

NAME: MARCKS family phosphorylation site domain.

CONSENSUS: E-T-P-K(5)-x(0,1)-F-S-F-K-K-x-F-K-L-S-G-x-S-F-K-[KR]-[NS]-[KR]-K-E.

NAME: Stathmin family signature 1.

CONSENSUS: P-[KQ]-[KR](2)-[DE]-x-S-L-[EG]-E.

NAME: Stathmin family signature 2.

CONSENSUS: A-E-K-R-E-H-E-[KR]-E-V.

NAME: GTP-binding elongation factors signature.

CONSENSUS: D-[KRSTGANQFYW]-x(3)-E-[KRAQ]-x-[RKQD]-[GC]-[IVMK]-[ST]-[IV]-x(2)-

CONSENSUS: [GSTACKRNQ].

NAME: Elongation factor 1 beta/beta'/delta chain signature 1.

CONSENSUS: [DE]-[DEG]-[DE](2)-[LIVMF]-D-L-F-G.

NAME: Elongation factor 1 beta/beta'/delta chain signature 2.

CONSENSUS: V-Q-S-x-D-[LIVM]-x-A-[FWM]-[NQ]-K-[LIVM].

NAME: Elongation factor 1 gamma chain profile.

NAME: Elongation factor Ts signature 1.

CONSENSUS: L-R-x(2)-T-[GDQ]-x-[GS]-[LIVMF]-x(0,1)-[DENKAC]-x-K-[KRNEQS]-[AV]-L.

NAME: Elongation factor Ts signature 2.
 CONSENSUS: E-[LIVM]-N-[SCV]-[QE]-T-D-F-V-[SA]-[KRN].

NAME: Elongation factor P signature.
 CONSENSUS: K-x-A-x(4)-G-x(2)-[LIV]-x-V-P-x(2)-[LIV]-x(2)-G.

NAME: Eukaryotic initiation factor 1A signature.
 CONSENSUS: [IM]-x-G-x-[GS]-[KRH]-x(4)-[CL]-x-D-G-x(2)-R-x(2)-[RH]-I-x-G.

NAME: Eukaryotic initiation factor 4E signature.
 CONSENSUS: [DE]-[IFY]-x(2)-F-[KR]-x(2)-[LIVM]-x-P-x-W-E-[DV]-x(5)-G-G-[KR]-W.

NAME: Eukaryotic initiation factor 5A hypusine signature.
 CONSENSUS: [PT]-G-K-H-G-x-A-K.

NAME: Initiation factor 2 signature.
 CONSENSUS: G-x-[LIVM]-x(2)-L-[KR]-[KRHNS]-x-K-x(5)-[LIVM]-x(2)-G-x-[DEN]-C-G.

NAME: Initiation factor 3 signature.
 CONSENSUS: [KR]-[LIVM](2)-[DN]-[FY]-[GSN]-[KR]-[LIVMFYS]-x-[FY]-[DEQT]-x(2)-[KR].

NAME: Translation initiation factor eIF1 signature.
 CONSENSUS: [LIVM]-[EQ]-[LIVM]-Q-G-[DEN]-[KHQ]-[KRV].

NAME: Prokaryotic-type class I peptide chain release factors signature.
 CONSENSUS: [AR]-[STA]-x-G-x-G-G-Q-[HNGCS]-V-N-x(3)-[ST]-A-[IV].

NAME: Transcription termination factor nusG signature.
 CONSENSUS: [LIVM]-F-G-[KRW]-x-T-P-[IV]-x-[LIVM].

NAME: Calponin family repeat.
 CONSENSUS: [LIVM]-x-[LS]-Q-[MAS]-G-[STY]-[NT]-[KRQ]-x(2)-[STN]-Q-x-G-x(3,4)-G.

NAME: CAP protein signature 1.
 CONSENSUS: [LIVM](2)-x-R-L-[DE]-x(4)-R-L-E.

NAME: CAP protein signature 2.
 CONSENSUS: D-[LIVMFY]-x-E-x-[PA]-x-P-E-Q-[LIVMFY]-K.

NAME: Calreticulin family signature 1.
 CONSENSUS: [KRHN]-x-[DEQN]-[DEQNK]-x(3)-C-G-G-[AG]-[FY]-[LIVM]-[KN]-[LIVMFY](2).

NAME: Calreticulin family signature 2.
 CONSENSUS: [LIVM](2)-F-G-P-D-x-C-[AG].

NAME: Calreticulin family repeated motif signature.
 CONSENSUS: [IV]-x-D-x-[DENST]-x(2)-K-P-[DEH]-D-W-[DEN].

NAME: Calsequestrin signature 1.
 CONSENSUS: [EQ]-[DE]-G-L-[DN]-F-P-x-Y-D-G-x-D-R-V.

NAME: Calsequestrin signature 2.
 CONSENSUS: [DE]-L-E-D-W-[LIVM]-E-D-V-L-x-G-x-[LIVM]-N-T-E-D-D-D.

NAME: S-100/ICaBP type calcium binding protein signature.
 CONSENSUS: [LIVMFYW](2)-x(2)-[LK]-D-x(3)-[DN]-x(3)-[DNSG]-[FY]-x-[ES]-[FYVC]-x(2)-
 CONSENSUS: [LIVMFS]-[LIVMF].

NAME: Hemolysin-type calcium-binding region signature.
 CONSENSUS: D-x-[LI]-x(4)-G-x-D-x-[LI]-x-G-G-x(3)-D.

NAME: HlyD family secretion proteins signature.
 CONSENSUS: [LIVM]-x(2)-G-[LM]-x(3)-[STGAV]-x-[LIVMT]-x-[LIVMT]-[GE]-x-[KR]-x-
 CONSENSUS: [LIVMFYW](2)-x-[LIVMFYW](3).

NAME: P-II protein uridylation site.
 CONSENSUS: Y-[KR]-G-[AS]-[AE]-Y.

NAME: P-II protein C-terminal region signature.
 CONSENSUS: [ST]-x(3)-G-[DY]-G-[KR]-[IV]-[FW]-[LIVM]-x(2)-[LIVM].

NAME: 14-3-3 proteins signature 1.
 CONSENSUS: R-N-L-[LIV]-S-[VG]-[GA]-Y-[KN]-N-[IVA].

NAME: 14-3-3 proteins signature 2.

CONSENSUS: Y-K-[DE]-S-T-L-I-[IM]-Q-L-[LF]-[RHC]-D-N-[LF]-T-[LS]-W-[TAN]-[SAD].

NAME: ATP1G1 / PLM / MAT8 family signature.

CONSENSUS: [DNS]-x-F-x-Y-D-x(2)-[ST]-[LIVM]-[RQ]-x(2)-G.

NAME: BTG1 family signature 1.

CONSENSUS: Y-x(2)-[HP]-W-[FY]-[AP]-E-x-P-x-K-G-x-[GA]-[FY]-R-C-[IV]-[RH]-[IV].

NAME: BTG1 family signature 2.

CONSENSUS: [LV]-P-x-[DE]-[LM]-[ST]-[LIVM]-W-[IV]-D-P-x-E-V-[SC]-x-[RQ]-x-G-E.

NAME: Cullin family signature.

CONSENSUS: [LIV]-K-x(2)-[LIV]-x(2)-L-I-[DEQ]-[KRHNQ]-x-Y-[LIVM]-x-R-x(6,7)-[FY]-x-

CONSENSUS: Y-x-[SA]>.

NAME: Cullin family profile.

NAME: Enhancer of rudimentary signature.

CONSENSUS: Y-D-I-[SA]-x-L-[FY]-x-F-[IV]-D-x(3)-D-[LIV]-S.

NAME: G10 protein signature 1.

CONSENSUS: L-C-C-x-[KR]-C-x(4)-[DE]-x-N-x(4)-C-x-C-R-V-P.

NAME: G10 protein signature 2.

CONSENSUS: C-x-H-C-G-C-[KRH]-G-C-[SA].

NAME: Glucokinase regulatory protein family signature.

CONSENSUS: G-[PA]-E-x-[LIV]-[STA]-G-S-[ST]-R-[LIVM]-K-[STGA](3)-x(2)-K.

NAME: GTP1/OBG family signature.

CONSENSUS: D-[LIVM]-P-G-[LIVM](2)-[DEY]-[GN]-A-x(2)-G-x-G.

NAME: HIT family signature.

CONSENSUS: [NQA]-x(4)-[GAV]-x-[QF]-x-[LIVM]-x-H-[LIVMFYT]-H-[LIVMFT]-H-[LIVMF](2)-

CONSENSUS: [PSGA].

NAME: Caseins alpha/beta signature.

CONSENSUS: C-L-[LV]-A-x-A-[LVF]-A.

NAME: Clathrin adaptor complexes medium chain signature 1.

CONSENSUS: [IVT]-[GSP]-W-R-x(2,3)-[GAD]-x(2)-[HY]-x(2)-N-x-[LIVMAFY](3)-D-[LIVM]-

CONSENSUS: [LIVMT]-E.

NAME: Clathrin adaptor complexes medium chain signature 2.

CONSENSUS: [LIV]-x-F-I-P-P-x-G-x-[LIVMFY]-x-L-x(2)-Y.

NAME: Clathrin adaptor complexes small chain signature.

CONSENSUS: [LIVM](2)-Y-[KR]-x(4)-L-Y-F.

NAME: Ependymins signature 1.

CONSENSUS: F-E-E-G-x-[LIVMF]-Y-[ED]-I-D-x(2)-N-[QE]-S-C-[RKH](2).

NAME: Ependymins signature 2.

CONSENSUS: [QE]-[LIVMA]-F-x(2)-P-[STA]-[FY]-C-[DE]-[GA]-[LIVM]-x(2)-[DE](2).

NAME: Syntaxin / epimorphin family signature.

CONSENSUS: [RQ]-x(3)-[LIVMA]-x(2)-[LIVM]-[ESH]-x(2)-[LIVMT]-x-[DEV]-[LIVM]-x(2)-

CONSENSUS: [LIVM]-[FS]-x(2)-[LIVM]-x(3)-[LIVT]-x(2)-Q-[GADEQ]-x(2)-[LIVM]-[DNQT]-x-

CONSENSUS: [LIVMF]-[DESV]-x(2)-[LIVM].

NAME: Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

CONSENSUS: [GDER]-H-[FYWH]-T-Q-[LIVM](2)-W-x(2)-[STN].

NAME: Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

CONSENSUS: [LIVMFYH]-[LIVMFY]-x-C-[NQRHS]-Y-x-[PARH]-x-[GL]-N-[LIVMFYWDN].

NAME: Fetuin family signature 1.

CONSENSUS: C-x(56)-C-x(10)-C-x(13)-C-x(17,18)-C-x(13)-C-x(2)-C-x(58)-C-x(10,11)-

CONSENSUS: C-x(10,12)-C-x(16,22)-C.

NAME: Fetuin family signature 2.

CONSENSUS: L-E-T-x-C-H-x-L-D-P-T-P.

NAME: Legume lectins beta-chain signature.

CONSENSUS: [LIV]-[STAG]-V-[DEQV]-[FLI]-D-[ST].

NAME: Legume lectins alpha-chain signature.

CONSENSUS: [LIV]-x-[EDQ]-[FYWKR]-V-x-[LIV]-G-[LF]-[ST].

NAME: Vertebrate galactoside-binding lectin signature.

CONSENSUS: W-[GEK]-x-[EQ]-x-[KRE]-x(3,6)-[PCTF]-[LIVMF]-[NQE GSKV]-x-[GH]-x(3)-[DENKHS]-[LIVMFC].

NAME: Lysosome-associated membrane glycoproteins duplicated domain signature.

CONSENSUS: [STA]-C-[LIVM]-[LIVMFYW]-A-x-[LIVMFYW]-x(3)-[LIVMFYW]-x(3)-Y.

NAME: LAMP glycoproteins transmembrane and cytoplasmic domain signature.

CONSENSUS: C-x(2)-D-x(3,4)-[LIVM](2)-P-[LIVM]-x-[LIVM]-G-x(2)-[LIVM]-x-G-[LIVM](2)-x-[LIVM](4)-A-[FY]-x-[LIVM]-x(2)-[KR]-[RH]-x(1,2)-[STAG](2)-Y-[EQ].

NAME: Glycophorin A signature.

CONSENSUS: I-I-x-[GAC]-V-M-A-G-[LIVM](2).

NAME: PMP-22 / EMP / MP20 family signature 1.

CONSENSUS: [LIVMF](4)-[SA]-T-x(2)-[DNKS]-x-W-x(9,13)-[LIV]-W-x(2)-C.

NAME: PMP-22 / EMP / MP20 family signature 2.

CONSENSUS: [RQ]-[AV]-x-M-[IV]-L-S-x-[LI]-x(4)-[GSA]-[LIVMF](3).

NAME: Oxysterol-binding protein family signature.

CONSENSUS: E-[KQ]-x-S-H-[HR]-P-P-x-[STACF]-A.

NAME: Yeast PIR proteins repeats signature.

CONSENSUS: S-Q-[IV]-[STGNH]-D-G-Q-[LIV]-Q-[AIV]-[STA].

NAME: Seminal vesicle protein I repeats signature.

CONSENSUS: [IVM]-x-G-Q-D-x-V-K-x(5)-[KN]-G-x(3)-[STLV].

NAME: Seminal vesicle protein II repeats signature.

CONSENSUS: [GSA]-Q-x-K-S-[FY]-x-Q-x-K-[SA].

NAME: Serum amyloid A proteins signature.

CONSENSUS: A-R-G-N-Y-[ED]-A-x-[QKR]-R-G-x-G-G-x-W-A.

NAME: Spermadhesins family signature 1.

CONSENSUS: C-G-x(2)-[LI]-x(4)-G-x-I-x(9)-C-x-W-T.

NAME: Spermadhesins family signature 2.

CONSENSUS: C-x-K-E-x-[LIVM]-E-[LIVM]-x-[DE]-x(3)-[GS]-x(5)-K-x-C.

NAME: Stress-induced proteins SRP1/TIP1 family signature.

CONSENSUS: P-W-Y-[ST](2)-R-L.

NAME: Glypicans signature.

CONSENSUS: C-x(2)-C-x-G-[LIVM]-x(4)-P-C-x(2)-[FY]-C-x(2)-[LIVM]-x(2)-G-C.

NAME: Syndecans signature.

CONSENSUS: [FY]-R-[IM]-[KR]-K(2)-D-E-G-S-Y.

NAME: Tissue factor signature.

CONSENSUS: W-K-x-K-C-x(2)-T-x-[DEN]-T-E-C-D-[LIVM]-T-D-E.

NAME: Translationally controlled tumor protein signature 1.

CONSENSUS: [IA]-G-[GAS]-N-[PA]-S-A-E-[GDE]-[PAGE]-x(0,1)-[DEG]-x-[DEN]-x(2)-[DE].

NAME: Translationally controlled tumor protein signature 2.

CONSENSUS: [FL]-[FY]-[IVT]-G-E-x-[MA]-x(2,5)-[DEN]-[GAS]-x-[LV]-[AV]-x(3)-[FY]-[KR]-[DE].

NAME: Tub family signature 1.

CONSENSUS: F-[KHQ]-G-R-V-[ST]-x-A-S-V-K-N-F-Q.

NAME: Tub family signature 2.

CONSENSUS: A-F-[AG]-I-[SAC]-[LIVM]-[ST]-S-F-x-[GST]-K-x-A-C-E.

NAME: HCP repeats signature.

CONSENSUS: H-R-H-R-G-H-x(2)-[DE](7).

NAME: Bacterial ice-nucleation proteins octamer repeat.
 CONSENSUS: A-G-Y-G-S-T-x-T.

NAME: Cell cycle proteins fisW / rodA / spoVE signature.
 CONSENSUS: [NV]-x(5)-[GTR]-[LIVMA]-x-P-[PTLIVM]-x-G-[LIVM]-x(3)-[LIVMFW](2)-S-[YSA]-
 CONSENSUS: G-G-[STN]-[SA].

NAME: Enterobacterial virulence outer membrane protein signature 1.
 CONSENSUS: G-[LIVMFY]-N-[LIVM]-K-Y-R-Y-E.

NAME: Enterobacterial virulence outer membrane protein signature 2.
 CONSENSUS: [FYW]-x(2)-G-x-G-Y-[KR]-F>.

NAME: Hydrogenases expression/synthesis hypA family signature.
 CONSENSUS: F-[CSA]-[FY]-[DE]-[LIVA](2)-x(3)-[ST]-[LIVM]-x(16)-C-x(2)-C-x(12,15)-
 CONSENSUS: C-P-x-C.

NAME: Hydrogenases expression/synthesis hupF/hupC family signature.
 CONSENSUS: <M-C-[LIV]-[GA]-[LIV]-P-x-[QKR]-[LIV].

NAME: Staphylocoagulase repeat signature.
 CONSENSUS: A-R-P-x(3)-K-x-S-x-T-N-A-Y-N-V-T-T-x(2)-[DN]-G-x(3)-Y-G.

NAME: 11-S plant seed storage proteins signature.
 CONSENSUS: N-G-x-[DE](2)-x-[LIVMF]-C-[ST]-x(11,12)-[PAG]-D.

NAME: Dehydrins signature 1.
 CONSENSUS: S(5)-[DE]-x-[DE]-G-x(1,2)-G-x(0,1)-[KR](4).

NAME: Dehydrins signature 2.
 CONSENSUS: [KR]-[LIM]-K-[DE]-K-[LIM]-P-G.

NAME: Germin family signature.
 CONSENSUS: G-x(4)-H-x-H-P-x-A-x-E-[LIVM].

NAME: Oleosins signature.
 CONSENSUS: [AG]-[ST]-x(2)-[AG]-x(2)-[LIVM]-[SAD]-T-P-[LIVMF](4)-F-S-P-[LIVM](3)-
 CONSENSUS: P-A.

NAME: Small hydrophilic plant seed proteins signature.
 CONSENSUS: G-[EQ]-T-V-V-P-G-G-T.

NAME: Pathogenesis-related proteins BtrvI family signature.
 CONSENSUS: G-x(2)-[LIVMF]-x(4)-E-x(2)-[CSTAEN]-x(8,9)-[GND]-G-[GS]-[CS]-x(2)-K-x(4)-
 CONSENSUS: [FY].

NAME: Pollen proteins Ole e I family signature.
 CONSENSUS: [EQ]-G-x-V-Y-C-D-T-C-R.

NAME: Thaumatin family signature.
 CONSENSUS: G-x-[GF]-x-C-x-T-[GA]-D-C-x(1,2)-G-x(2,3)-C.

NAME: Mrp family signature.
 CONSENSUS: W-x(2)-[LIVM]-D-[LIVMY](4)-D-x-P-P-G-T-[GS]-D.

NAME: Glucose inhibited division protein A family signature 1.
 CONSENSUS: [GS]-P-x-Y-C-P-S-[LIVM]-E-x-K-[LIVM]-x-[KR]-F.

NAME: Glucose inhibited division protein A family signature 2.
 CONSENSUS: A-G-Q-x-[NT]-G-x(2)-G-Y-x-E-[SAG](3)-[QS]-G-[LIVM](2)-A-G-[LIVMT]-N-A.

NAME: NOL1/NOP2/sun family signature.
 CONSENSUS: [FV]-D-[KRA]-[LIVMA]-L-x-D-[AV]-P-C-[ST]-[GA].

NAME: PET112 family signature.
 CONSENSUS: [DN]-x-[DN]-R-x(3)-P-L-[LIV]-E-[LIV]-x-[ST]-x-P.

NAME: Protein smpB signature.
 CONSENSUS: [TA]-G-[LIVM]-x-L-x-G-x-E-[LIVM]-[KQ]-[SA]-[LIVM].

NAME: Hypothetical cof family signature 1.
 CONSENSUS: [LIVFYAN]-[LIVMFA]-x(2)-D-[LIVMF]-[ND]-G-T-[LIV]-[LVY]-[STANLM].

NAME: Hypothetical cof family signature 2.

CONSENSUS: [LIVMF]-G-D-[GSANQ]-x-N-D-x(3)-[LIMFY]-x(2)-[AV]-x(2)-[GSCP]-x(2)-
CONSENSUS: [LMP]-x(2)-[GAS].

NAME: RIO1/ZK632.3/MJ0444 family signature.

CONSENSUS: [LIVM]-V-H-[GA]-D-L-S-E-[FY]-N-x-[LIVM].

NAME: SUA5/yciO/yrnC family signature.

CONSENSUS: [LIVMTA](3)-[LIVMFYC]-[PG]-T-[DE]-[STA]-x-[FY]-[GA]-[LIVM]-[GS].

NAME: Uncharacterized protein family UPF0001 signature.

CONSENSUS: [FW]-H-[FM]-[IV]-G-x-[LIV]-Q-x-[NKR]-K-x(3)-[LIV].

NAME: Uncharacterized protein family UPF0003 signature.

CONSENSUS: G-x-V-x(2)-[LIV]-x(3)-[SA]-x(6)-D-x(3)-[LIVT](3)-P-N-x(2)-[LIVMF](2)-
CONSENSUS: x(5)-N.

NAME: Uncharacterized protein family UPF0004 signature.

CONSENSUS: [LIVM]-x-[LIVMT]-x(2)-G-C-x(3)-C-[STAN]-[FY]-C-x-[LIVM]-x(4)-G.

NAME: Uncharacterized protein family UPF0005 signature.

CONSENSUS: G-[LIVM](2)-[SA]-x(5,8)-G-x(2)-[LIVM]-G-P-x-L-x(4)-[SAG]-x(4,6)-
CONSENSUS: [LIVM](2)-x(2)-A-x(3)-T-A-[LIVM](2)-F.

NAME: Uncharacterized protein family UPF0006 signature 1.

CONSENSUS: [LIVMFY](2)-D-[STA]-H-x-H-[LIVMF]-[DN].

NAME: Uncharacterized protein family UPF0006 signature 2.

CONSENSUS: P-[LIVM]-x-[LIVM]-H-x-R-x-[TA]-x-[DE].

NAME: Uncharacterized protein family UPF0006 signature 3.

CONSENSUS: [LVSA]-[LIVA]-x(2)-[LIVM]-[PS]-x(3)-L-[LIVM]-[LIVMS]-E-T-D-x-P.

NAME: Uncharacterized protein family UPF0007 signature.

CONSENSUS: V-L-[IV]-H-D-[GA]-A-R.

NAME: Uncharacterized protein family UPF0011 signature.

CONSENSUS: S-D-A-G-x-P-x-[LIV]-[SN]-D-P-G.

NAME: Uncharacterized protein family UPF0012 signature.

CONSENSUS: [GTA]-x(2)-[IVT]-C-Y-D-[LIVM]-x-F-P-x(9)-G.

NAME: Uncharacterized protein family UPF0015 signature.

CONSENSUS: [DE]-[LIVMF](3)-R-T-[SG]-G-x(2)-R-x-S-x-[FY]-[LIVM](2)-W-Q.

NAME: Uncharacterized protein family UPF0016 signature.

CONSENSUS: E-[LIVM]-G-D-K-T-F-[LIVMF](2)-A.

NAME: Uncharacterized protein family UPF0017 signature.

CONSENSUS: D-x(8)-[GN]-[LFY]-x(4)-[DET]-[LY]-Y-x(3)-[ST]-x(7)-[IV]-x(2)-[PS]-x-
CONSENSUS: [LIVM]-x-[LIVM]-x(3)-[DN]-D.

NAME: Uncharacterized protein family UPF0019 signature.

CONSENSUS: L-P-V-[VT]-[NQL]-F-[AT]-A-G-G-[LIV]-A-T-P-A-D-A-A-[LM].

NAME: Uncharacterized protein family UPF0020 signature.

CONSENSUS: D-P-[LIVMF]-C-G-[ST]-G-x(3)-[LI]-E.

NAME: Uncharacterized protein family UPF0021 signature.

CONSENSUS: C-K-x(2)-F-x(4)-E-x(22,23)-S-G-G-K-D.

NAME: Uncharacterized protein family UPF0023 signature.

CONSENSUS: D-x-D-E-[LIV]-L-x(4)-V-F-x(3)-S-K-G.

NAME: Uncharacterized protein family UPF0024 signature.

CONSENSUS: G-x-K-D-[KR]-x-A-[LV]-T-x-Q-x-[LIVF]-[SGC].

NAME: Uncharacterized protein family UPF0025 signature.

CONSENSUS: D-V-[LIV]-x(2)-G-H-[ST]-H-x(12)-[LIVMF]-N-P-G.

NAME: Uncharacterized protein family UPF0027 signature.

CONSENSUS: Q-[LIVM]-x-N-x-A-x-[LIVM]-P-x-I-x(6)-[LIVM]-P-D-x-H-x-G-x-G-x(2)-[IV]-G.

NAME: Uncharacterized protein family UPF0028 signature.

CONSENSUS: [GA]-[GS]-G-[GA]-A-R-G-x-[SA]-H-x-G-x(9)-[IV]-x-[IV]-D-x(2)-[GA]-G-x-S-
 CONSENSUS: x-G.

NAME: Uncharacterized protein family UPF0029 signature.

CONSENSUS: G-x(2)-[LIVM](2)-x(2)-[LIVM]-x(4)-[LIVM]-x(5)-[LIVM](2)-x-R-[FYW](2)-G-
 CONSENSUS: G-x(2)-[LIVM]-G.

NAME: Uncharacterized protein family UPF0030 signature.

CONSENSUS: [GA]-L-I-[LIV]-P-G-G-E-S-T-[STA].

NAME: Uncharacterized protein family UPF0031 signature 1.

CONSENSUS: [SAV]-[IVW]-[LVA]-[LIV]-G-[PNS]-G-L-[GP]-x-[DENQT].

NAME: Uncharacterized protein family UPF0031 signature 2.

CONSENSUS: [GA]-G-x-G-D-[TV]-[LT]-[STA]-G-x-[LIVM].

NAME: Uncharacterized protein family UPF0032 signature.

CONSENSUS: Y-x(2)-F-[LIVMA](2)-x-L-x(4)-G-x(2)-F-[EQ]-[LIVMF]-P-[LIVM].

NAME: Uncharacterized protein family UPF0033 signature.

CONSENSUS: L-[DN]-x(2)-[TAG]-x(2)-C-P-x-P-x-[LIVM].

NAME: Uncharacterized protein family UPF0034 signature.

CONSENSUS: [LIVM]-[DNG]-[LIVM]-N-x-G-C-P-x(3)-[LIVMASQ]-x(5)-G-[SAC].

NAME: Uncharacterized protein family UPF0035 signature.

CONSENSUS: L-L-T-x-R-[SA]-x(3)-R-x(3)-G-x(3)-F-P-G-G.

NAME: Uncharacterized protein family UPF0036 signature.

CONSENSUS: H-x-S-G-H-[GA]-x(3)-[DE]-x(3)-[LM]-x(5)-P-x(3)-[LIVM]-P-x-H-G-[DE].

NAME: Uncharacterized protein family UPF0038 signature.

CONSENSUS: G-x-[LI]-x-R-x(2)-L-x(4)-F-x(8)-[LIV]-x(5)-P-x-[LIV].

NAME: Uncharacterized protein family UPF0044 signature.

CONSENSUS: L-[ST]-x(3)-K-x(3)-[KR]-[SGA]-x-[GA]-H-x-L-x-P-[LIV]-x(2)-[LIV]-[GA]-
 CONSENSUS: x(2)-G.

NAME: Uncharacterized protein family UPF0047 signature.

CONSENSUS: S-X(2)-[LIV]-x-[LIV]-x(2)-G-x(4)-G-T-W-Q-x-[LIV].

NAME: Uncharacterized protein family UPF0054 signature.

CONSENSUS: H-[GS]-x-L-H-L-[LI]-G-[FYW]-D-H.

NAME: Uncharacterized protein family UPF0057 signature.

CONSENSUS: [LIV]-x-[STA]-[LIVF](3)-P-P-[LIVA]-[GA]-[IV]-x(4)-[GKN].

NAME: Hypothetical YER057c/yjjV family signature.

CONSENSUS: P-[AT]-R-[SA]-x-[LIVMY]-x(2)-[AK]-x-L-P-x(4)-[LIVM]-E.

NAME: Hypothetical hesB/yadR/yfhF family signature.

CONSENSUS: F-x-[LIVMFY]-x-N-[PG]-[NSK]-x(4)-C-x-C-[GS]-x-S-F.

NAME: Hypothetical yabO/yceC/sfhB family signature.

CONSENSUS: [NHY]-R-[LI]-D-x(2)-T-[ST]-G-[LIVMA]-[LIVMF](2)-[LIVMFG]-[SGAC].

We claim:

1. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_16c16; hfbr2_16f21; hfbr2_16g18; hfbr2_16i12; hfbr2_16k22; hfbr2_16l12; hfbr2_22f21; hfbr2_22h13; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8; hfbr2_23b10; hfbr2_23b21; hfbr2_23f2; hfbr2_23l24; hfbr2_23n16; hfbr2_23o24; hfbr2_23o5; hfbr2_2a2; hfbr2_2b17; hfbr2_2b5; hfbr2_2c1; hfbr2_2c17; hfbr2_2c18; hfbr2_2d15; hfbr2_2d17; hfbr2_2d20; hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2i17; hfbr2_2k14; hfbr2_2k19; hfbr2_3b16; hfbr2_3c18; hfbr2_3f16; hfbr2_3g8; hfbr2_3l2; hfbr2_4l1m15; hfbr2_62b11; hfbr2_62f10; hfbr2_62l19; hfbr2_62n10; hfbr2_62o17; hfbr2_64a11; hfbr2_64a15; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64j18; hfbr2_64k24; hfbr2_64o16; hfbr2_6a17; hfbr2_6b24; hfbr2_6i20; hfbr2_6o17; hfbr2_7l1o20; hfbr2_72b18; hfbr2_72d13; hfbr2_72l12; hfbr2_72m16; hfbr2_72n12; hfbr2_78c24; hfbr2_78d13; hfbr2_78k24; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22; hfbr2_7j4; hfbr2_82c20; hfbr1_10c20; hfbr2_82e17; hfbr1_10e17; hfbr2_82e4;; hfbr1_10e4; hfbr2_82g14;; hfbr1_10g14; hfbr2_82i17;; hfbr1_10; hfbr2_82i24;; hfbr1_10; hfbr2_82m16;; hfbr1_10; hfbr2_82m6;; hfbr1_10; hfkd2_1j9; hfkd2_24a15; hfkd2_24b15; hfkd2_24e23; hfkd2_24n20; hfkd2_24p5; hfkd2_3i13; hfkd2_3o17; hfkd2_46a6; hfkd2_46b10; hfkd2_46d13; hfkd2_46j20; hfkd2_46k19; hfkd2_46m4; hfkd2_47a4; hfkd2_4b6; hfkd2_4c8; hfkd2_4k14; hfkd2_4m11; hmcfl_1a11; hmcfl_1c23; hmcfl_1e15; hmcfl_1g13; htes3_1n3; htes3_14g5; htes3_14h21; htes3_14p14; htes3_14p7; htes3_15a13; Htes3_15c24; htes3_15c6; htes3_15g14; htes3_15h1; htes3_15i5; htes3_15j18; Htes3_15j3; htes3_15k11; htes3_17f10; htes3_17l17; htes3_17n12; htes3_17n18; Htes3_18f3; htes3_18l7; htes3_19f19; htes3_19j17; htes3_1cl1; htes3_1g13; htes3_1k11; htes3_20c21; htes3_20k2; htes3_20m18; htes3_21d4; htes3_21j15; htes3_21l16; htes3_21n23; htes3_22c23; htes3_22g2; htes3_22n13; htes3_23l11; htes3_23n19; Htes3_23n19; htes3_26g22; htes3_27d1; htes3_27k4; htes3_27o14; htes3_28d14; htes3_2a11; htes3_2a17; htes3_2d15; htes3_2e12; htes3_2f14; htes3_2g7; htes3_2h1; htes3_2h15; htes3_2l19; htes3_2m18; htes3_2m20; htes3_2n9; htes3_2ol3; htes3_30f4; Htes3_35b4; htes3_35b5; htes3_35e21; htes3_35g6; htes3_35k16; htes3_35k24; htes3_35n12; htes3_35n24; htes3_35n9; htes3_35p17; htes3_35p22; htes3_4b4; htes3_4f17; htes3_4f5; htes3_4h6; htes3_4o19; htes3_50j4; htes3_50n06;

htes3_50n23; htes3_6b21; htes3_6c11; htes3_6d16; htes3_72k11; Htes3_72k15;
 htes3_72p16; htes3_7b22; htes3_7d17; htes3_7j3; htes3_7j8; htes3_7p10; htes3_7p9;
 htes3_8e24; Htes3_8g11; Htes3_8g5; htes3_8m10; Htes3_8p7; Htes3_9e22; Htes3_9i20;
 Htes3_9k22; hute1_17k7; hute1_18c12; hute1_18i19; hute1_18i4; hute1_18l1;
 hute1_19f19; hute1_19g19; hute1_19g22; hute1_19h17; hute1_19j11; hute1_1i2;
 hute1_20b19; hute1_20g21; hute1_20h13; hute1_20m11; hute1_20m24; hute1_21d15;
 hute1_22d2; hute1_22e12; hute1_22n2; hute1_22o2; hute1_23e13; hute1_23g11;
 hute1_24c19; hute1_24e11; hute1_24j6; hute1_2h3; their complements; and variants thereof.

2. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_16c16; hfbr2_16f21; hfbr2_16g18; hfbr2_16i12; hfbr2_16k22; hfbr2_16l12; hfbr2_22f21; hfbr2_22h13; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8; hfbr2_23b10; hfbr2_23b21; hfbr2_23f2; hfbr2_23l24; ; hfbr2_23n16; hfbr2_23o24; hfbr2_23o5; hfbr2_2a2; hfbr2_2b17; hfbr2_2b5; hfbr2_2c1; hfbr2_2c17; hfbr2_2c18; hfbr2_2d15; hfbr2_2d17; hfbr2_2d20; hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2i17; hfbr2_2k14; hfbr2_2k19; hfbr2_3c18; hfbr2_3f16; hfbr2_3g8; hfbr2_3l2; hfbr2_4l15; hfbr2_62b11; hfbr2_62f10; hfbr2_62l19; hfbr2_62n10; hfbr2_62o17; hfbr2_64a11; hfbr2_64a15; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64j18; hfbr2_64k24; hfbr2_64o16; hfbr2_6a17; hfbr2_6b24; hfbr2_6i20; hfbr2_6o17; hfbr2_7l10; hfbr2_72b18; hfbr2_72d13; hfbr2_72l12; hfbr2_72m16; hfbr2_72n12; hfbr2_78c24; hfbr2_78d13; hfbr2_78k24; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22; hfbr2_7j4; hfbr2_82c20; hfbr1_10c20; hfbr2_82e17; hfbr1_10e17; hfbr2_82e4; hfbr1_10e4; hfbr2_82g14; hfbr1_10g14; hfbr2_82i17; hfbr1_10; hfbr2_82i24; hfbr1_10; hfbr2_82m16; hfbr1_10; hfbr2_82m6; hfbr1_10; their complements; and variants thereof.

3. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_16f21; hfbr2_16k22; hfbr2_22f21; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8; hfbr2_23f2; ; hfbr2_23o24; hfbr2_23o5; hfbr2_2a2; hfbr2_2c1; hfbr2_2c18; hfbr2_2d20; hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2k19; hfbr2_3f16; hfbr2_3l2; hfbr2_62n10; hfbr2_64a11; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64o16; hfbr2_6a17; hfbr2_6i20; hfbr2_7l10;

hfbr2_72d13; hfbr2_72m16; hfbr2_72n12; hfbr2_78d13; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22; hfbr2_7j4; hfbr2_82m16; and hfbr1_10.

4. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfkd2_1j9; hfkd2_24a15; hfkd2_24b15; hfkd2_24e23; hfkd2_24n20; hfkd2_24p5; hfkd2_3i13; hfkd2_3o17; hfkd2_46a6; hfkd2_46b10; hfkd2_46d13; hfkd2_46j20; hfkd2_46k19; hfkd2_46m4; hfkd2_47a4; hfkd2_4b6; hfkd2_4c8; hfkd2_4k14; hfkd2_4m11; their complements; and variants thereof.

5. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfkd2_1j9; hfkd2_24e23; hfkd2_46a6; hfkd2_46b10; hfkd2_46d13; hfkd2_4b6; hfkd2_4c8; their complements; and variants thereof.

6. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hmcfl_1a11; hmcfl_1c23; hmcfl_1e15; hmcfl_1g13; their complements; and variants thereof.

7. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hmcfl_1c23 hmcfl_1g13; their complements; and variants thereof.

8. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hhtes3_1n3; htes3_14g5; htes3_14h21; htes3_14p14; htes3_14p7; htes3_15a13; Htes3_15c24; htes3_15c6; htes3_15g14; htes3_15h1; htes3_15i5; htes3_15j18; Htes3_15j3; htes3_15k11; htes3_17f10; htes3_17i17; htes3_17n12; htes3_17n18; Htes3_18f3; htes3_18i7; htes3_19f19; htes3_19j17; htes3_1c1; htes3_1g13; htes3_1k11; htes3_20c21; htes3_20k2; htes3_20m18; htes3_21d4; htes3_21j15; htes3_21i16; htes3_21n23; htes3_22c23; htes3_22g2; htes3_22n13; htes3_23i11; htes3_23n19; Htes3_23n19; htes3_26g22; htes3_27d1; htes3_27k4; htes3_27o14; htes3_28d14; htes3_2a11; htes3_2a17; htes3_2d15; htes3_2e12; htes3_2f14; htes3_2g7; htes3_2h1; htes3_2h15; htes3_2i19; htes3_2m18; htes3_2m20; htes3_2n9; htes3_2o13; htes3_30f4; Htes3_35b4; htes3_35b5; htes3_35e21;

htes3_35g6; htes3_35k16; htes3_35k24; htes3_35n12; htes3_35n24; htes3_35n9;
htes3_35p17; htes3_35p22; htes3_4b4; htes3_4f17; htes3_4f5; htes3_4h6; htes3_4o19;
htes3_50j4; htes3_50n06; htes3_50n23; htes3_6b21; htes3_6c11; htes3_6d16; htes3_72k11;
Htes3_72k15; htes3_72p16; htes3_7b22; htes3_7d17; htes3_7j3; htes3_7j8; htes3_7p10;
htes3_7p9; htes3_8e24; Htes3_8g11; Htes3_8g5; htes3_8m10; Htes3_8p7; Htes3_9e22;
Htes3_9i20; Htes3_9k22; their complements; and variants thereof.

9. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: htes3_14g5; htes3_14p14; htes3_14p7; htes3_15a13; htes3_15g14; htes3_15h1; htes3_15j18; htes3_17f10; Htes3_18f3; htes3_19f19; htes3_19j17; htes3_20c21; htes3_21n23; htes3_22c23; htes3_22n13; Htes3_23n19; htes3_27o14; htes3_28d14; htes3_2a11; htes3_2d15; htes3_2f14; htes3_2g7; htes3_2h15; htes3_2i19; htes3_2m20; htes3_2n9; htes3_30f4; htes3_35g6; htes3_35n24; htes3_35p17; htes3_4b4; htes3_4f17; htes3_4o19; htes3_50j4; htes3_50n23; htes3_50n06; htes3_6b21; htes3_6d16; htes3_72k11; htes3_7d17; htes3_7j8; Htes3_8g11; Htes3_8g5; Htes3_8p7; Htes3_9e22; Htes3_9i20; Htes3_9k22; their complements; and variants thereof.

10. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_16g18; hfbr2_2k14; Htes3_35b4; htes3_35p22; htes3_7j3; htes3_7p10; hute1_20m11; their complements; and variants thereof.

11. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_16c16; hfbr2_2b5; htes3_15i5; htes3_18i7; htes3_1k11; Htes3_72k15; htes3_7b22; hute1_19g22; hute1_24j6; their complements; and variants thereof.

12. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_2d15; htes3_35e21; hute1_2h3; their complements; and variants thereof.

13. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_23i24; hfbr2_2i17; hfbr2_41m15; hfbr2_62f10; hfbr2_62i19; hfbr2_64j18;

hfkd2_24n20; hfkd2_24p5; hfkd2_4k14; htes3_1g13; htes3_21l16; htes3_23l11; htes3_26g22; htes3_4h6; htes3_72p16; hute1_19h17; hute1_20h13; hute1_24e11; their complements; and variants thereof.

14. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_3g8; hfbr2_62o17; hfbr2_6b24; hfbr2_78k24; hfkd2_24b15; hfkd2_3o17; hfkd2_46j20; htes3_17l17; htes3_17n18; htes3_27d1; htes3_2a17; htes3_35b5; htes3_35k16; htes3_35n12; htes3_35n9; hute1_20b19; hute1_20m24; hute1_23e13; their complements; and variants thereof.

15. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_23b10; hfbr2_3c18; hfbr2_64a15; hfbr2_6o17; hfbr2_72b18; hfbr2_72l12; hfbr2_82i24(hfbr1_10); htes3_14h21; Htes3_15j3; htes3_20m18; htes3_22g2; htes3_2m18; htes3_7p9; htes3_8m10; hute1_18l1; their complements; and variants thereof.

16. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_23b21; hfbr2_23n16; hfbr2_2c17; hfbr2_62b11; hfbr2_78c24; hfbr2_82e4 (hfbr1_10e4); hfbr2_82i17 (hfbr1_10); hfbr2_82m6 (hfbr1_10); hfkd2_46m4; htes3_15k11; htes3_1c1; hhtes3_1n3; htes3_20k2; htes3_21d4; htes3_23n19; htes3_4f5; htes3_6c11; htes3_8e24; hute1_20g21; hute1_22d2; hute1_22e12; their complements; and variants thereof.

17. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfbr2_16i12; hfbr2_16l12; hfbr2_22h13; hfbr2_2b17; hfbr2_2d17; hfbr2_64k24; hfbr2_82c20 (hfbr1_10c20); hfbr2_82e17 (hfbr1_10e17); hfbr2_82g14 (hfbr1_10g14); hfkd2_24a15; hfkd2_3i13; hfkd2_4m11; hmcfl_1a11; hmcfl_1e15; htes3_15c6; htes3_2o13; htes3_27k4; htes3_2h1; htes3_35k24; hute1_19f19; and hute1_24c19; their complements; and variants thereof.

18. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hfkd2_46k19; hfkd2_47a4;

htes3_2e12; htes3_21j15; htes3_17n12; hute1_18i19; hute1_1i2; their complements; and variants thereof.

19. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hute1_17k7; hute1_18c12; hute1_18i19; hute1_18i4; hute1_18l1; hute1_19f19; hute1_19g19; hute1_19g22; hute1_19h17; hute1_19j11; hute1_1i2; hute1_20b19; hute1_20g21; hute1_20h13; hute1_20m11; hute1_20m24; hute1_21d15; hute1_22d2; hute1_22e12; hute1_22n2; hute1_22o2; hute1_23e13; hute1_23g11; hute1_24c19; hute1_24e11; hute1_24j6; hute1_2h3; their complements; and variants thereof.

20. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: hute1_17k7; hute1_18c12; hute1_18i4; hute1_19g19; hute1_19j11; hute1_22n2; hute1_21d15; hute1_22o2; hute1_23g11; their complements; and variants thereof.

21. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hfbr2_16c16; hfbr2_16f21; hfbr2_16g18; hfbr2_16i12; hfbr2_16k22; hfbr2_16l12; hfbr2_22f21; hfbr2_22h13; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8; hfbr2_23b10; hfbr2_23b21; hfbr2_23f2; hfbr2_23l24; ; hfbr2_23n16; hfbr2_23o24; hfbr2_23o5; hfbr2_2a2; hfbr2_2b17; hfbr2_2b5; hfbr2_2c1; hfbr2_2c17; hfbr2_2c18; hfbr2_2d15; hfbr2_2d17; hfbr2_2d20; hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2i17; hfbr2_2k14; hfbr2_2k19; hfbr2_3c18; hfbr2_3f16; hfbr2_3g8; hfbr2_3l2; hfbr2_4l1m15; hfbr2_62b11; hfbr2_62f10; hfbr2_62l19; hfbr2_62n10; hfbr2_62o17; hfbr2_64a11; hfbr2_64a15; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64j18; hfbr2_64k24; hfbr2_64o16; hfbr2_6a17; hfbr2_6b24; hfbr2_6i20; hfbr2_6o17; hfbr2_71o20; hfbr2_72b18; hfbr2_72d13; hfbr2_72l12; hfbr2_72m16; hfbr2_72n12; hfbr2_78c24; hfbr2_78d13; hfbr2_78k24; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22; hfbr2_7j4; hfbr2_82c20; hfbr1_10c20; hfbr2_82e17; hfbr1_10e17; hfbr2_82e4;; hfbr1_10e4; hfbr2_82g14;; hfbr1_10g14; hfbr2_82i17;; hfbr1_10; hfbr2_82i24;; hfbr1_10; hfbr2_82m16;; hfbr1_10; hfbr2_82m6;; hfbr1_10; hfkd2_1j9; hfkd2_24a15; hfkd2_24b15; hfkd2_24e23; hfkd2_24n20; hfkd2_24p5; hfkd2_3i13; hfkd2_3o17; hfkd2_46a6;

hfkd2_46b10; hfkd2_46d13; hfkd2_46j20; hfkd2_46k19; hfkd2_46m4; hfkd2_47a4;
 hfkd2_4b6; hfkd2_4c8; hfkd2_4k14; hfkd2_4m11; hmcfl_1a11; hmcfl_1c23; hmcfl_1e15;
 hmcfl_1g13; hhtes3_1n3; htes3_14g5; htes3_14h21; htes3_14p14; htes3_14p7;
 htes3_15a13; Htes3_15c24; htes3_15c6; htes3_15g14; htes3_15h1; htes3_15i5;
 htes3_15j18; Htes3_15j3; htes3_15k11; htes3_17f10; htes3_17l17; htes3_17n12;
 htes3_17n18; Htes3_18f3; htes3_18l7; htes3_19f19; htes3_19j17; htes3_1c1; htes3_1g13;
 htes3_1k11; htes3_20c21; htes3_20k2; htes3_20m18; htes3_21d4; htes3_21j15;
 htes3_21l16; htes3_21n23; htes3_22c23; htes3_22g2; htes3_22n13; htes3_23l11;
 htes3_23n19; Htes3_23n19; htes3_26g22; htes3_27d1; htes3_27k4; htes3_27o14;
 htes3_28d14; htes3_2a11; htes3_2a17; htes3_2d15; htes3_2e12; htes3_2f14; htes3_2g7;
 htes3_2h1; htes3_2h15; htes3_2l19; htes3_2m18; htes3_2m20; htes3_2n9; htes3_2o13;
 htes3_30f4; Htes3_35b4; htes3_35b5; htes3_35e21; htes3_35g6; htes3_35k16;
 htes3_35k24; htes3_35n12; htes3_35n24; htes3_35n9; htes3_35p17; htes3_35p22;
 htes3_4b4; htes3_4f17; htes3_4f5; htes3_4h6; htes3_4o19; htes3_50j4; htes3_50n06;
 htes3_50n23; htes3_6b21; htes3_6c11; htes3_6d16; htes3_72k11; Htes3_72k15;
 htes3_72p16; htes3_7b22; htes3_7d17; htes3_7j3; htes3_7j8; htes3_7p10; htes3_7p9;
 htes3_8e24; Htes3_8g11; Htes3_8g5; htes3_8m10; Htes3_8p7; Htes3_9e22; Htes3_9i20;
 Htes3_9k22; hute1_17k7; hute1_18c12; hute1_18i19; hute1_18i4; hute1_18l1;
 hute1_19f19; hute1_19g19; hute1_19g22; hute1_19h17; hute1_19j11; hute1_1i2;
 hute1_20b19; hute1_20g21; hute1_20h13; hute1_20m11; hute1_20m24; hute1_21d15;
 hute1_22d2; hute1_22e12; hute1_22n2; hute1_22o2; hute1_23e13; hute1_23g11;
 hute1_24c19; hute1_24e11; hute1_24j6; hute1_2h3; their complements; and variants thereof.

22. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of:

hfbr2_16c16; hfbr2_16f21; hfbr2_16g18; hfbr2_16i12; hfbr2_16k22; hfbr2_16l12;
 hfbr2_22f21; hfbr2_22h13; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8;
 hfbr2_23b10; hfbr2_23b21; hfbr2_23f2; hfbr2_23l24; ; hfbr2_23n16; hfbr2_23o24;
 hfbr2_23o5; hfbr2_2a2; hfbr2_2b17; hfbr2_2b5; hfbr2_2c1; hfbr2_2c17; hfbr2_2c18;
 hfbr2_2d15; hfbr2_2d17; hfbr2_2d20; hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2i17;
 hfbr2_2k14; hfbr2_2k19; hfbr2_3c18; hfbr2_3f16; hfbr2_3g8; hfbr2_3l2; hfbr2_4l15;
 hfbr2_62b11; hfbr2_62f10; hfbr2_62l19; hfbr2_62n10; hfbr2_62o17; hfbr2_64a11;

hfbr2_64a15; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64j18;
 hfbr2_64k24; hfbr2_64o16; hfbr2_6a17; hfbr2_6b24; hfbr2_6i20; hfbr2_6o17;
 hfbr2_71o20; hfbr2_72b18; hfbr2_72d13; hfbr2_72i12; hfbr2_72m16; hfbr2_72n12;
 hfbr2_78c24; hfbr2_78d13; hfbr2_78k24; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22;
 hfbr2_7j4; hfbr2_82c20; hfbr1_10c20; hfbr2_82e17; hfbr1_10e17; hfbr2_82e4;
 hfbr1_10e4; hfbr2_82g14; hfbr1_10g14; hfbr2_82i17; hfbr1_10; hfbr2_82i24; hfbr1_10;
 hfbr2_82m16; hfbr1_10; hfbr2_82m6; hfbr1_10; complements of the nucleic acid
 sequences; and variants thereof.

23. A computer readable medium, comprising in electronic form at least one
 nucleic acid or protein sequence of a clone selected from the group consisting of:
 hfbr2_16f21; hfbr2_16k22; hfbr2_22f21; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8;
 hfbr2_23f2; ; hfbr2_23o24; hfbr2_23o5; hfbr2_2a2; hfbr2_2c1; hfbr2_2c18; hfbr2_2d20;
 hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2k19; hfbr2_3f16; hfbr2_3i2; hfbr2_62n10;
 hfbr2_64a11; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64k24;
 hfbr2_64o16; hfbr2_6a17; hfbr2_6i20; hfbr2_71o20; hfbr2_72d13; hfbr2_72m16;
 hfbr2_72n12; hfbr2_78d13; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22; hfbr2_7j4; hfbr2_82m16;
 hfbr1_10; complements of the nucleic acid sequences; and variants thereof.

24. A computer readable medium, comprising in electronic form at least one
 nucleic acid or protein sequence of a clone selected from the group consisting of:
 hfkd2_1j9; hfkd2_24a15; hfkd2_24b15; hfkd2_24e23; hfkd2_24n20; hfkd2_24p5;
 hfkd2_3i13; hfkd2_3o17; hfkd2_46a6; hfkd2_46b10; hfkd2_46d13; hfkd2_46j20;
 hfkd2_46k19; hfkd2_46m4; hfkd2_47a4; hfkd2_4b6; hfkd2_4c8; hfkd2_4k14;
 hfkd2_4m11; complements of the nucleic acid sequences; and variants thereof.

25. A computer readable medium, comprising in electronic form at least one
 nucleic acid or protein sequence of a clone selected from the group consisting of: hfkd2_1j9;
 hfkd2_24e23; hfkd2_46a6; hfkd2_46b10; hfkd2_46d13; hfkd2_4b6; hfkd2_4c8;
 complements of the nucleic acid sequences; and variants thereof.

26. A computer readable medium, comprising in electronic form at least one
 nucleic acid or protein sequence of a clone selected from the group consisting of:

hmcfl_1a11; hmcfl_1c23; hmcfl_1e15; hmcfl_1g13; complements of the nucleic acid sequences; and variants thereof.

27. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hmcfl_1c23; hmcfl_1g13; complements of the nucleic acid sequences; and variants thereof.

28. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hhtes3_1n3; htes3_14g5; htes3_14h21; htes3_14p14; htes3_14p7; htes3_15a13; Htes3_15c24; htes3_15c6; htes3_15g14; htes3_15h1; htes3_15i5; htes3_15j18; Htes3_15j3; htes3_15k11; htes3_17f10; htes3_17l17; htes3_17n12; htes3_17n18; Htes3_18f3; htes3_18l7; htes3_19f19; htes3_19j17; htes3_1c1; htes3_1g13; htes3_1k11; htes3_20c21; htes3_20k2; htes3_20m18; htes3_21d4; htes3_21j15; htes3_21l16; htes3_21n23; htes3_22c23; htes3_22g2; htes3_22n13; htes3_23l11; htes3_23n19; Htes3_23n19; htes3_26g22; htes3_27d1; htes3_27k4; htes3_27o14; htes3_28d14; htes3_2a11; htes3_2a17; htes3_2d15; htes3_2e12; htes3_2f14; htes3_2g7; htes3_2h1; htes3_2h15; htes3_2l19; htes3_2m18; htes3_2m20; htes3_2n9; htes3_2o13; htes3_30f4; Htes3_35b4; htes3_35b5; htes3_35e21; htes3_35g6; htes3_35k16; htes3_35k24; htes3_35n12; htes3_35n24; htes3_35n9; htes3_35p17; htes3_35p22; htes3_4b4; htes3_4f17; htes3_4f5; htes3_4h6; htes3_4o19; htes3_50j4; htes3_50n06; htes3_50n23; htes3_6b21; htes3_6c11; htes3_6d16; htes3_72k11; Htes3_72k15; htes3_72p16; htes3_7b22; htes3_7d17; htes3_7j3; htes3_7j8; htes3_7p10; htes3_7p9; htes3_8e24; Htes3_8g11; Htes3_8g5; htes3_8m10; Htes3_8p7; Htes3_9e22; Htes3_9i20; Htes3_9k22; complements of the nucleic acid sequences; and variants thereof.

29. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: htes3_14g5; htes3_14p14; htes3_14p7; htes3_15a13; htes3_15g14; htes3_15h1; htes3_15j18; htes3_17f10; htes3_17n18; Htes3_18f3; htes3_19f19; htes3_19j17; htes3_20c21; htes3_21n23; htes3_22c23; htes3_22n13; Htes3_23n19; htes3_27o14; htes3_28d14; htes3_2a11; htes3_2d15; htes3_2f14; htes3_2g7; htes3_2h15; htes3_2l19; htes3_2m20; htes3_2n9; htes3_30f4; htes3_35g6; htes3_35n24; htes3_35p17; htes3_4b4; htes3_4f17;

htes3_4o19; htes3_50j4; htes3_50n23; htes3_50n06; htes3_6b21; htes3_6d16; htes3_72k11; htes3_7d17; htes3_7j8; Htes3_8g11; Htes3_8g5; Htes3_8p7; Htes3_9e22; Htes3_9i20; Htes3_9k22; complements of the nucleic acid sequences; and variants thereof.

30. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hfbr2_16g18; hfbr2_2k14; Htes3_35b4; htes3_35p22; htes3_7j3; htes3_7p10; hute1_20m11; complements of the nucleic acid sequences; and variants thereof.

31. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hfbr2_16c16; hfbr2_2b5; htes3_15i5; htes3_18l7; htes3_1k11; Htes3_72k15; htes3_7b22; hute1_19g22; hute1_24j6; complements of the nucleic acid sequences; and variants thereof.

32. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hfbr2_2d15; htes3_35e21; hute1_2h3; complements of the nucleic acid sequences; and variants thereof.

33. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hfbr2_23l24; hfbr2_2i17; hfbr2_41m15; hfbr2_62f10; hfbr2_62l19; hfbr2_64j18; hfkd2_24n20; hfkd2_24p5; hfkd2_4k14; htes3_1g13; htes3_21l16; htes3_23l11; htes3_26g22; htes3_4h6; htes3_72p16; hute1_19h17; hute1_20h13; hute1_24e11; complements of the nucleic acid sequences; and variants thereof.

34. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hfbr2_3g8; hfbr2_62o17; hfbr2_6b24; hfbr2_78k24; hfkd2_24b15; hfkd2_3o17; hfkd2_46j20; htes3_17l17; Htes3_17n18; htes3_27d1; htes3_2a17; htes3_35b5; htes3_35k16; htes3_35n12; htes3_35n9; hute1_20b19; hute1_20m24; hute1_23e13; complements of the nucleic acid sequences; and variants thereof.

35. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of:

hfbr2_23b10; hfbr2_3c18; hfbr2_64a15; hfbr2_6o17; hfbr2_72b18; hfbr2_72l12;
hfbr2_82i24(hfbr1_10); htes3_14h21; Htes3_15j3; htes3_20m18; htes3_22g2; htes3_2m18;
htes3_7p9; htes3_8m10; hute1_18l1; complements of the nucleic acid sequences; and
variants thereof.

36. A computer readable medium, comprising in electronic form at least one
nucleic acid or protein sequence of a clone selected from the group consisting of:
hfbr2_23b21; hfbr2_23n16; hfbr2_2c17; hfbr2_62b11; hfbr2_78c24; hfbr2_82e4
(hfbr1_10e4); hfbr2_82i17 (hfbr1_10); hfbr2_82m6 (hfbr1_10); hfkd2_46m4; htes3_15k11;
htes3_1c1; hhtes3_1n3; htes3_20k2; htes3_21d4; htes3_23n19; htes3_4f5; htes3_6c11;
htes3_8e24; hute1_20g21; hute1_22d2; hute1_22e12; complements of the nucleic acid
sequences; and variants thereof.

37. A computer readable medium, comprising in electronic form at least one
nucleic acid or protein sequence of a clone selected from the group consisting of:
hfbr2_16i12; hfbr2_16l12; hfbr2_22h13; hfbr2_2b17; hfbr2_2d17; hfbr2_64k24;
hfbr2_82c20 (hfbr1_10c20); hfbr2_82e17 (hfbr1_10e17); hfbr2_82g14 (hfbr1_10g14);
hfkd2_24a15; hfkd2_3i13; hfkd2_4m11; hmcf1_1a11; hmcf1_1e15; htes3_15c6;
htes3_2ol3; htes3_27k4; htes3_2h1; htes3_35k24; hute1_19f19; and hute1_24c19;
complements of the nucleic acid sequences; and variants thereof.

38. A computer readable medium, comprising in electronic form at least one
nucleic acid or protein sequence of a clone selected from the group consisting of:
hfkd2_46k19; hfkd2_47a4; htes3_2e12; htes3_21j15; htes3_17n12; hute1_18i19;
hute1_1i2; complements of the nucleic acid sequences; and variants thereof.

39. A computer readable medium, comprising in electronic form at least one
nucleic acid or protein sequence of a clone selected from the group consisting of:
hute1_17k7; hute1_18c12; hute1_18i19; hute1_18i4; hute1_18l1; hute1_19f19;
hute1_19g19; hute1_19g22; hute1_19h17; hute1_19j11; hute1_1i2; hute1_20b19;
hute1_20g21; hute1_20h13; hute1_20m11; hute1_20m24; hute1_21d15; hute1_22d2;
hute1_22e12; hute1_22n2; hute1_22o2; hute1_23e13; hute1_23g11; hute1_24c19;
hute1_24e11; hute1_24j6; hute1_2h3; complements of the nucleic acid sequences; and
variants thereof.

40. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: hutel_17k7; hutel_18c12; hutel_18i4; hutel_19g19; hutel_19j11; hutel_22n2; hutel_21d15; hutel_22o2; hutel_23g11; complements of the nucleic acid sequences; and variants thereof.

41. A nucleic acid molecule having the sequence of a clone selected from the group consisting of hfbr2_16c16; hfbr2_16f21; hfbr2_16g18; hfbr2_16i12; hfbr2_16k22; hfbr2_16l12; hfbr2_22f21; hfbr2_22h13; hfbr2_22h13; hfbr2_22i4; hfbr2_22k3; hfbr2_22k8; hfbr2_23b10; hfbr2_23b21; hfbr2_23f2; hfbr2_23l24; hfbr2_23n16; hfbr2_23o24; hfbr2_23o5; hfbr2_2a2; hfbr2_2b17; hfbr2_2b5; hfbr2_2c1; hfbr2_2c17; hfbr2_2c18; hfbr2_2d15; hfbr2_2d17; hfbr2_2d20; hfbr2_2g18; hfbr2_2h1; hfbr2_2h10; hfbr2_2i17; hfbr2_2k14; hfbr2_2k19; hfbr2_3b16; hfbr2_3c18; hfbr2_3f16; hfbr2_3g8; hfbr2_3l2; hfbr2_41m15; hfbr2_62b11; hfbr2_62f10; hfbr2_62l19; hfbr2_62n10; hfbr2_62o17; hfbr2_64a11; hfbr2_64a15; hfbr2_64c16; hfbr2_64c4; hfbr2_64h6; hfbr2_64i20; hfbr2_64j18; hfbr2_64k24; hfbr2_64o16; hfbr2_6a17; hfbr2_6b24; hfbr2_6i20; hfbr2_6o17; hfbr2_71o20; hfbr2_72b18; hfbr2_72d13; hfbr2_72l12; hfbr2_72m16; hfbr2_72n12; hfbr2_78c24; hfbr2_78d13; hfbr2_78k24; hfbr2_78n23; hfbr2_7a24; hfbr2_7e22; hfbr2_7j4; hfbr2_82c20; hfbr1_10c20; hfbr2_82e17; hfbr1_10e17; hfbr2_82e4;; hfbr1_10e4; hfbr2_82g14;; hfbr1_10g14; hfbr2_82i17;; hfbr1_10; hfbr2_82i24;; hfbr1_10; hfbr2_82m16;; hfbr1_10; hfbr2_82m6;; hfbr1_10; hfkd2_1j9; hfkd2_24a15; hfkd2_24b15; hfkd2_24e23; hfkd2_24n20; hfkd2_24p5; hfkd2_3i13; hfkd2_3o17; hfkd2_46a6; hfkd2_46b10; hfkd2_46d13; hfkd2_46j20; hfkd2_46k19; hfkd2_46m4; hfkd2_47a4; hfkd2_4b6; hfkd2_4c8; hfkd2_4k14; hfkd2_4m11; hmcfl_1a11; hmcfl_1c23; hmcfl_1e15; hmcfl_1g13; htes3_1n3; htes3_14g5; htes3_14h21; htes3_14p14; htes3_14p7; htes3_15a13; Htes3_15c24; htes3_15c6; htes3_15g14; htes3_15h1; htes3_15i5; htes3_15j18; Htes3_15j3; htes3_15k11; htes3_17f10; htes3_17l17; htes3_17n12; htes3_17n18; Htes3_18f3; htes3_18l7; htes3_19f19; htes3_19j17; htes3_1c1; htes3_1g13; htes3_1k11; htes3_20c21; htes3_20k2; htes3_20m18; htes3_21d4; htes3_21j15; htes3_21l16; htes3_21n23; htes3_22c23; htes3_22g2; htes3_22n13; htes3_23l11; htes3_23n19; Htes3_23n19; htes3_26g22; htes3_27d1; htes3_27k4; htes3_27o14; htes3_28d14; htes3_2a11; htes3_2a17; htes3_2d15; htes3_2e12; htes3_2f14; htes3_2g7; htes3_2h1; htes3_2h15; htes3_2l19; htes3_2m18;

htes3_2m20; htes3_2n9; htes3_2o13; htes3_30f4; Htes3_35b4; htes3_35b5; htes3_35e21; htes3_35g6; htes3_35k16; htes3_35k24; htes3_35n12; htes3_35n24; htes3_35n9; htes3_35p17; htes3_35p22; htes3_4b4; htes3_4f17; htes3_4f5; htes3_4h6; htes3_4o19; htes3_50j4; htes3_50n06; htes3_50n23; htes3_6b21; htes3_6c11; htes3_6d16; htes3_72k11; Htes3_72k15; htes3_72p16; htes3_7b22; htes3_7d17; htes3_7j3; htes3_7j8; htes3_7p10; htes3_7p9; htes3_8e24; Htes3_8g11; Htes3_8g5; htes3_8m10; Htes3_8p7; Htes3_9e22; Htes3_9i20; Htes3_9k22; hute1_17k7; hute1_18c12; hute1_18i19; hute1_18i4; hute1_18l1; hute1_19f19; hute1_19g19; hute1_19g22; hute1_19h17; hute1_19j11; hute1_1i2; hute1_20b19; hute1_20g21; hute1_20h13; hute1_20m11; hute1_20m24; hute1_21d15; hute1_22d2; hute1_22e12; hute1_22n2; hute1_22o2; hute1_23e13; hute1_23g11; hute1_24c19; hute1_24e11; hute1_24j6; hute1_2h3; their complements; and variants thereof.

42. A polypeptide encoded by the nucleic acid molecule according to claim 41.

43. An antibody or fragment thereof that is capable of binding to a specific portion of the peptide according to claim 42.

44. A pharmaceutical composition, comprising (a) an effective amount of a pharmaceutical agent, wherein said pharmaceutical agent is selected from the group consisting of the polypeptide according to claim 42, variants or functional derivatives thereof, and antibodies thereto; and (2) a physiologically acceptable carrier or excipient.

45. An expression vector comprising the nucleic acid molecule of claim 41 or a fragment thereof, and optionally a promoter operably linked to said nucleic acid molecule or said fragment.

46. A method for recombinantly producing a desired peptide, comprising expressing in a host cell a peptide encoded by the nucleic acid molecule according to claim 41.

